

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 21.3633 Seconds
(without alignments)
2141.995 Million cell updates/sec

Title: US-09-758-173-12

Perfect score: 2549

Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHNYHTOKSLSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1763	69.2	330	1 GHU	Ig gamma-1 chain C
2	1626.5	63.8	377	2 A23511	Ig gamma-3 chain C
3	1624.5	63.7	377	2 A60764	Ig gamma-3 chain C
4	1600	62.8	326	1 G2HU	Ig gamma-2 chain C
5	1586.5	62.2	327	1 G4HU	Ig gamma-4 chain C
6	1567	61.5	470	2 S22080	Ig heavy chain pre
7	1548	60.7	472	2 S31459	Ig gamma-1 chain -
8	1547	60.7	374	2 S69339	Ig heavy chain V r
9	1426.5	56.0	469	2 S37483	Ig gamma-2a chain
10	1392	54.6	446	2 S40295	Ig gamma-2a chain
11	1382.5	54.2	444	2 PC4436	monoclonal antibody
12	1369.5	53.7	475	2 S01321	Ig gamma-2b chain
13	1362	53.4	474	1 G2WS11	Ig gamma-2b chain
14	1259	49.4	328	2 I47159	Ig gamma 2a chain
15	1256	49.3	255	4 S31866	Ig gamma-1 chain C
16	1253	49.2	328	2 I47160	Ig gamma 2b chain
17	1250	49.0	234	2 PT0207	Ig gamma chain C r
18	1227	48.1	328	2 I4715B	Ig gamma 1 chain C
19	1226.5	48.1	323	1 GHRB	Ig gamma 3 chain C
20	1223	48.0	328	2 I47161	Ig gamma-2 chain C
21	1212.5	47.6	329	1 G2GP	Ig heavy chain C r
22	1157.5	45.4	308	2 C30554	Ig gamma-3 heavy C
23	1152	45.2	289	1 G3HUI	Ig gamma-1 chain C
24	1148	45.0	326	2 PS0017	Ig gamma-2b chain C
25	1142.5	44.8	333	2 G1MS	Ig gamma-1 chain C
26	1138	44.6	324	1 G1MSC	Ig gamma-3 chain C
27	1137	44.6	329	1 G3WSM	Ig gamma-1 chain C
28	1133	44.4	393	1 G1WSM	Ig gamma-3 chain C
29	1126	44.2	398	1 G3WSM	Ig gamma-3 chain C

RESULT 1

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999

C;Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELT>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) marker

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid se

A;Reference number: A90563; MUID:71064024; PMID:5489771

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96, R, 98-135 <CUN>

A;Note: this sequence has the Gln(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A;Reference number: A90564; MUID:71064025; PMID:5530842

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240-241, 'M'

A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primaerstruktur eines monoklonalen IGG1-Immunglobulins (Myelomprotein N

Query Match 63.7%; Score 1624.5; DB 2; Length 377;
Best Local Similarity 81.7%; Pred. No. 3.2e-86;
Matches 308; Conservative 10; Mismatches 12; Indels 47; Gaps 1;
QY 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 206
Db 1 ASTKGPSVFPLAPCSRSTSGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 207 GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKA----- 244
Db 61 GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKRVELKPLGLDTHTCPRCEPKSC 120
QY 245 -----EPKSCDKTHTCPCPAPPELLGGPSVFLPCKPKDT 279
Db 121 DTPPCPCPCPKSCDTPPCPCPCPKSCDTPPCPCPAPPELLGGPSVFLPCKPKDT 180
QY 280 LMISTPTEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQNSTYRVSVLTVLH 339
Db 181 LMISTPTEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQNSTFRVSVLTVLH 240
QY 340 QDWLNGKEYCKVKSNKALPAPAEKTIKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 399
Db 241 QDWLNGKEYCKVKSNKALPAPAEKTIKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 300
QY 400 GFPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHE 459
Db 301 GFPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHE 360
QY 460 ALHNHYTOKSLSLSPGK 476
Db 361 ALHNHYTOKSLSLSPGK 377
RESULT 4
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PID:G6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132

A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amida
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
P:20-85/Domain: immunoglobulin homology <IM1>
P:133-202/Domain: immunoglobulin homology <IM2>
P:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 62.8%; Score 1600; DB 1; Length 326;
Best Local Similarity 90.9%; Pred. No. 6.8e-85;
Matches 300; Conservative 12; Mismatches 14; Indels 4; Gaps 2;
QY 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 206
Db 1 ASTKGPSVFPLAPCSRSTSGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 207 GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKAPKSCDKTHTCPCPAPPELLGG 266
Db 61 GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKAPKSCDKTHTCPCPAPPELLGG 116
QY 267 PSVLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 326
Db 117 PSVLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 176
QY 327 STYRVSVTLTVLHQDWLNGKEYCKVKSNKALPAPAEKTIKAKGQPREPOVYTLPPSRDE 386
Db 177 STFRVSVTLTVLHQDWLNGKEYCKVKSNKALPAPAEKTIKAKGQPREPOVYTLPPSRDE 236
QY 387 LTKNOVSLTCLVKGYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 446
Db 237 LTKNOVSLTCLVKGYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 296
QY 447 QGQNVFSCVMHEALHNHYTOKSLSPGK 476
Db 297 QGQNVFSCVMHEALHNHYTOKSLSPGK 326
RESULT 5
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933
 A;Molecule type: DNA
 A;Residues: 1-327 <ELL>
 A;Note: the sequence was determined from the germline gene
 R;Pink, J.R.L.; Butterly, S.H.; De Vries, G.M.; Milstein, C.
 Biochem. J. 117, 33-47, 1970
 A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
 A;Reference number: A90249; MUID:70207560; PMID:4192699
 A;Accession: A90249
 A;Molecule type: protein
 A;Residues: 1-30,81-326 <PIN>
 C;Genetics:
 A;Gene: GDB:IGHG4

A;Cross-references: GDB:119340; OMIM:147130
 A;Map position: 14q32.33-14q32.33
 A;Introns: 99/1; 111/1; 221/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:99-110/Region: hinge
 F:134-203/Domain: immunoglobulin homology <IM2>
 F:240-307/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide Bonds: Interchain (to light chain) #status experimental
 F:27-83,141-201,247-305/Disulfide bonds: #status predicted
 F:106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.2%; Score 1586.5; DB 1; Length 327;
 Best Local Similarity 90.6%; Pred. No. 4.1e-84;
 Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

QY 147 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 206
 Db 1 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
 QY 207 GLYSLSVTVPPSSSLGTQYICNNVHKPSNTKVDKAEPSKCDKTHTCPPCPAPELILGG 266
 Db 61 GLYSLSVTVPPSSSLGTQYICNNVHKPSNTKVDKAEPSKCDKTHTCPPCPAPELILGG 117
 QY 267 PSVFLPPPKPDKTLMLSRTEPVTVVVDVSHDEPKVFNWVDGVEVHNATKPREQYN 326
 Db 118 PSVFLPPPKPDKTLMLSRTEPVTVVVDVSHDEPKVFNWVDGVEVHNATKPREQYN 177
 QY 327 STYRVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTIKAKQPREPQVYTLPPSRDE 386
 Db 178 STYRVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTIKAKQPREPQVYTLPPSRDE 237
 QY 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSLKLTVDKSRW 446
 Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSLKLTVDKSRW 297
 QY 447 QQGNVFSCSWMEALHNHYTQKSLSLSPGK 476
 Db 298 QQGNVFSCSWMEALHNHYTQKSLSLSPGK 327

RESULT 6

S22080
 Ig heavy chain precursor (B/WT.4A.17.H5.A5) - bovine
 N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S22080; S06610; A31303
 R;Sanders, P.G.
 submitted to the EMBL Data Library, November 1991
 A;Reference number: S22080
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-470 <SAN>
 A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
 Mol. Immunol. 26, 841-850, 1989

A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and
 A;Reference number: S06610; MUID:90097956; PMID:2513487

A;Molecule type: DNA
 A;Residues: 142-470 <SYM>
 A;Cross-references: EMBL:X16701
 A;Note: the sequence was determined from the germline gene
 C;Genetics:
 A;Gene: IG CH gamma-1

A;Introns: 98/1; 111/1; 221/1
 A;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
 F:161-225/Domain: immunoglobulin homology <IMW>
 F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.5%; Score 1567; DB 2; Length 470;
 Best Local Similarity 63.7%; Pred. No. 8.1e-83;
 Matches 305; Conservative 56; Mismatches 106; Indels 12; Gaps 8;

QY 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGSISGGYGMWIRQP 60
 Db 1 MNPLWTLFLVLSAPIGVLSQVQLRESGFLVKPSQTLSTCTVSGFSL-SYALTWVROA 59
 QY 61 PGKCLEWIGSFYSSSGNTYNNPSLKSQVITSTDTSKNPFSLKLNMTAADTAVYCVDRD 120
 Db 60 PGKALEWVGIT-TSGGTTYNNPALKSRSLTKENSKQVLSVSSVTPEDTATYYCAR-- 116
 QY 121 LFSVVGVMYNNWF-DVMGPGVLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYF 179
 Db 117 --STYGEVGDGAIDANGQGLLVTVSSASTTAPKYPLSSCCGDKSSSTVTGLCLVSSYM 174
 QY 180 PEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVTPSSSLGTQYICNNVHKPSNTK 239
 Db 175 PEPTVTVNSGALKSGVHTFPAVLQSSGLYSLSSVTVVTPGTSQ-QTFTCNVAHPASSTK 233
 QY 240 VDKAEPSKCDKTHTCPPCPAPELILGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHED 299
 Db 234 VDKAVDP-TC-KPSPCCDCCPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVDVGHDD 291
 QY 300 PEKFNWYVDGVEVHNATKPREQYNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKALPA 359
 Db 292 PEKFSWFVDVDEVTATTTPREQFNSTYRVVSALRIQHODWTGKFKCKVHNEGLPA 351
 QY 360 PIEKTIKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--E 417
 Db 352 PIVRTISRTKGPAREPQVYVLAAPPQEELSKSTVSLTCMVTSTFYPDYIAVEWQNGQPESE 411
 QY 418 NNYKTTTPPVLDSGSPFLYSLKLTVDKSRWQGNVFSVMEALHNHYTQKSLSLSPGK 476
 Db 412 DKYGTTPQLDADSSVFLYSKLVRDRNSWEGDYYTCVVMHEALHNHYTQKSTKSAGK 470

RESULT 7

S31459
 Ig gamma-1 chain - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C;Accession: S31459
 R;Patel, S.; Nau, F.
 submitted to the EMBL Data Library, December 1992
 A;Reference number: S31459
 A;Accession: S31459
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-472 <PAT>
 A;Cross-references: EMBL:X69797
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F:277-346/Domain: immunoglobulin homology <IMW>
 Query Match 60.7%; Score 1548; DB 2; Length 472;

Qy	127	MVYNNWFDMVNGPGLVTVTVSSASTGKSGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVTS	186
Db	123	YGQYRPHSGWGQGLTVTVSS-----	142
Qy	187	WNSGALTSGVHTTPPAVLQSSGLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAPP	246
Db	143	-----EP	144
Qy	247	KSCDKTHCTCPPELPGSPSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNN	306
Db	145	KSCDKTHCTCPPELPGSPSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNN	204
Qy	307	YVDGVEVHNAAKTPRGEQYNSTRYVVSVLTVLHODWLNKEYKCKVSNKALPAPIETKTS	366
Db	205	YVDGVEVHNAAKTPRGEQYNSTRYVVSVLTVLHODWLNKEYKCKVSNKALPAPIETKTS	264
Qy	367	KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV	426
Db	265	KAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV	324
Qy	427	LDSGSEFFLYSKLTVDKSRNQQGNVSCSVMHAEALHNHHYTKQSLSLSPGK	476
Db	325	LDSGSEFFLYSKLTVDKSRNQQGNVSCSVMHAEALHNHHYTKQSLSLSPGK	374
RESULT 9			
S37483			
Ig gamma-2a chain - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999			
C:Accession: S37483			
R:Ducancel, F.F.D.			
submitted to the EMBL Data Library, February 1993			
A:Reference number: S37483			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-469 <DUC>			
C:Cross-references: EMBL:X70423; NID:G406252; PID:CAA49868.1; PID:G406253			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
C:Keywords: immunoglobulin			
F:276-345/Domain: immunoglobulin homology <IMM>			
Query Match 56.0%; Score 1426.5; DB 2; Length 469;			
Best Local Similarity 57.2%; Pred. No. 9.3e-75;			
Matches 271; Conservative 71; Mismatches 121; Indels 11; Gaps			
Qy	5	WFFLLVAAPRWLVLSQLOESGPGVKPSETLSLTCVSGSGISGGYGMGWIRQPPGKG	64
Db	5	WIFLUSGTAGVHCQIQLOQSGPELVKPGASVKISKASGYTFT-DYINYNWQKPPGOG	63
Qy	65	LEWIGSYSSSGNTYINPFLSKSVTISTDTSKNQFSLKLNMTAABTVVYCVDRDLFSV	124
Db	64	LKWIGIYIPASGNTKYNEFKKATLTVDTSSTSTAYWQLSSLTSEDVAVVFCAR----	118
Qy	125	VGMYNNWFVWVGPGVLTVYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPV	184
Db	119	MGAT-ATLLDYWGQGTTLTVSSAKTTAPSVYPLAPVCGDGTGSSVTLGCLVKGYFPEPV	177
Qy	185	VSMNSGALTGVHTFPFPAVLQSSGLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKKA	244
Db	178	LTMNSGSLSSGVHTFPFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDDKI	236
Qy	245	EPKSCDKTHCTCP--CPAPELLGGSPSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEV	302
Db	237	EPRG-PTIKPCPPCKCAPNLLGGSPSVIFIPPKIKDVLMSISPIVTCVVVDVSEDDPOV	295
Qy	303	KFNWVVDGVEVHNAAKTPRGEQYNSTRYVVSVLTVLHODWLNKEYKCKVSNKALPAPIE	362
Db	296	QISFVNVEVHTAQOTHRDYNSTRLVVSALPIQHDDWMSKEFKCKVNNKDLPAPIE	355
Qy	363	KTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT	422

Db 356 RTISKPKGSVRAPQVYVLPPLPPPEEMTKKQVTLTCMVTDMPEDYVVEWTNKGKTELNYKN 415

QY 423 TPVVLDSGSLYSLKLTVDKSRWQGNVFSQVMEALHNHYTKSLSPGK 476

Db 416 TEPVLDSGSLYSLKLTVDKSRWQGNVFSQVMEALHNHYTKSLSPGK 469

RESULT 10

S40295

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999

C:Accession: S40295

R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Prosch, M.; Weisgerber, C.; Bl submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against

A:Reference number: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

C:Genetics:

A:Map position: 12

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CHR>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F:360-427/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted

F:132/Disulfide bonds: interchain (to light chain) #status predicted

F:224,227,229/Disulfide bonds: interchain #status predicted

F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.6%; Score 1392; DB 2; Length 446;

Best Local Similarity 57.6%; Pred. No. 8.4e-73;

Matches 264; Conservative 68; Mismatches 112; Indels 14; Gaps 5;

QY 20 QVQLQESGPGLVKPSSETLSLTCAVSGSGISGGYCWGWIRQPPGKLEWIGSYSSSGNTY 79

Db 1 QIQQLQSGPELVKPSGKISCKAGSYFT-DYIHWKQREGEGLWIGWYPSGNGTK 59

QY 80 YNPGLSKQVITSTDTSKNQFSLKLSMTAADTAVYVCVDRDLFSVVMYNNWFDVWGP 139

Db 60 YNEKPKGKATLTDTSSSTAYNQLSLSEDSAVFCARGKFAM-----DYWGQ 110

QY 140 VLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSMNSGALTSGVHTF 199

Db 111 TSVTVSSAKTTAPSYVPLAPYCGDITGSSVTLGCLVKGYFPEPVTLTWNSSGLSGVHTF 170

QY 200 PAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTKVDKAEKPKSCDKTHCPP-- 257

Db 171 PAVLQSD-LYTLSSSVTVSSTPWSPQSTCNVAHPASSTKVDKKEIPRG-PTIKPCPPCK 228

QY 258 CPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Db 229 CPAPNLLGGPSVFLPFPKIKDVLMLSLSPMTVCVVVDVSEDDPDVQISFVNVEVLTAQ 288

QY 318 TKPREEQNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKGQREPOV 377

Db 289 TQTHREDYNSTLRVVSALPIQHDQWMSKEFKCRVNNKDLPAPIETKISKPGSVRAPQV 348

QY 378 YTLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYS 437

Db 349 YVLPPLPPEEMTKKQVTLTCMVTDMPEDYVVEWTNKGKTELNYKNTEPVLDSDGSFYMS 408

QY 438 KLTVDKSRWQGNVFSQVMEALHNHYTKSLSPG 475

Db 409 KLRVEKKQWVERNSYSCSVHVEGLNHNHTTKSFSRTPG 446

RESULT 11

PC4436

monoclonal antibody 13-1 heavy chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: PC4436

R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp

A:Reference number: JC5810; MUID:98063277; PMID:9398605

A:Accession: PC4436

A:Molecule type: protein

A:Residues: 1-444 <AKA>

C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed ag

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:251-320/Domain: immunoglobulin homology <IMM>

F:22/Disulfide bonds: interchain (to 98) #status predicted

F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 54.2%; Score 1382.5; DB 2; Length 444;

Best Local Similarity 56.5%; Pred. No. 2.9e-72;

Matches 262; Conservative 68; Mismatches 107; Indels 27; Gaps 8;

QY 20 QVQLQESGPGLVKPSSETLSLTCAVSGSGISGGYCWGWIRQPPGKLEWIGSYSSSGN-- 77

Db 1 EVQVETGGGLVPRGNSLKSLTSGFTFS-NYRMHWLRQPPGKRLEWIAVITVKSDNYG 59

QY 78 TYYNPLSKQVITSTDTSKNQFSLKLSMTAADTAVYVCVDRDLFSVVMYNNW---FD 134

Db 60 AKYAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCR-----TPWVYAMD 108

QY 135 VMPGVLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSMNSGALT 194

Db 109 CWGQGSYVIVSSAKTTPPSYVPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTWSGSLSS 168

QY 195 GVHTFAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTKVDKAEKPKSCDKTH 254

Db 169 GVHTFAVLQSD-LYTLSSSVTVTPSSTPWSPSETVTCNVAHPASSTKVDKIVPRDCG--- 223

QY 255 CPP--CPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 312

Db 224 CKPCICTVPEV---SSVFIFFPKPKDVLITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 280

QY 313 VHNATKPREEQNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKG 372

Db 281 VHTAQTQPREEQNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKG 340

QY 373 REPQVTVLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGQPENNYKTTTPPVLDSDGS 432

Db 341 KAPQVYTIPTPKPKQMAKDKVSLTCTMITDFPEDITVWQWNGQPAENYKNTQPIIMDTG 400

QY 433 FLYYSLKLTVDKSRWQGNVFSQVMEALHNHYTKSLSPGK 476

Db 401 YFVYSLKLVQKSNWEAGNTFTCSVLHGLNHNHTTKSLSHSPGK 444

RESULT 12

S01321

Ig gamma-2b chain precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999

C:Accession: S01321

R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.

Eur. J. Biochem. 176, 287-295, 1988

A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe

A:Reference number: S01320; MUID:88329081; PMID:3138116

A:Accession: S01321

A:Molecule type: mRNA

A:Residues: 1-475 <DE1>

A:Cross-references: EMBL:X13188; NID:gs1780; PIDN:CAA31580.1; PID:gs1781

A>Note: this sequence was determined from the differentiated gene

[illegible]

RESULT 14

I47159

I9 gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47159

R:KacsKovics, I.; Sun, J.; Butler, J.E.

J: Immunol. 153, 3565-3573, 1994

A:title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47159

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124

C:Genetics:

A:Gene: I9G2a

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match	49.4%;	Score 1259;	DB 2;	Length 328;
Best Local Similarity	69.3%;	Pred. No. 2.5e-65;		
Matches 230;	Conservative	43;	Mismatches 53;	Indels 6;
Gaps	12;			

QY	147	ASTKGPSVFPLAPSSKSTSGGTAA	GLCLVKDYFPEPVTVSWNSGALNSGVH	TFPAVLQSS	206
DB					
	1	APKTAPSYVPLAPCSRDTSG	FNVALGCLASFFPEPVTVWNSGALSGVHTF	PSVQLQPS	60
QY	207	GLXSLSSWVTVPPSSSLGTQTY	ICNVNHKPSNTKVDKKAEPKSCDK	TKHTCTPCCPAPELGG	266
DB	61	GLXSLSSWVTVPPASSLSKSY	TCNVNHPATTTKVDKRVG	TKTKPCPCPACESP	116
QY	267	PSVFLPPPKPKDTLMISRTPE	VTCTVVDVSHEDDEVKFNWTV	DGVGVNATKTPREQYN	326
DB	117	PSVFIFFPKPKDTLMISRTPO	VTCTVVDVSDQENPEVQFSW	TVDGVGVNATKTRPKEQFN	176
QY	327	STYRVSVSLTVLHDDWLNGEY	KCYKCVSNKALPAPIEXTI	ISKAKGQPREPVYITPPSRDE	386
DB	177	STYRVSVSLFIQHDWLNGEY	KFCCKVANKDLPAPIRIIS	ISKAKGQPREPVYITPPHAAE	236
QY	387	LTKNQVSLTCLVKGFYPSDIA	VENESGQ--PENNYKTTTPP	VLDSGDSFFLYSKLTVDKKS	444
DB	237	LSRSKVSITCLVGFYPPDID	VEWRNGQPEPEGNYRITPP	QQDVGDGYFLYSKESVDKA	296
QY	445	RWQGNVFSSCVMHEALHNHY	TQKSLSLPGK	476	
DB	297	SWGGGIFQCAVMHEALHNHY	TQKSISKTGK	328	

```

RESULT 15
S1866
U31866
C31866
S31866
A:Species: synthetic
A:Name: Hsma-1 chain C region - synthetic
A:Date: 06-Jan-1995
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
#sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Eilpula, D.

```

submitted to the EMBL Data Library, February 1993
A;Description: Screening method for protein-protein interactions of cloned gene products
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

	Query Match	49.3%	Score 1256	DB 4	Length 255	
	Best Local Similarity	97.1%	Pred. NO. 2.8e-65			
	Matches 23	Conservative 0	Mismatches 7	Indels 0	Gaps 0	
Qy	238	TKVDKKAEPKSKDKTHTCPCCPAPPELLGGGSVFLFPKPKD	TLMSIRTPETVCVVVDVSH	297		
Db	17	TVAQADVESKSKDKTHTCPCCPAPPELLGGGSVFLFPKPKD	TLMSIRTPETVCVVVDVSH	76		
Qy	298	EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLT	VLHODLWLNKGEYKCKVSNNKAL	357		
Db	77	EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLT	VLHODLWLNKGEYKCKVSNNKAL	136		
Qy	358	PAPIEKTISKAGQPREPQYVTLPPSRDELTKNQVSLTCLVKGF	YPSPDIAVEWESNQPE	417		
Db	137	PAPIEKTISKAGQPREPQYVTLPPSRDELTKNQVSLTCLVKGF	YPSPDIAVEWESNQPE	196		
Qy	418	NNYKTTPLVLDSDGSFFLYSKLTVDKSRWQQGNVFC	GSVMHEALHNHYTKQSLSLSPGK	476		
Db	197	NNYKTTPLVLDSDGSFFLYSKLTVDKSRWQQGNVFC	GSVMHEALHNHYTKQSLSLSPGK	255		

Search completed: March 29, 2003, 09:16:21
Job time : 22.3633 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 11.3492 Seconds
(without alignments)
1739.566 Million cell updates/sec

Title: US-09-758-173-12
Perfect score: 2549
Sequence: 1 MKHLWFLLLVAAPRWLSQ.....MHEALHNHYTKSLSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1763	69.2	330	GCL_HUMAN	P01857 homo sapien
2	1600	62.8	326	GC2_HUMAN	P01859 homo sapien
3	1586.5	62.2	327	GC4_HUMAN	P01861 homo sapien
4	1266.5	48.1	323	GC_RABIT	P01870 oryctolagus
5	1212.5	47.6	329	GC2_CAVPO	P01862 cavia porce
6	1157	45.4	290	GC3_HUMAN	P01860 homo sapien
7	1148	45.0	326	GC1_RAT	P20759 rattus norv
8	1142.5	44.8	333	GC8_RAT	P20761 rattus norv
9	1138	44.6	324	GC1_MOUSE	P01868 mus musculu
10	1137	44.6	329	GC3_MOUSE	P22436 mus musculu
11	1133	44.4	393	GC1M_MOUSE	P01869 mus musculu
12	1126	44.2	398	GC3M_MOUSE	P03987 mus musculu
13	1122	44.0	330	GC3A_MOUSE	P01863 mus musculu
14	1119.5	43.9	335	GCAB_MOUSE	P01864 mus musculu
15	1117	43.8	399	GCAM_MOUSE	P01865 mus musculu
16	1114.5	43.7	329	GCC_RAT	P20762 rattus norv
17	1108	43.5	322	GCA_RAT	P20760 rattus norv
18	1085	42.6	336	GCB_MOUSE	P01866 mus musculu
19	1080	42.4	405	GCBM_MOUSE	P01867 mus musculu
20	489	19.2	428	EPC_HUMAN	P01854 homo sapien
21	483.5	19.0	429	EPC_RAT	P01855 rattus norv
22	465	18.2	421	EPC_MOUSE	P06336 mus musculu
23	458	18.0	146	HV2I_HUMAN	P06331 homo sapien
24	442	17.3	454	MUC_HUMAN	P01871 homo sapien
25	437	17.1	458	MUC_RABIT	P03988 oryctolagus
26	432.5	17.0	455	MUC_MOUSE	P01872 mus musculu
27	427	16.8	479	MUCM_RABIT	P04221 oryctolagus
28	425	16.7	457	MDC_SUNMU	P20768 suncus muri
29	422.5	16.6	476	MUCM_MOUSE	P01873 mus musculu
30	420	16.5	129	HV2F_HUMAN	P01824 homo sapien
31	420	16.5	450	MUC_CANFA	P01874 canis famil
32	415.5	16.3	454	MUC_MESAU	P06337 mesocricetu
33	403	15.8	391	MUCB_HUMAN	P04220 homo sapien

RESULT 1

ID	GCL_HUMAN	STANDARD	PRT	330 AA
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	IG gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=62274238; PubMed=6287432;			
RA	Ellison J.W., Barson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RN	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RN	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RL	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RL	peptides and discussion of the complete structure."			
RN	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P01822 mus musculu
P23085 heterodontu
P23087 heterodontu
P23088 heterodontu
P23084 heterodontu
P01876 homo sapien
P20758 gorilla gor
P18531 mus musculu
P23086 heterodontu
P01825 homo sapien
P18532 mus musculu

ALIGNMENTS

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RX MEDLINE=770267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from *Staphylococcus*
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272
 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig like; 1.
 DR SMART; SM00407; IGH1; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180 N-LINKED (GLCNAC...).
 FT MOD RES 330 330 REMOVED POST-TRANSLATIONALLY.
 FT VARIANT 97 97 K -> R (IN GIM(3) MARKER).
 FT VARIANT 239 239 /FTID=VAR_003886.
 FT VARIANT 241 241 D -> E (IN GIM(NON-1) MARKER).
 FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).
 FT STRAND 123 126 /FTID=VAR_003886.

FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT TURN 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770BE106C2FA33D CRC64;
 Query Match 69.2%; Score 1763; DB 1; Length 330;
 Best Local Similarity 99.7%; Pred. No. 1.8e-113;
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 147 ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 206
 DB 1 ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
 QY 207 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKAEPKSCDKTHTCTPCCPAPPELLGG 266
 DB 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKAEPKSCDKTHTCTPCCPAPPELLGG 120
 QY 267 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
 DB 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
 QY 327 STYRVVSVLTVQLHQLMNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 386
 DB 181 STYRVVSVLTVQLHQLMNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
 QY 387 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 446
 DB 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
 QY 447 QQGNVFSCSMHEALHNHYTQKSLSLSPGK 476
 DB 301 QQGNVFSCSMHEALHNHYTQKSLSLSPGK 330
 RESULT 2
 GC2 HUMAN
 ID GC2 HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obara M., Nikaido T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 evolution of a gene family.";
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbits T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes.";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung B., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milestein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milestein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; J00230; AAB59393.1; -.
 PIR; A02148; G2HU.
 HSP; P01857; IFC1.
 Genew; HGNC:5526; IGHG2.
 MIM; 147110; -.
 InterPro; IPR003006; Ig_MHC.
 InterPro; IPR003597; Ig_C1.
 InterPro; IPR003600; Ig_Like.
 Pfam; PF00047; Ig; 3.
 SMART; SM00407; Ig_Like; 1.
 SMART; SM00410; IGH1; 2.
 PROSITE; PS00290; IG_MHC; 2.
 Immunoglobulin domain; Immunoglobulin C region.
 NON_TER 1
 DOMAIN 1 98 CHI.
 DOMAIN 99 110 HINGE.
 DOMAIN 111 219 CH2.
 DOMAIN 220 326 CH3.
 DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 DISULFID 27 83
 DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 DISULFID 140 200
 DISULFID 246 304
 SITE 156 156
 MOD_RES 326 326
 VARIANT 60
 CONFLICT 109 109 /FTID=VAR_003889.
 SEQUENCE 326 AA; 35884 MW; 831087C6878CF9C CRC64;
 Query Match 62.8%; Score 1600; DB 1; Length 326;
 Best Local Similarity 90.9%; Pred. No. 2.4e-102;
 Matches 300; Conservative 12; Mismatches 14; Indels 4; Gaps 2;
 QY 147 ASTGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVNSWGALTSGVHTFPAVLQSS 206
 DB 1 ASTGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVNSWGALTSGVHTFPAVLQSS 60
 QY 207 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKYDKAEPKSCDKTHRTCPCPAPELGG 266
 DB 61 GLYSLSVVTVPSSNFGTQTYTCNVHDKPSNTKYDKTVERKCCVE--CPPCPAPP-VAG 116
 QY 267 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVVHNATKPREEOYN 326
 DB 117 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVVHNATKPREEOYN 176
 QY 327 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIETISKAKQPREPVYVITLPPSRDE 386
 DB 177 STFRVSVLTIVHODWLNKGEYKCKVSNKGLPAPIETISKAKQPREPVYVITLPPSRDE 236
 QY 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 446
 DB 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 296
 QY 447 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 476
 DB 297 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 326
 RESULT 3
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RL "Human immunoglobulin subclasses. Partial amino acid sequence of the
 constant region of a gamma 4 chain.";
 Biochem. J. 117:33-47(1970).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DE EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A02150; G4HU.
 DR HSSP; P01842; 7FAB.
 DR Genew; HGNC:5528; IGHG4.
 DR MIM; 147130;
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGC1; 2.
 DR PROSITE; PS00290; Ig_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EBDD811EF208E7A CRC64;
 Query Match 62.2%; Score 1586.5; DB 1; Length 327;
 Best Local Similarity 90.6%; Pred. No. 2e-101;
 Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;
 QY 147 ASTKGSVFLAPSSKSTSGTAAALCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 206
 DB 1 ASTKGSVFLAPSSKSTSGTAAALCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60
 QY 207 GLYSLSVVTVFSSSLGTQYICNVNPKPSNTKVDKKAEPKSCDKTHCTCPCPAPELGG 266
 DB 61 GLYSLSVVTVFSSSLGTQYICNVNPKPSNTKVDKRVESK---YGPCCSCPAPEFLGG 117
 QY 267 PSVELPPPKKOTLMISRPEVTCVVVDVSHEDPEVKFNWYGVQVEVHNKATKPRBEQYN 326
 DB 118 PSVELPPPKKOTLMISRPEVTCVVVDVSHEDPEVKFNWYGVQVEVHNKATKPRBEQFN 177
 QY 327 STYRVSVLTVLHQDLWNGKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 386
 |||||

Db 178 STYRVSVLTVLHQDLWNGKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 237
 QY 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
 Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 297
 QY 447 QOQNVFSCVMHEALHNYHTOKSLSPGK 476
 Db 298 QEGNVFSCVMHEALHNYHTOKSLSPGK 327
 RESULT 4
 GC_RABIT ID GC_RABIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84030930; PubMed=6313520;
 RA Bernstein K.E., Alexander C.B., Mage R.G.;
 RL "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 F-1 haplotype.";
 Immunogenetics 18:387-397(1983).
 RN [2]
 RP SEQUENCE OF 1-128.
 RX MEDLINE=76135469; PubMed=1243651;
 RA Pratt D.M., Mole L.E.;
 RL "Sequence studies on the constant region of the Fd sections of rabbit
 immunoglobulin G of different allotype.";
 Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RL "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
 heavy chain and identification of two genomic C gamma genes.";
 Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RL "Sequence studies of the Fd section of the heavy chain of rabbit
 immunoglobulin G.";
 Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (In) Killander J. (eds.);
 Stockholm (1967).
 CC 1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 MARKERS AND REF.5 THE E15 MARKER.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DE EMBL; M16426; AAA31289.1;
 DR PIR; A02161; GHRB.
 DR HSSP; P01857; 1FC1.
 DR InterPro; IPR003006; Ig_MHC.

```

DR InterPro; IPR003597; Ig_c1.
DR SMART; SM00407; Ig_2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REP. 2).
FT CONFLICT 71 71 V -> VPV (IN REP. 2).
FT CONFLICT 144 144 Q -> E (IN REP. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REP. 5).
FT CONFLICT 187 187 Q -> E (IN REP. 5).
FT CONFLICT 201 201 N -> D (IN REP. 5).
FT CONFLICT 218 218 E -> Q (IN REP. 5).
FT CONFLICT 233 233 E -> G (IN REP. 5).
FT CONFLICT 246 246 E -> G (IN REP. 5).
FT CONFLICT 256 256 N -> D (IN REP. 5).
FT CONFLICT 260 260 N -> D (IN REP. 5).
FT CONFLICT 266 266 N -> D (IN REP. 5).
FT CONFLICT 280 280 Y -> W (IN REP. 5).
FT CONFLICT 284 284 N -> S (IN REP. 5).
SQ SEQUENCE 323 AA; 3540 MW; 69E8AA118D579A8B CRC64;

Query Match 48.1%; Score 1226.5; DB 1; Length 323;
Best Local Similarity 69.7%; Pred. No. 7.6e-77;
Matches 228; Conservative 34; Mismatches 58; Indels 7; Gaps 2;

QY 150 KPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQSSGLY 209
Db 4 KAPSVPPLAPCCGDPSSSTVTTLGCLVKGLPEPVTVTWNSGTLTGVTFTFVSQSSGLY 63
QY 210 SLSSVVTVPSSSLGQTQYICNVNHPKSTKVDKKAEPKSCDKTHTCPPCPAPELGGPSV 269
Db 64 SLSSVSVTSSS--QPVTCTVAHPATNTKVDKTAPESTCSK---PTCPPELGGPSV 116
QY 270 FLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWVVDGVEVINATKPREQYNSTY 329
Db 117 FLPPPKPKDTLMISRTPEVTCVVDVSDQDEPVQFTWVNNQVARTAPPLREQGFNSTI 176
QY 330 RVVSVLTVLHODWLNKGEYKCKVSKNKAIPAEIKTISKAKGQPPQVYVTLPPSRDELTK 389
Db 177 RVVSTLPITQDLWLRKEFKCKVHNKALPAIEKTIKARGQPLEKPKVYVTWGPPEELSS 236
QY 390 NOVSLTCLVKGYPSDIAVEWESNGPENNYKTTTPVLDSGFSFLYSLKLTVDKSRWQOG 449
Db 237 RVSLTCLMNGFYPSDISVEWENKGAEDNYKITPAVLDSGFSFLYSLKLTVDKSRWQOG 296
QY 450 NVFSCVMHEALHNHYTQKSLSLSPK 476
Db 297 DVFTCSVMHEALHNHYTQKSISPSPK 323

RESULT 5
G22_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
ON NCBI_TaxId=10141;
RX Trischmann T.M.;
RP SEQUENCE OF 1-3.
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K.; Huseain Q.Z.; Cebra J.J.;

```

```

RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J.; Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 11. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E.; Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M.; Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B.; Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 N-LINKED (GLCNAC. . .).
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1PBA9 CRC64;

Query Match 47.6%; Score 1212.5; DB 1; Length 329;
Best Local Similarity 70.1%; Pred. No. 7.1e-76;
Matches 234; Conservative 28; Mismatches 63; Indels 9; Gaps 4;

QY 146 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQ 205
Db 1 SARTAPSVFPPLAASCVDVTSGSMWTLGCLVKGYFPEPTVKWNSGALTSGVHTFPAVLQ- 59
QY 206 SGLYSLSSVTVFPSSSLGQTQYICNVNHPKSTKVDKKAEPKSCDKTH--TCPPCPAPEL 263
Db 60 SGLYSLTSMVTVFPSSQKAT---CNVAHPASSTKVDKTVPEFTPTPBPCTCKPCPPEN 115
QY 264 LGGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNATKPREE 323
Db 116 LGGSPVFIFFPKPKDTLMISLTPTVTCVVDVSDQDEPVQFTWFDNKPVGNAETKPRVE 175
QY 324 QYNSTRVSVLTVLHODWLNKGEYKCKVSKNKAIPAEIKTISKAKGQPPQVYVTLPPS 383

```

Db 176 QYNTTFVESVLPQHQDLWLGKFEKCKVYNKALPAPIEKTISKTKGAPRMPDVVTLPPS 235
QY 384 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDGFFLYSKLTV 441
Db 236 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDGFFLYSKLTV 295
QY 442 DKSRWQGNVFCSCVMHEALHNHVTQKSLSPG 475
Db 296 DKSANDQGVTVTCVMHEALHNHVTQKSLSPG 329
RESULT 6
GC3 HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC) .
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=8101548; PubMed=674747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL Biochemistry 19:4304-4308 (1980).
RN [2]
RP REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RL quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:1883-889 (1977).
RN [3]
RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RL Structure of the FC fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914 (1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RT Franklin E.C., Hood L., Buxbaum J.N.;
RL "Gamma Heavy chain disease in man: cDNA sequence supports partial
RL gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264 (1982).
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC REF. 2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC AND ALL OF THE CH1 REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC OF THE CH1 REGION AND PART OF THE HINGE COMPARED WITH NORMAL
CC GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC SEGMENT (12-28).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outpost -

the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.eib-eib.ch/announce/>
or send an email to license@eib-eib.ch)

CC EMBL; J00231; AAS2805.1; ALT_SEQ.
DR PIR; A02149; G3HUI.
DR HSP; P01857; IFC1.
DR Genew; HGNC:5527; IGHG3.
DR MIM; 147120; .
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGHG1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT DOMAIN 12 73
FT DOMAIN 74 183
FT DOMAIN 184 289
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7
FT DISULFID 24 24
FT DISULFID 27 27
FT DISULFID 33 33
FT DISULFID 39 39
FT DISULFID 42 42
FT DISULFID 48 48
FT DISULFID 54 54
FT DISULFID 57 57
FT DISULFID 63 63
FT DISULFID 69 69
FT DISULFID 72 72
FT CARBOHYD 140 140
FT MOD_RES 290 290
FT VARIANT 126 127
FT VARIANT 134 134
FT VARIANT 139 139
FT VARIANT 182 182
FT VARIANT 227 227
FT VARIANT 227 227
FT VARIANT 279 279
SQ SEQUENCE 290 AA; 32331 MW; E69CB95705B2F46 CRC64;
Query Match 45.4%; Score 1157; DB 1; Length 290;
Best Local Similarity 76.2%; Pred. No. 3.7e-72;
Matches 218; Conservative 20; Mismatches 26; Indels 22; Gaps 2;
QY 210 SLSSVTVTPSSSLGTQYICNVNHPKNTKV-----DKKAEPKSCD 250
Db 8 TVSSSELTTP---LGDTHTCRCPEPKSCDTPPCRCPEPKSCDTPPCRCPEPKSCD 64
QY 251 KTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 310
Db 65 TPPECPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 124
QY 311 VEYHNATKREEQYNSTYRVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKG 370
Db 125 VQVHNATKREEQYNSTYRVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKG 184

```

QY 371 QREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 430
DB 185 QREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 244
QY 431 GSFPLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTOKLSLSLSPGK 476
DB 245 GSFPLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTOKLSLSLSPGK 290

RESULT 7
GCB_RAT ID GCB_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RL "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
DR Gene 74:473-482(1988).
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.0%; Score 1148; DB 1; Length 326;
Best Local Similarity 63.1%; Pred. No. 1.8e-71;
Matches 210; Conservative 52; Mismatches 61; Indels 10; Gaps 4;

QY 147 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 206
DB 1 AETATSVPLAPSGTALKNSMTLGLVKGYFPEPTVYSWNSGALTSGVHTFPAVLQ-S 59
QY 207 GLYSLSVTVPPSSLGDTQYICNVNHPKNTKVDKAEKPKCDKTHTCPCPAELGG 266
DB 60 GLYTLTSSVTVPPSSLGDTQYICNVNHPKNTKVDKAEKPKCDKTHTCPCPAELGG 113
QY 267 ---PSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNKTPREE 323
DB 114 SEVSSVFIFPPKPKDVLITLTKPVTCVVDVSHEDPEVKFNWYVDGVVHNKTPREE 173
QY 324 QYNSTYRVSVLTIVHQDLNGLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPS 383
DB 174 QFNSTFRSVSELPILHQLDMLNGLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPS 233
QY 384 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLYVDK 443
DB 234 KEEMTQNEVSICTWCKGFGFPDPIYVWQMNGQPENNYKTTPPVLDSDGSFFLYSLYVDK 293

```

```

QY 444 SRWQQGNVSCSVMHEALHNHYTOKLSLSLSPGK 476
DB 294 EKQQQGNVSCSVMHEALHNHYTOKLSLSLSPGK 326

RESULT 8
GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RL "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
DR Gene 74:473-482(1988).
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 44.8%; Score 1142.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 4.3e-71;
Matches 214; Conservative 44; Mismatches 69; Indels 9; Gaps 3;

QY 147 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 206
DB 1 AQTTPASVYPLAPSGDTTSSTVTLGCLVKGYFPEPTVYSWNSGALTSGVHTFPAVLQ-S 59
QY 207 GLYSLSVTVPPSSLGDTQYICNVNHPKNTKVDKAEKPKS-----CDKTHTCPCPA 260
DB 60 GLYTLTSSVTVPPSSLGDTQYICNVNHPKNTKVDKAEKPKS-----CDKTHTCPCPA 117
QY 261 PELLGGSVLPFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNKTP 320
DB 118 PELLGGSVLPFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNKTP 177
QY 321 REEQYNSTYRVSVLTIVHQDLNGLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTL 380
DB 178 REEQYNSTYRVSVLTIVHQDLNGLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTL 237
QY 381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLT 440
DB 238 GPPEQTEQVTSVLTCLTSGFLPNDIGVETSNGHLEKNTPEVNDSDGSFFLYSLT 297
QY 441 VDKSRWQQGNVSCSVMHEALHNHYTOKLSLSLSPGK 476
DB 298 VERSRWDSRAPFVCSVVHGLNHNHVEKISRPPEGK 333

```

RESULT 9
GCL MOUSE
ID GCL MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 19 gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T.; Obata M.; Yamawaki-Kataoka Y.; Kataoka T.; Kawakami T.;
RA Takahashi N.; Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene."
RL Cell 18:559-568(1979).
[2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M.; Yamawaki-Kataoka Y.; Takahashi N.; Kataoka T.; Shimizu A.;
RA Mano Y.; Seidman J.G.; Peterlin B.M.; Leder P.; Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid."
RL Gene 9:87-97(1980).
[3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J.; Clarke P.; Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain."
RL Nucleic Acids Res. 5:3305-3321(1979).
[4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma 1 chain."
RL J. Biol. Chem. 253:6068-6075(1978).
[5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J.; Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein."
RL Biochem. J. 126:837-850(1972).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; V00793; CAA24172.1;
DR EMBL; V00793; CAA24173.1;
DR EMBL; V00793; CAA24174.1;
DR EMBL; V00793; CAA24175.1;
DR EMBL; V00793; CAA24176.1;
DR PIR; A02159; GIWS.
DR HSSP; P01842; 7FAB.
DR GlycoSuiteDB; P01868;
DR MGD; MGI:96446; Igh-4;
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003597; Igh_C1.
DR Pfam; PF00047; Igh; 3.
DR SMART; SM00407; Igh1; 2.
DR PROSITE; PS00290; Igh_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 1 97
FT DOMAIN 98 110
FT DOMAIN 111 217
FT DOMAIN 218 324
FT DISULFID 27 82
FT DISULFID 102 102
FT DISULFID 104 104
FT DISULFID 107 107
FT DISULFID 109 109
FT DISULFID 138 198
FT CARBOHYD 174 174
FT DISULFID 244 302
FT MOD_RES 324 324
FT CONFLICT 276 276
FT CONFLICT 278 278
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
Query Match 44.6%; Score 1138; DB 1; Length 324;
Best Local Similarity 62.0%; Pred. No. 8.5e-71;
Matches 206; Conservative 55; Mismatches 61; Indels 10; Gaps 4;
Qy 147 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 206
Db 1 AKTPPSVYPLAPGSAQTNSMTLGLCLVKGYFPEPTVTVWSGSLSSGVHTFPAVLQSD 60
Qy 207 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNTKVDKAEKPSCKDKHTHTCPP--CPAPELL 264
Db 61 -LYTLSSVTVFPSSPRPSETVTCNVAHPASSTKVDDKTIPTVPCDQ---CKPCICTVPEV- 114
Qy 265 GGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPREQ 324
Db 115 --SVVFPFPKPKDVLITLIPKTCVVVDVSKDDPEVFQFVDFVDDVHVAQTQPREQ 172
Qy 325 YNSTVRVSVLTVLHQDLNKGKEYCKVSKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
Db 173 FNSTFRSVSELPIMHQDLNKGKFCRVNSAFAPIEKTISKTKGRPKAPQVYTIPTPK 232
Qy 385 DELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFYYLSSKLTVDKS 444
Db 233 EQMAKDKVSLTCLMITDFPEDITVEQWQNGQPAENYKNTQIMNTNGSYFYVYSLKLVQKS 292
Qy 445 RWOQGVFSCVMHEALHNHTQKSLSPQK 476
Db 293 NWEAGNTFTCSVLNHEGLHNHTKSLSHSPQK 324
RESULT 10
GCL MOUSE
ID GCL MOUSE STANDARD; PRT; 329 AA.
AC P02436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 19 gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wals J.A.; Word C.J.; Rimm D.; Der-Balan G.P.; Martinez H.M.;
RA Tucker P.W.; Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene."
RL EMBO J. 3:2041-2046(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: J00451; -; NOT_ANNOTATED_CDS.
PIR: B02156; G3MSC.
HSSP: P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; P45827174182BAD6 CRC64;
Query Match 44.4%; Score 1137; DB 1; Length 329;
Best Local Similarity 64.0%; Pred. No. 1e-70;
Matches 212; Conservative 46; Mismatches 69; Indels 4; Gaps 3;
QY 148 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNWSGALTSGVHTTTPAVLSGG 207
Db 1 TTTAPSVPLVPGSGDSIGSSVTLCLVKGYFPEPTVKNNYGLSSGVRTVSSVLQ-SG 59
QY 208 LYLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKAEPKSCDKHTHCP--PCPAPELIG 265
Db 60 FYSLSSLVTPSSSTWPSQTVCINVAHPASKTELKRIEPR-IPKPSPTPGSSCPGCGNIG 118
QY 266 GPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDDEVGFKNWTVGVGVNNAKTKPREQY 325
Db 119 GPSVFIFPPPKDALMSLTPEKVKTCVVVDVSDDDPDVHVSFVFNKVEHTAWTQPREAQ 178
QY 326 NSTYRVSVLTVTLQHDMLNGKEYKCKVKNKALPAPIEKTIISKAKGQPREPPQVYTLPPSRD 385
Db 179 NSTFRVVSALPIQHQDWRGKEFKCKVKNKALPAPIERTISPKGKAQTPQVYTIIPPRE 238
QY 386 ELTKQNSVLTCLVKGFPSDPIAVENESGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSR 445
Db 239 QMSKKKYSVLTCLVNTFFSEALISVEVERNGELEQDYKNTTPILDSDGTFLYSKLTVDTDS 298
QY 446 WQGNVFTSCVMHEALNHHYTKSLSPGK 476
Db 299 WLQGEIFTCSVVEALNHHHTQKLSRSPGK 329
RESULT 11
GC1M_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]

SEQUENCE OF 323-393 FROM N.A.
MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6792907;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: V00793; CAA24172.1; -;
DR EMBL; V00793; CAA24173.1; -;
DR EMBL; V00793; CAA24174.1; -;
DR PIR; B02159; G1MSM.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 N-LINKED (GLCNAC. . .).
FT CARBOHYD 174 174 POTENTIAL.
FT DISULFID 244 302 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 340 357
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;
Query Match 44.4%; Score 1133; DB 1; Length 393;
Best Local Similarity 61.9%; Pred. No. 2.4e-70;
Matches 205; Conservative 55; Mismatches 61; Indels 10; Gaps 4;
QY 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNWSGALTSGVHTTTPAVLSGG 206

```
Db 1 AKTTPSVVPLAPCSAQTSMVTLGCLVKGYPFPEVTVTNWNSGSLSGVHTFPVAVLQSD 60
Qy 207 GLYSLSVTVTPSSSLGTQTVICNVNKKPSNTKVDKAEKSCDKTHTCP--CPAPELL 264
Db . 61 -LYTSSSVTVSPSPRSETVTCNVAHPASSTKVDKIVPRDCG----CKPCICTVPEV- 114
Qy 265 GQPSVFLFPKPKDRTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 324
Db 115 --SSVFIFPPKPKDVLITITLTKVTCVVVDISKDPEVQFSWFVDVDEVHTAQTQPREQ 172
Qy 325 YNSTRVSVTLVHQLDNLNGKEYCKVSKNKKALPAPIETKISKAKGQPREPQVYTLPPSR 384
Db 173 FNSTRFVSGELPIMHODWLNKGEKFCRVNSAFAPIETKISKTKGRPRAPQVYTIPTPPK 232
Qy 385 DELTKNOVSLTCLVKGYPSPDIAVEWESNGOPENNYKTPPVLDSDGSPFLYSKLTVDKS 444
Db 233 EQAKDKVSLTCMTDFPFEDITVEWQNGQPAENYKNTQIPMNTNGSYFVYSKLVNQKS 292
Qy 445 RWOQGNVFCSCVNHEALHNHYTKQSLSPG 475
Db 293 NWEAGNTFCVSLHLEGLHNHHTKSLSHSPG 323

RESULT 12
GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314259;
RA Konaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00451; AAB59655.1;
DR EMEL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A02155; G3MSM.
DR HSPR; P01857; 1FC1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER '1
```

```
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 44.2%; Score 1126; DB 1; Length 398;
Best Local Similarity 63.8%; Pred. No. 7.2e-70;
Matches 210; Conservative 46; Mismatches 69; Indels 4; Gaps 3;

Qy 148 STKGSVPLAPSSKSTSGTAALGCLVKGYPFPEVTVTNWNSGALTSGVHTFPVAVLQSSG 207
Db 1 TTTAPSVPLVPGCSDTSGSSVTGLCLVKGYPFPEVTVTNWNSGALTSGVHTFPVAVLQ- 59
Qy 208 LYSLSVTVTPSSSLGTQTVICNVNKKPSNTKVDKAEKSCDKTHTCP--CPAPELLG 265
Db 60 FYLSLTVTPSSTWPSQIVICNVAHPASKTELKRIEPR-IPKSTPFGSSCPPGNILG 118
Qy 266 GPSVFLFPKPKDRTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 325
Db 119 GPSVFLFPKPKDALMISLTPKVTCCVVVDVSEDDPDVHVSFWVDNKEVHTAMTQPREAQ 178
Qy 326 NSTYRVSVTLVHQLDNLNGKEYCKVSKNKKALPAPIETKISKAKGQPREPQVYTLPPSRD 385
Db 179 NSTFRVVSALPIQHDWNRGKFKCKVNNKALPAPIETKISKPKGRAQTQVYTIPTPPRE 238
Qy 386 ELTKNOVSLTCLVKGYPSPDIAVEWESNGOPENNYKTPPVLDSDGSPFLYSKLTVDKSR 445
Db 239 QMSKKVSLTCLVTNFFSEAISEWERNGELEQDYKNTPTPILDSGDTFLYSKLTVDTS 298
Qy 446 WQGNVFCSCVNHEALHNHYTKQSLSP 474
Db 299 WLQGEIFTCVVVHEALHNHHTQKNLSRSP 327

RESULT 13
GCAA_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 19 gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollio R., Auffray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
suggests that exons can be exchanged between genes in a multigenic
RT
```


family.⁴;
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446 (1981).
 RN [4]
 RX MYELOMA PROTEIN MOPC 173.
 RA MEDLINE=74175517; PubMed=4831970;
 RT Bourgeois A., Fougereau M., Rocca-Serra J.;
 "Determination of the primary structure of a mouse IgG2a
 immunoglobulin amino-acid sequence of the Fc fragment. Implications
 for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435 (1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=73056887; PubMed=4565406;
 RA de Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma G2a
 immunoglobulin. Identification of the disulfide bridges.";
 RL Eur. J. Biochem. 30:452-462 (1972).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch.
 CC -----
 DR ENBL; V00798; CAA24178.1; -;
 DR PIR; A02152; G2MSA.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00410; Ig like; 1.
 DR SMART; SM00407; IGL1; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region.
 KW NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
 SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;
 Query Match 44.0%; Score 1122; DB 1; Length 330;
 Best Local Similarity 63.6%; Pred. No. 1.1e-69;
 Matches 211; Conservative 43; Mismatches 74; Indels 4; Gaps 3;
 QY 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSVHTFPAVLQSS 206
 DB 1 AKTAPSVYPLPVCVGGTIGSSVTGLCLVKGYFPEPTVLTWNSGSSGSGVHTFPAVLQSD 60
 QY 207 GLYSLSVVTPSSSLGTQTYICNVNHPKSNKVKDKAEPKSCDKHTCTCPP--CPAPELL 264
 DB 61 -LYTSSSVTVTSSTWPSQSIICNVNHPASSTKVDKKIEPRG-PTIKPCPPKCPAPNLL 118
 QY 265 GGPVSFLFPKPKDPTLMSRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKREEQ 324
 DB 119 GGPVSFTFPKPKDPTLMSRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKREEQ 178
 QY 325 YNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTPPSR 384
 DB 179 YNSTLRVVSALPIQHDWMSGKPKCKVNNKDLPAPIERTISKPKGVRAPQVYVLPPE 238
 QY 385 DELTKQVSLTCLYKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLYTDKS 444
 DB 239 EEMTKQVLTLCWTFDMPEDYVETWNTNGKTELNYKNTPEVLDSGYSFMYSKLRVEKK 298
 QY 445 RWQGNVFCSSVMHEALHNHYTQKSLSLSPGK 476

DB 299 NWVERNSYSCSYVHEGLNHHHTTKSFSTRPGK 330
 RESULT 14
 GCAB MOUSE
 ID GCAB MOUSE STANDARD; PRT; 335 AA.
 AC P01864;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE IG gamma-2A chain C region, B allele.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6;
 RX MEDLINE=82037861; PubMed=6170065;
 RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
 RT "Multiple differences between the nucleic acid sequences of the
 RT IGG2aa and IGG2ab alleles of the mouse."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499 (1981).
 RN [2]
 RP SEQUENCE
 RX MEDLINE=82037777; PubMed=6794027;
 RA Dognin M.J., Lauwerys M., Strosberg A.D.;
 RT "Multiple amino acid substitutions between murine gamma 2a heavy
 RT chain Fc regions of Ig1a and Ig1b allotypic forms."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035 (1981).
 CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
 CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch.
 CC -----
 DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
 DR PIR; A02153; G2MSAB.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00410; Ig like; 1.
 DR SMART; SM00407; IGL1; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region.
 KW NON_TER 1
 FT SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
 Query Match 43.9%; Score 1119.5; DB 1; Length 335;
 Best Local Similarity 61.3%; Pred. No. 1.6e-69;
 Matches 206; Conservative 52; Mismatches 71; Indels 7; Gaps 2;
 QY 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSVHTFPAVLQSS 206
 DB 1 AKTAPSVYPLPVCVGGTIGSSVTGLCLVKGYFPEPTVLTWNSGSSGSGVHTFPAVLQ-S 59
 QY 207 GLYSLSVVTPSSSLGTQTYICNVNHPKSNKVKDKAEPK-----SCDKHTCTCPPCA 260
 DB 60 GLYTLSSSVTVTSSTWPSQSIICNVNHPASSTKVDKKIEPRVITONPCPPHQRVPVPCA 119
 QY 261 BELLGPSVFLPFPKPKDPTLMSRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKP 320
 DB 120 PLLLGPSVFIPIPKIKVDVLSLSPWTCVVVDVSEDDPDVQISFWVNNVEVHTAQOT 179
 QY 321 RBEQNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 380

```
Db 180 HREDYNSTRVVSALPIQHODMSKFEKCKVNNKALSPKIEKTSKPRGPVAPQVYVL 239
Qy 381 PPSDELTKNOVSTCLVKGYPSDIAVWESNGOPENNYKTPPVLDSDGSFFLYSKLT 440
Db 240 PPPAEETKFEFSLTGMTGLPABIAVDWTNGRTEQNYKNTATVLDSDGSFYFYSKLR 299
Qy 441 VDKSRWOGNVPFSCVMEALHNNHYTKSLSPGK 476
Db 300 VOKSTWGRSLFACSVVHEVLHNLTKTIIRSLGK 335

RESULT 15
GCAM MOUSE
ID GCAM MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END ENCODED
CC IN SEPARATE EXONS. THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
CC THE A ALLELE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00471; AAB59661.1; ALT_INIT.
CC FIR; A02154; G2MSAM..
CC HSSP; P01842; 7FAB.
CC MGD; MGI:96443; Igh-1.
CC InterPro; IPR003106; Ig_MHC.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00410; IG_Like; 1.
CC SMART; SM00407; IGCL; 2.
CC PROSITE; PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT DISULFID 346 363
FT TRANSMEM 364 399
FT DOMAIN 364 399
FT CARBOHYD 380 180
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT N-LINKED (GLCNAC... ) (POTENTIAL).
```

```
SO SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;
Query Match 43.8%; Score 1117; DB 1; Length 399;
Best Local Similarity 63.4%; Pred. No. 3e-69;
Matches 210; Conservative 43; Mismatches 74; Indels 4; Gaps 3;
Qy 147 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS 206
Db 1 AKTAPSVIFPLAPVCGDTIGSSVTLGCLVKGYFPEPVTLITWNSGSLSSGVHTFPAVLQSD 60
Qy 207 GLYSLSSVVTVPFSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKHTHTCPP--CPAPELL 264
Db 61 -LYTLSSSVTVTSSWPSQSITCNVAHPASSTKVDKIEPRG-PTIKPCPPCKCPAPNLL 118
Qy 265 GGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREQ 324
Db 119 GGPSVFIPTPKIKDVLMSLSFIVTCVVVDVSEDDPDQVQISFWNNVEVHTAQTQTHRED 178
Qy 325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSR 384
Db 179 YNSTLRVVVSALFIQHDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPE 238
Qy 385 DELTKNOVSLTCLVKGYFVPSPDIAVWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKS 444
Db 239 EEMTKKQVTLTCMVTDFMPEDIIYVEWTNNKTELNYKNTEPVLDSDGSFYFYSKLRVEKK 298
Qy 445 RWQOGNVFSCSVMEALHNNHYTKSLSPG 475
Db 299 NWVERNSYSCSVVHEGLNHHHTTKSFSTRTPG 329
```

Search completed: March 29, 2003, 09:11:17
Job time : 13.3492 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 43.1716 Seconds
(without alignment)
2271.829 Million cell updates/sec

Title: US-09-758-173-12

Perfect score: 2549

Sequence: 1 MKHLFFLLVAAPRWLSQ.....MHEALHNYTKSLSPGK 476

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2102.5	82.5	471	4 Q8TC77	Q8TC77 homo sapien
2	2075	81.4	473	4 Q8TC63	Q8TC63 homo sapien
3	1473.5	57.8	463	11 Q99LC4	Q99LC4 mus musculus
4	1437.5	56.4	473	11 Q98DL4	Q98DL4 mus musculus
5	1434	56.3	469	11 Q8R3V9	Q8R3V9 mus musculus
6	1430.5	56.1	437	11 Q8R1A4	Q8R1A4 mus musculus
7	1416	55.6	468	11 Q99LJ1	Q99LJ1 mus musculus
8	1394.5	54.7	473	11 Q99L25	Q99L25 mus musculus
9	1367	53.6	474	11 Q8R3H6	Q8R3H6 mus musculus
10	1365.5	53.6	473	11 Q91Z05	Q91Z05 mus musculus
11	1268	49.7	701	4 Q96PQ8	Q96PQ8 homo sapien
12	1262.5	49.5	337	6 Q95M34	Q95M34 equus caball
13	973	38.2	613	4 Q96EY0	Q96EY0 homo sapien
14	948.5	37.2	597	4 Q8BU10	Q8BU10 homo sapien
15	944.5	37.1	597	4 Q96B58	Q96B58 homo sapien
16	938.5	36.8	588	4 Q8WUX4	Q8WUX4 homo sapien

17	938.5	36.8	618	4	Q96AA6	Q96AA6 homo sapien
18	915	35.9	496	4	Q96KX8	Q96KX8 homo sapien
19	770.5	30.2	597	4	Q96BB9	Q96BB9 homo sapien
20	762	29.9	613	4	Q8WUK1	Q8WUK1 homo sapien
21	746.5	29.3	479	11	Q99M22	Q99M22 mus musculus
22	726	28.5	613	11	Q8VCX7	Q8VCX7 mus musculus
23	725	28.4	278	11	Q921K1	Q921K1 mus musculus
24	702	27.5	494	4	Q96K68	Q96K68 homo sapien
25	700	27.5	482	11	Q91X92	Q91X92 mus musculus
26	692.5	27.2	614	4	Q96GA6	Q96GA6 homo sapien
27	667.5	26.2	497	4	Q8WY24	Q8WY24 homo sapien
28	655.5	25.7	479	11	Q91WP5	Q91WP5 mus musculus
29	655	25.7	488	11	Q91WR1	Q91WR1 mus musculus
30	654.5	25.7	487	11	Q99KA4	Q99KA4 mus musculus
31	652	25.6	486	11	Q91207	Q91207 mus musculus
32	645	25.3	500	4	Q9BSV0	Q9BSV0 homo sapien
33	637.5	25.0	481	11	Q91WT1	Q91WT1 mus musculus
34	636	25.0	496	4	Q96DK0	Q96DK0 homo sapien
35	635.5	24.9	481	11	Q8VCV5	Q8VCV5 mus musculus
36	631.5	24.8	480	11	Q91XE1	Q91XE1 mus musculus
37	626.5	24.6	489	11	Q8VCX4	Q8VCX4 mus musculus
38	623.5	24.5	484	11	Q8VEA0	Q8VEA0 mus musculus
39	614	24.1	484	11	Q99LA6	Q99LA6 mus musculus
40	590.5	23.2	481	11	Q91WT3	Q91WT3 mus musculus
41	583.5	22.9	150	4	Q95973	Q95973 homo sapien
42	576	22.6	416	4	Q9NPP6	Q9NPP6 homo sapien
43	538	21.1	573	4	Q8WU38	Q8WU38 homo sapien
44	503	19.7	426	11	Q9DCD9	Q9DCD9 mus musculus
45	465	18.2	384	4	Q9UP60	Q9UP60 homo sapien

ALIGNMENTS

RESULT 1

ID	Q8TC77	PRELIMINARY;	PRT;	471 AA.
AC	Q8TC77;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Hypothetical 51.8 kDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI	taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SPLEEN;			
RA	Strausberg R.;			
RL	Submitted (PEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC024289; AAH24289.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 471 AA; 51791 MW; 388774CF588660E CRC64;			

Query Match	82.5%;	Score	2102.5;	DB	4;	Length	471;
Best Local Similarity	85.2%;	Pred. No.	1.1e-159;				
Matches	403;	Conservative	16;	Mismatches	45;	Indels	9;
Gaps							
Qy	5	WFFLLVAAPRWLSQVQLQESGPGLVKPSPTLSLTCAVSGGSISGGYGMGWIRQPPGKG	64				
Db	7	WVF-LVAALSGVQCEVQLVSGGGLVKPGSLRLSCAASGFTFS-SYSMNWVRAQAPKG	63				
Qy	65	LEWIGSFSSSGNYNPSLKSQVTISTDTSKNQFSLKLSMTAADTAIVYCVDRLEFSV	124				
Db	64	LEWSSMSSSSYIYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYICARD-----	118				
Qy	125	VGMYNNH-FDVWGPGLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV	183				
Db	119	LRLQTSYWFYFLWGRGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV	178				
Qy	184	TVSNNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSKTKVDKK	243				

```

Db 179 TVSNWNGALTSVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKK 238
Qy 244 AEPKSCDKHTCPCPCAPPELLGGSVFLFPKPKDITLMISRPETVTVVVDVSHEDPEVK 303
Db 239 VEPKSCDKHTCPCPCAPPELLGGSVFLFPKPKDITLMISRPETVTVVVDVSHEDPEVK 298
Qy 304 FNVWVDGVEVHNKTKPREQYNSYRVRVSVLTVLHODWLNKGYKCKVSNKALPAPTEK 363
Db 299 FNVWVDGVEVHNKTKPREQYNSYRVRVSVLTVLHODWLNKGYKCKVSNKALPAPTEK 358
Qy 364 TISAKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPNNTKT 423
Db 359 TISAKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPNNTKT 418
Qy 424 PPVLDSGGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 476
Db 419 PPVLDSGGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 471

RESULT 2
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAR25985.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 81.4%; Score 2075; DB 4; Length 473;
Best Local Similarity 83.2%; Pred. No. 1.8e-157;
Matches 397; Conservative 29; Mismatches 39; Indels 12; Gaps 5;

Qy 1 MKHLWFFLLVAAPRWVLSQVLOESGPGLVKPKSETLSLTCAVSGGST-SGGYWGWIRO 59
Db 8 MKHLWFFLLVAAPRWVLSRLQESGPGLVKPKSETLSLTCTVSGDSVASSSYTWGWRQ 67
Qy 60 PPGKLEWIGSFYSSSGNTYINPGLKSVTLTSTDKNQFSLKLSNMTAADTAVYCVRD 119
Db 68 PPGKLEWIGTI-NFSGNMYSPSLRSRVMTSADMSENSEFYLKLDSTVTAADTAVYCAAG 126
Qy 120 RLFSVGMVYNNWFDVWGPGLVTVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYF 179
Db 127 HL--VMGFGAH-----WGQGLSVSPASTKGPVFPPLAPCSRSTSTSTAAALGCLVKDYF 179
Qy 180 PEPVTVSNWNGALTSVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTK 239
Db 180 PEPVTVSNWNGALTSVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTK 239
Qy 240 VDKAEPKSCDKHTCPCPCAPPELLGGPSVFLFPKPKDITLMISRPETVTVVVDVSHED 299
Db 240 VDKRVESK--YGPCCPCAPPELLGGPSVFLFPKPKDITLMISRPETVTVVVDVSHED 296
Qy 300 PEVKFNWYVDGVEVHNKTKPREQYNSYRVRVSVLTVLHODWLNKGYKCKVSNKALPA 359
Db 297 PEVQFNWYVDGVEVHNKTKPREQYNSYRVRVSVLTVLHODWLNKGYKCKVSNKALPA 356
Qy 360 PAKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPNNT 419
Db 357 SIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPNNT 416
Qy 420 YKTTTPPVLDSDGGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 476

```

```

Db 417 YKTTTPPVLDSDGGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 473

RESULT 3
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Similar to riken cDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAR03435.1; -.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BB30783 CRC64;

Query Match 57.8%; Score 1473.5; DB 11; Length 463;
Best Local Similarity 56.3%; Pred. No. 1.9e-109;
Matches 269; Conservative 84; Mismatches 108; Indels 17; Gaps 6;

Qy 1 MKHLWFFLLVAAPRWVLSQVLOESGPGLVKPKSETLSLTCAVSGGST-SGGYWGWIRO 60
Db 1 MEWIFLFLISLTAGVHSQVLOQSGAELAPGASVPLSCASGYTFT-GYGVSWVKOR 59
Qy 61 PKGLEWIGSFYSSSGNTYINPGLKSVTLTSTDKNQFSLKLSNMTAADTAVYCVRD 120
Db 60 TGOGLEWVGEIYPGSGNTYIYSEKFKGATLTDDKSSSTAYMHLSSLTSEDVAVFCAHSS 119
Qy 121 LFSVGMVYNNWFDVWGPGLVTVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYF 180
Db 120 YSY-----DLFAYWGGTGLTVSAAKTTTPSVYPLAPGSAQAOTNSMVTGLGCLVKDYF 173
Qy 181 EPTVTVSNWNGALTSVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTK 240
Db 174 EPTVTVSNWNGALTSVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTK 232
Qy 241 DKAEPKSCDKHTCPCPCAPPELLGGPSVFLFPKPKDITLMISRPETVTVVVDVSHED 298
Db 233 DKKIVPRDCG---CKPCICTVPEV---SSVFIPPKPKDITLTTPKTCVVDVSHED 285
Qy 299 DPEVKFNWYVDGVEVHNKTKPREQYNSYRVRVSVLTVLHODWLNKGYKCKVSNKALP 358
Db 286 DPEVQFNWYVDGVEVHNKTKPREQYNSYRVRVSVLTVLHODWLNKGYKCKVSNKALP 345
Qy 359 APIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPN 418
Db 346 APIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPN 405
Qy 419 NYKTTTPPVLDSDGGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 476
Db 406 NYKNTQIMTDDGGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 463

```

RESULT 4
Q9DBL4 PRELIMINARY; PRT; 473 AA.
AC Q9DBL4; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1810060009RIK protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H., Aeshburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher M., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wu L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Igh.
DR InterPro; IPR003597; Igh.c1.
DR InterPro; IPR003600; Igh-like.
DR InterPro; IPR003006; Igh.MHC.
DR InterPro; IPR003596; Igh.v.
DR Pfam; PF00047; Igh; 4.
DR SMART; SM00409; Igh; 2.
DR SMART; SM00407; Igh; 3.
DR SMART; SM00406; Igh; 1.
DR SMART; SM00410; Igh like; 1.
DR PROSITE; PS00290; Igh.MHC; UNKNOWN 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 56.4%; Score 1437.5; DB 11; Length 473;
Best Local Similarity 55.8%; Pred. No. 1.5e-106;
Matches 269; Conservative 80; Mismatches 118; Indels 15; Gaps 5;
QY 1 MKELWFLLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGSGISGGYGMWIRQP 60
DB 1 MENSWVFLFLSVTAGVCHQVQLKQSGAELVKPESGKISCKASGYTF-DYYINWVKQR 59
QY 61 PGKLEWIGSFYSSGNTYINPSLKQVITSTDTSKNQFSLKNSMTAADTAVYVCVRD 120
DB 60 PGGLEWIGKIGCSGSTYINPKFKALITADKSSYAMQSSUTSDESAVFCARS- 118
QY 121 LFSVGVGNVNNFDVWPGVLTVTSASTKGPSVFPPLAPSSKSTSGTAAALCLVKDYFP 180
DB 119 -----GDYD-DWFAVGGQGLTVTSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGYPP 172
QY 181 EPVTVSNMGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKY 240
DB 173 EPVTLTNWSSGLSSGVTTPALLO-SGLYTLSSSVTVTNTWPSQTITCNVAHPASSSTKY 231

QY 241 DKKAEPK-----SDKTHCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD 294
DB 232 DKKIEPRVPIQNPCCPLKECPAAPPDLLGGPSVFIFFPKIKDVLMSLSPNVTCVVD 291
QY 295 VSHEDPEVKFNWYVDGVEVHNNAKTPREBOYNSTYRVSVLTVLHODWLNKGYKCKVSN 354
DB 292 VSEDDPDVQISWFWNNVVEVHTAQTHREDYNSTLRVSAALPIHQDWMMSGKEFKCKVNN 351
QY 355 KALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEESNG 414
DB 352 RALPSPIETKISKPRGPVRAQVYVLPPEAEWTKKEFSLTCTMTGLPAEIAVDVTSNG 411
QY 415 QPENNYKTTPVLDDSGSFLYSLKLTVDKSRWQGNVFCSSNHEALHNHYTKSLSP 474
DB 412 RTEQNYKNTATVLDSDGSYFMYSLRVQKSWERGSVHGVHGHNNHTTKTIRSL 471
QY 475 GK 476
DB 472 GK 473
RESULT 5
Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024405; AAH24405.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
Query Match 56.3%; Score 1434; DB 11; Length 469;
Best Local Similarity 57.1%; Pred. No. 2.8e-106;
Matches 274; Conservative 76; Mismatches 110; Indels 20; Gaps 10;
QY 4 LWF-FLLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGSGISGGYGMWIRQP 62
DB 3 LWNWIFLVTLNGIQCEVNLVSGGGLVQPGGSLRLSCAASGFTFT-DYYMSWVRQPPG 61
QY 63 KGLEWIGSFYSSGNTY---YNPSLKSOVITSTDTSKNQFSLKNSMTAADTAVYVCVRD 119
DB 62 KALEWLG-FIRNKANGYTYEYSASVKGRFTISRDNQSILYLQMNALRAEDSATYTCARD 120
QY 120 RLFVGVGNVNNW-FDVMGPGVLTVTSASTKGPSVFPPLAPSSKSTSGTAAALCLVKDY 178
DB 121 RRS-YYISGTSFAYWGGTGLTVTSAAKTTTPSVYPLAPGAAQNSMTVTCVVDIS 177
QY 179 FPEPTVTVSNMGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNT 238
DB 178 FPEPTVTVSNMGSLSSGVTTPVAVLQSD-LYTLSSSVTVPSSTWPSQTVTCNVAHPASST 236
QY 239 KVDKAEPSKCDKTHCTCP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS 296
DB 237 KVDKKIVPRDQ----CKPICVPEV---SSVIFPPKPKDVLTLTLTKVTCVVDIS 289
QY 297 HEDPEVKFNWYVDGVEVHNNAKTPREBOYNSTYRVSVLTVLHODWLNKGYKCKVSNKA 356
DB 290 KDDPEVQFQFVDDVEVHTAQTKPREBOYNSTFRSVSELPIMHQDWMNGKEFKCKVNSAA 349
QY 357 LPAPIETKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEESNGQP 416
DB 350 FPAPIETKISKGRPKAPQVYTIPTPPKEQMAKDKVSLTCTMTDFFPEDITVEMQWNGQP 409


```

Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 181006009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA03888.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG1; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGV_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 473 AA; 52449 MW; BE98987986D1A55 CRC64;

Query Match 54.7%; Score 1394.5; DB 11; Length 473;
Best Local Similarity 55.8%; Pred. No. 4.1e-103;
Matches 269; Conservative 71; Mismatches 127; Indels 15; Gaps 6;

QY 1 MKHLWFLVLAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSGISGGYGMWIRP 60
DB 1 MENSWFLFLSVTTGVHSQVQLQDAELVKGASVKISCKRVGVTFT-DHTIHWKQR 59

QY 61 PGKLEWIGSYSSNGTYNPSLKSQVLTSTDTSKNQFSLKLNMSMTAADAATVYCVDR 120
DB 60 PEQGLEWIGYIPRDGSKYNEKFKGKATLTADKSSSTAYMQLNLSLTSDSAFCVCSRG- 118

QY 121 LFSVVGVMVNN----WFDVWGPGVLVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVK 176
DB 119 -----GSIYGYGLYFDYWGQGTITVSSAKTAPSVFLAPVCGDITGSSVTLGCLVK 173

QY 177 DYPEPVTWNSGALTSQVHTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKS 236
DB 174 GYFPEPVTWNSGSLSSGVHTTPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPAS 232

QY 237 NTKVDKKAEPKSCDKTHTCPP--CPAPELGGPSVFLFPKPKDITLMISRTPEVTCVVVD 294
DB 233 STKVDKKIEPRG-PTIKPCPCCKCPAPNLLGGPSVFIAPPKIDVLMISLSPMVTICVVVD 291

QY 295 VSHDEPEVKNVYDGVGVHNAKTKPREOYNSTYRVSVTLVLDHODWLNKGEYKCKVSN 354
DB 292 VSDDDPDVQISWVNNVEVTAQTQTHREDYNSTLRVVSALPIQHODWMSGKEFKCKVNN 351

QY 355 KALPAPIETKISKAGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNG 414
DB 352 KALPAPIERTISKPGSVRAPOVYVILPPPEEEMTKKQVTLTCMTVDFMPEDIVVETWNG 411

QY 415 QPENNYKTPPVLDSOGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 474
DB 412 KTELNYKNTPEVLDSOGSYFMYSLKRVKKNVERNISYSCVVHGLAHNHTTKFSRTP 471

QY 475 GK 476
DB 472 GK 473

RESULT 9
Q983H6

```

```

ID Q983H6 PRELIMINARY; PRT; 474 AA.
AC Q983H6;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -
DR Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 53.6%; Score 1367; DB 11; Length 474;
Best Local Similarity 54.8%; Pred. No. 6.5e-101;
Matches 261; Conservative 75; Mismatches 124; Indels 16; Gaps 5;

QY 8 LLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSGISGGYGMWIRPQPKGLEW 67
DB 8 LFLLSVTEGVHSQVQLQSGPELVKPGASVKISCRASGYAFKSW-MNWVKRRFGKGLEW 66

QY 68 IGSFYSSSGNTYNNPSLKSQVLTSTDTSKNQFSLKLNMSMTAADAATVYCVDRDLFSVVG 127
DB 67 IGRIFPGDGDTHYSKFGKAKLTADKSSVTAFLLQLTSLTSEDSAVYFCARD-----S 119

QY 128 VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPBPVTWS 187
DB 120 DYGDYFDWGGQATVTVSSAKTTPPSVPLAPGCGDITGSSVTLGCLVKGYFPESVITW 179

QY 188 NSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSTKVDKKAEPK 247
DB 180 NSGSLSSSVHTFPALLO-SGLYTNSSSVTPSSWPSVTVCVAHPASSTVDDKLEPS 238

QY 248 SCDXT-HTCPT-----CPAPELGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDP 300
DB 239 GPISITINPCPCCKCHKCPAPNLEGPSVFIAPPKIDVLMISLTPKVTCTVVDVSDDP 298

QY 301 BVKNWVYDGVGVHNAKTKPREOYNSTYRVSVTLVLDHODWLNKGEYKCKVSNKALPAP 360
DB 299 DVQISWVNNVEVTAQTQTHREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPS 358

QY 361 IEKTSKAGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
DB 359 IERTISKIKGLVRAPOVYVILPPPAEQLSRKDVSLTCLVVGFPNPGDISVETNSGHTTE 418

QY 421 KTTTPPVLDSOGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 476
DB 419 KDTAPVLDSOGSYFMYSLKIDIKTSKWEKTDSPSCNVRHEGLKNYYLTKTISRSPGK 474

RESULT 10
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -

```

```

DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00181; EGF_2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00111; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 473 AA; 51946 MW; CF625F0089332AF12 CRC64;

Query Match 53.6%; Score 1365.5; DB 11; Length 473;
Best Local Similarity 55.6%; Pred. No. 8.5e-101;
Matches 265; Conservative 70; Mismatches 123; Indels 19; Gaps 6;

QY 7 FLLVAAPRWYLSOVQLQESGGLVKPSETLSLTCAVSGGSGISGGYGGWIRQPPGKGL 66
DB 1 FLVLIL--KGVCQEVQLVESGGLVKPGSRKLSCAASGFTFS--DYGMMHWVQAPKGL 65

QY 67 WIGSFYSSGNTYNNPLSKSQVTISTDTSKNQFSLKUNMTAADTAVYYCVRDLFSVVG 126
DB 66 WVAYINGSGTIIYADTVKGRFTISRDNAKNTLFLQMTSLRSEDYAMYICARE----- 118

QY 127 MVYNNWFDVWPGVGLVTVSSASTKGPVFPPLAPSSKTSGGTAALGCLVKDYFPPPTVS 186
DB 119 -LWLRRIDYWGQGITITVSSAKTTPPVYPLAPGCGDTTGSSTVLGCLVKGYFPESVT 177

QY 187 NWSGALTSGVHTFPAVLOSGGLYSSVVTVPSSSLGTQTYICNVNHPKTKYDKKALP 246
DB 178 NWSGSLSSSVHTFPALLQ--SGLYTWSSSVTVPSSTWPSQTVCVAHPASSTTVDDKLEP 236

QY 247 KSCDKT--HTCPP-----CPAPELLGSPSVFLPFPKPKDTLMISRTPEVTCVVDVSHED 299
DB 237 SGPISTINPCPPCKECHKCAPNLEGGSPVIFPPENIKDVLMLSLTPKVTCCVVDVSEDD 296

QY 300 PEVFNWVVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPA 359
DB 297 PDVQISFNWVNVVHTAGTQTHREDYNSITIRVVSALPQHQWMSGKGFCKVSNKALDPS 356

QY 360 PIETISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
DB 357 PIETISKIKGLVAPQVYIILPPPAEQLSKRDVSLTCLVWGFNPGDISVENTVSGHTTEEN 416

QY 420 YKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 476
DB 417 YKDTAPVLDSDGSPFYIYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 473

RESULT 11
Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Factor VII active site mutant immunocofugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RZ Hu Z.; Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT calls for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.

```

```

DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF_2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00111; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 49.7%; Score 1268; DB 4; Length 701;
Best Local Similarity 82.7%; Pred. No. 9.1e-93;
Matches 244; Conservative 4; Mismatches 29; Indels 18; Gaps 3;

QY 185 VSNWSGALTSGVHTFPAVLOSGGLYSSVVTVPSSSLGTQTYICNVNHPKPS--NTKVD 241
DB 422 VSWGQGCATVG-----HFGVY-----TRVSYIEWLQKLMRSEPRGVLLRAFP 466

QY 242 KKAEPKSCDKTHTCPDPAPELLGSPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPE 301
DB 467 GSABPKSCDKTHTCPDPAPELLGSPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPE 526

QY 302 VKFNWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPI 361
DB 527 VKFNWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPI 586

QY 362 EKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 421
DB 587 EKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 646

QY 422 TTPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 476
DB 647 TTPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 701

RESULT 12
Q95M34 PRELIMINARY; PRT; 337 AA.
AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region
DE (Fragment).
GN IGHCL.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX Wagner B.;
RP Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B.; Overesch G.; Sheoran A.; Holmes M.; Richards C.;
RA Leibold W.; Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199:105-119(1998).
DR EMBL; AJ300675; CAC4624.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR NON_TER 1
FT

```


SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
 Query Match 49.5%; Score 1262.5; DB 6; Length 337;
 Best Local Similarity 69.2%; Pred. No. 9e-93;
 Matches 234; Conservative 42; Mismatches 53; Indels 9; Gaps 3;

QY 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSNWNGALTSVHTFPAVLQSS 206
 DB 1 ASTARFVALAPGCGGTSDSITVALGCLVSGYFPFPVKVSNWNGSLTSVHTFPAVLQSS 60

QY 207 GLYSLSVTVTPSSSLGCTTYICNVNHPKSNKTKVKKAE-----KSCDKTHTCPPCPA 260
 DB 61 GFYSLSSMTVPASTWTSETYICNVVHAASNFKVDKRIEIPDNHQKVCDSM-KCPKCPA 119

QY 261 PELLGGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 320
 DB 120 PELLGGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 179

QY 321 REEYNSTRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKQPREPOVYL 380
 DB 180 KEQFNSTRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKQPREPOVYL 239

QY 381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLDSDGSFELYSK 438
 DB 240 AHPDELKSKSVTCLVKDFYPPRIEINWQSNQGPDELTKYSTTQAQDSGDSYFLYSK 299

QY 439 LTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPK 476
 DB 300 LSVDRNRWQGTTCGVWHEALHNNHYTKSNVSKNPK 337

RESULT 13
 Q96EYO PRELIMINARY; PRT; 613 AA.
 AC Q96EYO; 01-JUN-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Unknown (protein for MGC:20337).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-CELL;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AAH11857.1; -
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 38.2%; Score 973; DB 4; Length 613;
 Best Local Similarity 38.5%; Pred. No. 2.8e-69;
 Matches 224; Conservative 75; Mismatches 163; Indels 120; Gaps 19;

QY 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGSISGGYGVGWIROP 60
 DB 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGSIS-SYVNSWIROP 59

QY 61 PGKLEWISGFYSSSGNTYNNPSLKSOVITSTDTSKNQFSLKLNMTAATAVYVCVRDR 120
 DB 60 AGKLEWIGRIY-TSGSTYNNPSLKSRVTMSVDTSKNQFSLKLSSTAAATAVYCASOP 118

QY 121 L-FSVYGVYNNWFDVWGPVLTVVSASTKGPSVFLAPSSKSTSG-GTAALGCLVKDY 178
 DB 119 WELPTVGLFY-----WGQGLTVTVSSGASAPTLFPLVSCENSPSDTSVAVGCLAQDF 172

QY 179 PPEPVTYSW--NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNH 233
 DB 173 LPDSITFSWKYKNNKDISSTRGFPVSLR--GGKYAATSQVLLPSKOVNQGTDEHVVKVQH 231

QY 234 KPSN-----TKVDKKAEPK-----CKTHTCP----- 256

DB 232 PNGNKEKNVLPVIAELPPKVSFVPPRDGFGNPKRSLICQATGFSRQIQVSWLREG 291

QY 257 -----PCPAPELLGGPS----- 268

DB 292 KQVSGVTTDQVQAEKESGPTTVKVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQGNASS 351

QY 269 -----VFLFPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

DB 352 MCVDPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTLDTLTYD-SVTISWTRQNGEAVKTH 409

QY 318 TKPREQYNSYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKQPREPO 376

DB 410 TNISESHPNATFSVAGEASICEDDWSNGERTCTVTHDLPSPKQTIISRPKGVALLHRPD 469

QY 377 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLD--SDG 431

DB 470 VYLLPPAREQLNRESATITCLVTGFSPADVFQVMQMGQPLSPEKYVTSAPMPEQAPG 529

QY 432 SFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSL 473

DB 530 RYFAHSILTVEEENWGTETTCVVAHEALPNRVTERTVKDS 571

RESULT 14
 Q9BU10 PRELIMINARY; PRT; 597 AA.
 AC Q9BU10; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 65.3 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPH;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002963; AAH02963.1; -
 DR HSP; P01825; 7FAB.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003600; IG_like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 4.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8PB7E055851 CRC64;

Query Match 37.2%; Score 948.5; DB 4; Length 597;
 Best Local Similarity 37.5%; Pred. No. 2.4e-67;
 Matches 219; Conservative 76; Mismatches 176; Indels 113; Gaps 17;

QY 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGSISGGYGVGWIROP 60
 DB 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGSIS-GYYNSWIROP 59

QY 61 PGKLEWISGFYSSSGNTYNNPSLKSOVITSTDTSKNQFSLKLNMTAATAVYVCVRDR 120
 DB 60 PGKLEWIGEI-NHSGSTYNNPSLKSRVTISVDTSKKQLSLKLSVNAADATVYICARV 118

Qy 121 LFSVGVYNNWFDVWGPGVLVTVSSASTKGPSPVPLAPSSKSTSG-GTAALGCLVNDYF 179
 Db 119 TRASPGLDGRYGMVWGPGVLTVTSSGASAPTLFPLVSCNSPSTSSVAVGCLAQDFL 178
 Qy 180 PEPVTVSW--NSGALTSGVHTFPVAVLQSSGLYSLSVVTPSSSL--GTQTY-ICNVNKH 234
 Db 179 PDSITFSWKYNNSDISSTRGFPVLR--GGKYAATSVLLPSKDVQMGQTDHVVCKVQHP 237
 Qy 235 PSN-----TKVDKKAEPKS-----CDKHTCP----- 256
 Db 238 NGNKEKNVPLVIAELPKVSVFVPPDRGFGNPKRSKLI COATGFSRQIQVSWLRGK 297
 Qy 257 -----PCPAPELLGGPS----- 268
 Db 298 QVGSVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRLTFOQNASSM 357
 Qy 269 -----VFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNAKT 318
 Db 358 CVPDQTAIRVFAIPPS--FASIFLTKSTKLCLVTLDTTYD--SVTISWTRQNGEAVKTHT 415
 Qy 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQP--REPOV 377
 Db 416 NISSEHPNATFSVGEASICEDDNGSERFTCTVHTDLPSPKQTSRPGKVALHRPDV 475
 Qy 378 YTLPPSRDELTA-KNOVSLTCLVKGFPYPSDIAVWESNGQP--ENNYKTPPVLD--SDGS 432
 Db 476 YLLPPAREQLNRESATITCLVTGFSADVFQVMQGPUSPEKYVTSAPMPPEQAPGR 535
 Qy 433 FFYLSKLTVDKSRWQOQNVFSCVMHEALHNHYTKLSLSPGK 476
 Db 536 YFAHSILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK 579

RESULT 15

Q9BQ88 PRELIMINARY; PRT; 597 AA.
 AC Q9BQ88; 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE Unknown (protein for MGC:1905) (protein for MGC:1228).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIMPH;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AAH06180.1; -
 DR EMBL; BC001872; AAH01872.1; -
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 4.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
 SQ SEQUENCE .597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match

37.1%; Score 944.5; DB 4; Length 597;

Best Local Similarity 37.5%; Pred. No. 5.1e-67;
 Matches 219; Conservative 75; Mismatches 177; Indels 113; Gaps 17;

Qy 1 MKHLWFFLLVAAPRWVLSQVLOESGPGLVKPSSETLSITCAVSGSGISGGYGMWIRQP 60
 Db 1 MKHLWFFLLVAAPRWVLSQVLOESGPGLVKPSSETLSITCGVYGSFS-GYYWSWIRQP 59
 Qy 61 PGKLEWITGSYSNGNTYNNPSLKSQVTISTDSKQFSLKNSMTAADTAVYVCVRRR 120
 Db 60 PGKLEWITGEI-NHSGITNYPNPSLKSRTVISTDSKQFSLKNSMTAADTAVYCARVI 118
 Qy 121 LFSVGVYNNWFDVWGPGVLVTVSSASTKGPSPVPLAPSSKSTSG-GTAALGCLVNDYF 179
 Db 119 TRASPGLDGRYGMVWGPGVLTVTSSGASAPTLFPLVSCNSPSTSSVAVGCLAQDFL 178
 Qy 180 PEPVTVSW--NSGALTSGVHTFPVAVLQSSGLYSLSVVTPSSSL--GTQTY-ICNVNKH 234
 Db 179 PDSITFSWKYNNSDISSTRGFPVLR--GGKYAATSVLLPSKDVQMGQTDHVVCKVQHP 237
 Qy 235 PSN-----TKVDKKAEPKS-----CDKHTCP----- 256
 Db 238 NGNKEKNVPLVIAELPKVSVFVPPDRGFGNPKRSKLI COATGFSRQIQVSWLRGK 297
 Qy 257 -----PCPAPELLGGPS----- 268
 Db 298 QVGSVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRLTFOQNASSM 357
 Qy 269 -----VFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNAKT 318
 Db 358 CVPDQTAIRVFAIPPS--FASIFLTKSTKLCLVTLDTTYD--SVTISWTRQNGEAVKTHT 415
 Qy 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQP--REPOV 377
 Db 416 NISSEHPNATFSVGEASICEDDNGSERFTCTVHTDLPSPKQTSRPGKVALHRPDV 475
 Qy 378 YTLPPSRDELTA-KNOVSLTCLVKGFPYPSDIAVWESNGQP--ENNYKTPPVLD--SDGS 432
 Db 476 YLLPPAREQLNRESATITCLVTGFSADVFQVMQGPUSPEKYVTSAPMPPEQAPGR 535
 Qy 433 FFYLSKLTVDKSRWQOQNVFSCVMHEALHNHYTKLSLSPGK 476
 Db 536 YFAHSILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK 579

Search completed: March 29, 2003, 09:14:42

Job time : 45.1716 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 18.2478 Seconds
(without alignments)
1531.829 Million cell updates/sec

Title: US-09-758-173-12

Perfect score: 2549

Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHHYTKSLSLSPCK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
- 7: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pap.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pap.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pap.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pap.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2549	100.0	476	9 US-10-124-905-12	Sequence 12, Appl
2	2549	100.0	476	9 US-09-948-4298-12	Sequence 12, Appl
3	2309	90.6	476	9 US-10-124-905-4	Sequence 4, Appl
4	2309	90.6	476	9 US-09-948-4298-4	Sequence 4, Appl
5	2127	83.4	451	9 US-09-925-179-66	Sequence 66, Appl
6	2126	83.4	451	10 US-09-920-171-18	Sequence 18, Appl
7	2124	83.3	451	9 US-09-925-179-65	Sequence 65, Appl
8	2124	83.3	451	10 US-09-920-171-14	Sequence 14, Appl
9	2124	83.3	451	10 US-09-920-171-16	Sequence 16, Appl
10	2122.5	83.3	450	9 US-09-996-288-218	Sequence 218, Appl
11	2122.5	83.3	450	9 US-09-996-288-250	Sequence 250, Appl
12	2122.5	83.3	450	10 US-09-796-848A-43	Sequence 43, Appl
13	2122.5	83.3	475	10 US-09-740-002-25	Sequence 25, Appl
14	2121	83.2	450	9 US-09-925-179-68	Sequence 68, Appl
15	2120.5	83.2	450	9 US-09-996-288-216	Sequence 216, Appl
16	2120.5	83.2	450	10 US-09-796-848A-49	Sequence 49, Appl
17	2119.5	83.2	450	9 US-09-996-288-222	Sequence 222, Appl
18	2119.5	83.2	450	9 US-09-996-288-224	Sequence 224, Appl
19	2119.5	83.2	450	10 US-09-796-848A-39	Sequence 39, Appl

20	2119.5	83.2	450	10 US-09-796-848A-41	Sequence 41, Appl
21	2118.5	83.1	450	9 US-09-996-288-220	Sequence 220, Appl
22	2118.5	83.1	450	10 US-09-796-848A-37	Sequence 37, Appl
23	2117.5	83.1	450	9 US-09-996-288-226	Sequence 226, Appl
24	2117.5	83.1	450	9 US-09-996-288-252	Sequence 252, Appl
25	2117.5	83.1	450	9 US-09-996-288-254	Sequence 254, Appl
26	2117.5	83.1	450	9 US-09-996-288-256	Sequence 256, Appl
27	2117.5	83.0	450	10 US-09-796-848A-45	Sequence 45, Appl
28	2116.5	83.0	450	9 US-09-996-288-232	Sequence 232, Appl
29	2116.5	83.0	450	9 US-09-996-288-234	Sequence 234, Appl
30	2116.5	83.0	450	9 US-09-996-288-236	Sequence 236, Appl
31	2115.5	83.0	450	9 US-09-996-288-212	Sequence 212, Appl
32	2115.5	83.0	450	9 US-09-996-288-214	Sequence 214, Appl
33	2115.5	83.0	450	10 US-09-796-848A-51	Sequence 51, Appl
34	2115.5	83.0	450	10 US-09-796-848A-53	Sequence 53, Appl
35	2114.5	83.0	450	9 US-09-996-288-228	Sequence 228, Appl
36	2114.5	83.0	450	10 US-09-796-848A-47	Sequence 47, Appl
37	2112.5	82.9	450	9 US-09-996-288-238	Sequence 238, Appl
38	2112.5	82.9	450	9 US-09-996-288-242	Sequence 242, Appl
39	2112.5	82.9	450	9 US-09-996-288-244	Sequence 244, Appl
40	2112.5	82.9	450	9 US-09-996-288-246	Sequence 246, Appl
41	2106.5	82.6	450	9 US-09-996-288-210	Sequence 210, Appl
42	2106.5	82.6	450	9 US-09-996-288-240	Sequence 240, Appl
43	2105.5	82.6	450	9 US-09-996-288-208	Sequence 208, Appl
44	2105.5	82.6	450	9 US-09-996-288-248	Sequence 248, Appl
45	2095	82.2	451	9 US-09-996-288-230	Sequence 230, Appl

ALIGNMENTS

RESULT 1
US-10-124-905-12
; Sequence 12, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-12

Query Match 100.0%; Score 2549; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e-129;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAAPRWVLSQVQLQESGPGLVKPSSETLSLTCAVSGGSIISGGYGMWIRQP 60
DB 1 MKHLWFFLLVAAAPRWVLSQVQLQESGPGLVKPSSETLSLTCAVSGGSIISGGYGMWIRQP 60
QY 61 PGKLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNMTAADTAVYVCVRDR 120
DB 61 PGKLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNMTAADTAVYVCVRDR 120
QY 121 LFSVVGVMYNNWFDVWGPGVLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFP 180
DB 121 LFSVVGVMYNNWFDVWGPGVLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFP 180
QY 181 EPTVSNWNSGALTSQVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKV 240
DB 181 EPTVSNWNSGALTSQVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKV 240
QY 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 361 IEKTIKAKQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTIKAKQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DB 421 KTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 2

US-09-948-429B-12
; Sequence 12, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-948-429B-12

Query Match 100.0%; Score 2549; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e-129;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAAPRWVLSQVQLQESGPGLVKPSSETLSLTCAVSGGSIISGGYGMWIRQP 60
DB 1 MKHLWFFLLVAAAPRWVLSQVQLQESGPGLVKPSSETLSLTCAVSGGSIISGGYGMWIRQP 60
QY 61 PGKLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNMTAADTAVYVCVRDR 120
DB 61 PGKLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNMTAADTAVYVCVRDR 120
QY 121 LFSVVGVMYNNWFDVWGPGVLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFP 180
DB 121 LFSVVGVMYNNWFDVWGPGVLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFP 180
QY 181 EPTVSNWNSGALTSQVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKV 240
DB 181 EPTVSNWNSGALTSQVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKV 240
QY 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 361 IEKTIKAKQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTIKAKQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DB 421 KTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 3

US-10-124-905-4
; Sequence 4, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-4

```

```

Query Match          90.6%; Score 2309; DB 9; Length 476;
Best Local Similarity 91.2%; Pred. No. 1.7e-116;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWLSQVLOESGPGLVKPSFTLSLTCVAVSGGSLSGGYGWCWIRQP 60
DB 1 MKHLWFFLLVAAPRWLSQVLOESGPGLVKPSFTLSLTCVAVSGGSLSGGYGWCWIRQT 60

QY 61 PKGLEWIGTSFYSSSGNTYNNPSLKSQVTISTDTSKNQFSLKLNMTAADTAVYVCVRDR 120
DB 61 PKGLEWIGHIYNGGATTNNPSLKSRTISKDTSKNQFFLNLSVTDADTAVYVCARGP 120

QY 121 LFSVGVGVNNMFDVWGPGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALCLVKDYFP 180
DB 121 RPDCTTCYGGWVDVWGPGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALCLVKDYFP 180

QY 181 EPTVSNWNGALTSQVHTTTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKV 240
DB 181 EPTVSNWNGALTSQVHTTTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKV 240

QY 241 DKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDP 300

QY 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

QY 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

QY 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQOQGVNFSCVMHEALHNHYTQKSLSLSPGK 476
DB 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQOQGVNFSCVMHEALHNHYTQKSLSLSPGK 476

```

```

RESULT 4
US-09-948-429B-4
; Sequence 4, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

```

```

; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-4

```

```

Query Match          90.6%; Score 2309; DB 9; Length 476;
Best Local Similarity 91.2%; Pred. No. 1.7e-116;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWLSQVLOESGPGLVKPSFTLSLTCVAVSGGSLSGGYGWCWIRQP 60
DB 1 MKHLWFFLLVAAPRWLSQVLOESGPGLVKPSFTLSLTCVAVSGGSLSGGYGWCWIRQT 60

QY 61 PKGLEWIGTSFYSSSGNTYNNPSLKSQVTISTDTSKNQFSLKLNMTAADTAVYVCVRDR 120
DB 61 PKGLEWIGHIYNGGATTNNPSLKSRTISKDTSKNQFFLNLSVTDADTAVYVCARGP 120

QY 121 LFSVGVGVNNMFDVWGPGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALCLVKDYFP 180
DB 121 RPDCTTCYGGWVDVWGPGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALCLVKDYFP 180

QY 181 EPTVSNWNGALTSQVHTTTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKV 240
DB 181 EPTVSNWNGALTSQVHTTTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKV 240

QY 241 DKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDP 300

QY 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

QY 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

QY 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQOQGVNFSCVMHEALHNHYTQKSLSLSPGK 476
DB 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQOQGVNFSCVMHEALHNHYTQKSLSLSPGK 476

```

```
; Sequence 18, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

Query Match      83.4%; Score 2126; DB 10; Length 451;
Best Local Similarity 87.6%; Pred.No.9.6e-107;
Matches 401; Conservative 17; Mismatches 32; Indels 8; Gaps

QY    20 QVQLQSGLVKPSFTLSLTCAVGSGSISGGYGWGIQPPKPKGLEWIGSYSSGNTY 79
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     1 EVLVESGGGLVPGGSLRLSCAVSGYSITSGYSWNIRQAPKGLEWVASI-KYSGETK 59
```

Matches	401; Conservative	17; Mismatches	32; Indels	8; Gaps
QY	20	QVQLQESGGGLVQPSSTLSLTCAVSGGSGTSGGNGWIRQPPQKGLIEWGTSGFYSSSGNTY	79	
Db	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMRIQAPQKGLIEWVASI-KYSGETK	59	
QY	80	YNPSLAKSQVITISDTSKNQPSFLKLNLSMTAADTAVYYCVDRDLFSVVGVMVYNNW-FDVWGP	138	
Db	60	YNFSVKGRITISRDDSKNTFYLQMSLRAEDTAVYYCARGSHY-----FGWHFAVMWQ	113	
QY	139	GLVLTVSSASTKGPSVFPLAPSSKSTSGGTGAALGLVQDYFEPPTVTSWNSGALTSGVHT	198	
Db	114	GLTUVTVSSASTKGPSVFPLAPSSKSTSGGTGAALGLVQDYFEPPTVTSWNSGALTSGVHT	173	
QY	199	FPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC	258	
Db	174	FPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC	233	
QY	259	PAPELLGGPSVFLPFPKPKDTLMSRTPETVTCVVDVSHEDPEVKENWYVDGVEVHNAKT	318	
Db	234	PAPELLGGPSVFLPFPKPKDTLMSRTPETVTCVVDVSHEDPEVKENWYVDGVEVHNAKT	293	
QY	319	KPREQYNSTYRVSVLTVTHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVY	378	
Db	294	KPREQYNSTYRVSVLTVTHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVY	353	
QY	379	TLPPSRDELTKNQVSLTCLVKGPYPSDIAVWESNQGPNNTKTPPVLDSDGCSFFLYSK	438	
Db	354	TLPPSRDEMTKNQVSLTCLVKGPYPSDIAVWESNQGPNNTKTPPVLDSDGCSFFLYSK	413	
QY	439	LTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK	476	
Db	414	LTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK	451	

RESULT 7
 US-09-925-179-65
 ; Sequence 65, Application US/09925179
 ; Publication No. US20030044858A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardieu, Paula M.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
 ; FILE REFERENCE: P0718P2C1D1C1US
 ; CURRENT APPLICATION NUMBER: US/09/925,179
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 08/466,163

; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860
 ; PRIOR FILING DATE: 1992-08-14
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 68

```

; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain
US-09-925-179-65

```

Query Match	83.3%	Score 2124;	DB 9;	Length 451;
Best Local Similarity	87.3%	Pred. No. 1.2e-106;		

Query Match	83.3%	Score 2124;	DB 9;	Length 451;
Best Local Similarity	87.3%;	Pred. No. 1.2e-106;		
Matches 400;	Conservative	19;	Mismatches 31;	Indels 8;
				Gaps 3;

Db	60	YNPSKGRITISRDSDSKNTFYIQMSLRADTA	VYVYCAR	GS	HY	-----FGWHFVWGQ	113
QY	139	GVLTVTSSASTKGPSVFPLAPSSKSTSG	SGTAALGCLV	KDYFPEP	VTVSN	SGALTSQVHT	198
Db	114	GTLTVTSSASTKGPSVFPLAPSSKSTSG	TAALGCLV	KDYFPEP	VTVSN	SGALTSQVHT	173

199	QY	FPAVLQSSGLYSLSSVTVVPSSSLGTQTQYICNVNHHKPSNTKYVDKKAPKSPKSCDTHTCPPC	258
174	Db	FPAVLQSSGLYSLSSVTVVPSSSLGTQTQYICNVNHHKPSNTKYVDKKVBPSPKSCDTHTCPPC	233
259	QY	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVNNAKT	318

```
Query Match      83.3%; Score 2124; DB 10; Length 451;
Best Local Similarity 87.3%; Pred. No. 1.2e-106;
Matches 400; Conservative 19; Mismatches 31; Indels 8; Gaps 3;

Qy 20 QVQLQESGPGGLVKKPSETLSLTCAVSGGSIISGGYGMGWIROPKGLGEMIGSFYSSSGNTY 79
Db 1 EVQLVESGGELVQPGSLRLSCLAVSGYSITSGYSNNWIROPKGLGEMIASI-TYDGSN 59
Qy 80 YNPSLKSOVITSDTSKNQFSLKNSMTAADTAVYYCVDRDLFSVGMVYNNW-FDVWGP 138
Db 60 YNPVKGRITTRSDSKNTFLQMNLSRAEDTAVYYCARGSHY-----FGHWFPAVMGQ 113
Qy 139 GVLTVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 198
Db 114 GTLVTVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 173
Qy 199 FPAVLQSSGLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPPC 258
Db 174 FPAVLQSSGLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPPC 233
Qy 259 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 318
Db 234 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 293
Qy 319 KPREBOYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 378
Db 294 KPREBOYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 353
Qy 379 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSK 438
Db 354 TLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSK 413
Qy 439 LTVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 476
Db 414 LTVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 10
US-09-996-288-218
; Sequence 218, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996.288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-218

Query Match      83.3%; Score 2122.5; DB 9; Length 450;
Best Local Similarity 87.3%; Pred. No. 1.5e-106;
Matches 400; Conservative 18; Mismatches 31; Indels 9; Gaps 3;

Qy 20 QVQLQESGPGGLVKKPSETLSLTCAVSGGSIISGGYGMGWIROPKGLGEMIGSFYSSSGNT 78
Db 1 QVTLRESGPALVKPTQTLTLCTSFSGFSLTAGMSVGMIRPPGKALEWLADIW-WDGKK 59
Qy 79 YNPSLKSOVITSDTSKNQFSLKNSMTAADTAVYYCVDRDLFSVGMVYNNWFDVWGP 138
Db 60 HYNFSLKDRLLISKDTSKNQVVLKTNMDPADTATYYCARD-----MIFNWFYDVWGP 112
Qy 139 GVLTVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 198
Db 113 GTTVTVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 172
Qy 199 FPAVLQSSGLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPPC 258
Db 173 FPAVLQSSGLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPPC 232
Qy 259 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 318
Db 233 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 292
Qy 319 KPREBOYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 378
Db 293 KPREBOYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 352
Qy 379 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSK 438
Db 113 GTTVTVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 172
```

```
Qy 139 FPAVLQSSGLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPPC 258
Db 173 FPAVLQSSGLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPPC 232
Qy 259 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 318
Db 233 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 292
Qy 319 KPREBOYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 378
Db 293 KPREBOYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 352
Qy 379 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSK 438
Db 353 TLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSK 412
Qy 439 LTVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 476
Db 413 LTVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 450

RESULT 11
US-09-996-288-250
; Sequence 250, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996.288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 250
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-250

Query Match      83.3%; Score 2122.5; DB 9; Length 450;
Best Local Similarity 87.3%; Pred. No. 1.5e-106;
Matches 400; Conservative 18; Mismatches 31; Indels 9; Gaps 3;

Qy 20 QVQLQESGPGGLVKKPSETLSLTCAVSGGSIISGGYGMGWIROPKGLGEMIGSFYSSSGNT 78
Db 1 QVTLRESGPALVKPTQTLTLCTSFSGFSLTAGMSVGMIRPPGKALEWLADIW-WDGKK 59
Qy 79 YNPSLKSOVITSDTSKNQFSLKNSMTAADTAVYYCVDRDLFSVGMVYNNWFDVWGP 138
Db 60 HYNFSLKDRLLISKDTSKNQVVLKTNMDPADTATYYCARD-----MIFNWFYDVWGP 112
Qy 139 GVLTVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 198
Db 113 GTTVTVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 172
Qy 199 FPAVLQSSGLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPPC 258
Db 173 FPAVLQSSGLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPPC 232
Qy 259 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 318
Db 233 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 292
Qy 319 KPREBOYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 378
Db 293 KPREBOYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 352
Qy 379 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSK 438
Db 113 GTTVTVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 172
```


Db 353 TLPSREEMTKNQVSLTCLVKGFPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSK 412
Qy 439 LTVDKSRWQOGNVFSCSVNHEALHNHYTKQSLSPGK 476
Db 413 LTVDKSRWQOGNVFSCSVNHEALHNHYTKQSLSPGK 450

RESULT 12

US-09-796-848A-43
; Sequence 43, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Heiren
; APPLICANT: Watkins, Jeffery D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; TITLE OF INVENTION: Producing Them
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-43

Query Match 83.3%; Score 2122.5; DB 10; Length 450;
Best Local Similarity 87.3%; Pred. No. 1.5e-106;
Matches 400; Conservative 18; Mismatches 31; Indels 9; Gaps 3;
Qy 20 QVQLQESGPGLVKPSSETLSLTCAVSGGSGIS-GGYGMGWIRPPGKLEWISFYSSSGNT 78
Db 1 QVTLRESGPALVKPTQTTLTCTSGFSLTAGMSVGMIRPPGKALEWADIW-WDGKK 59
Qy 79 YNPSLKSQVLTISTDTSKNQPSLKLNSMTAADTAVYYCVRDLRFVSVGMVYNNHFDVWGP 138
Db 60 HYNPSLKSRLTISKDTSKNQVVKVNNWDPADTATYYCARD-----MIFNWYFDVWQG 112
Qy 139 GVLVTVSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYPPPEPTVTVSWNSGALTSVHT 198
Db 113 GTTVTVVSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYPPPEPTVTVSWNSGALTSVHT 172
Qy 199 PPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKNTKVDKAEKPSKCDKTHTCPPC 258
Db 173 PPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKNTKVDKAEKPSKCDKTHTCPPC 232
Qy 259 PAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 233 PAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 292
Qy 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVY 378
Db 293 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVY 352
Qy 379 TLPSRDELTKNQVSLTCLVKGFPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSK 438
Db 353 TLPSREEMTKNQVSLTCLVKGFPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSK 412
Qy 439 LTVDKSRWQOGNVFSCSVNHEALHNHYTKQSLSPGK 476
Db 413 LTVDKSRWQOGNVFSCSVNHEALHNHYTKQSLSPGK 450

RESULT 13

US-09-740-002-25
; Sequence 25, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-25

Query Match 83.3%; Score 2122.5; DB 10; Length 475;
Best Local Similarity 86.4%; Pred. No. 1.5e-106;
Matches 406; Conservative 20; Mismatches 41; Indels 3; Gaps 3;
Qy 8 LLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSGIS-GYGMGWIRPPGKLE 66
Db 8 LFLVAVATRVLSQVQLQESGPGVYVVKPTETLTCTVSGFSLNPRMGTWIRQPPGKALE 67
Qy 67 WIGSFYSSSGNTYYNPSLKSQVLTISTDTSKNQPSLKLNSMTAADTAVYYCVRDLRFVWVG 126
Db 68 WLGNIFSGSDEKS-FPSLSKSLRLTTSQDTSRSQVVLSTLVNVDVDTATYYCARVGLYD-IN 125
Qy 127 MYNNWFDVWGPVLTVTVSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYPPPEPTVVS 186
Db 126 AYLYLYLDYWGQGTFLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYPPPEPTVVS 185
Qy 187 WNSGALTSGVHTTTPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKNTKVDKKAEP 246
Db 186 WNSGALTSGVHTTTPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKNTKVDKKAEP 245
Qy 247 KSCDKTHTCPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 306
Db 246 KSCDKTHTCPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 305
Qy 307 YVDGVEVHNAKTTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 366
Db 306 YVDGVEVHNAKTTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 365
Qy 367 KAKGQPREPOVYTLPSRDELTKNQVSLTCLVKGFPDIAVEWESNGQPENNYKTTTPV 426
Db 366 KAKGQPREPOVYTLPSRDELTKNQVSLTCLVKGFPDIAVEWESNGQPENNYKTTTPV 425
Qy 427 LDSGSEFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTKQSLSPGK 476
Db 426 LDSGSEFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTKQSLSPGK 475

RESULT 14

US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044859A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163

; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68

; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table

US-09-928-179-68

Query Match 83.2%; Score 2121; DB 9; Length 451;
Best Local Similarity 87.6%; Pred. No. 1.8e-106;
Matches 401; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

QY 20 QVQLQESGPGLVKPSVETLSITCAVSGSISGGYGMWIRPPGKGLWIGSFYSSSGNTY 79
Db 1 EVLVESGGGLVPGGSLRUSCAVGSYISITSGYSWIRAPGKGLWIGSI-RYDGSIN 59

QY 80 YNPGLSKQVITSTDTSKNQPSLKLNSMTAADTAVYICVDRDLFSVGMVYNNW-FDYWGP 138
Db 60 YNDSLKGRITVSRDSDSKNTFYQLNSARAEDTAVYICARGSHY-----FGHWFAVWQG 113

QY 139 GVLVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
Db 114 GVLVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173

QY 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKPSNTKVDKABPKSCDKTHTCPPC 258
Db 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKPSNTKVDKABPKSCDKTHTCPPC 233

QY 259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 234 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293

QY 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353

QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYISK 438
Db 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYISK 413

QY 439 LTVDKSRWQOGNVPFSCSVMEALHNNHYTQKSLSLSPGK 476
Db 414 LTVDKSRWQOGNVPFSCSVMEALHNNHYTQKSLSLSPGK 451

RESULT 15

US-09-996-288-216
; Sequence 216; Application US/09996288
; Patent No. US2002017128A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 216

; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-996-288-216

Query Match 83.2%; Score 2120.5; DB 9; Length 450;
Best Local Similarity 87.3%; Pred. No. 1.9e-106;
Matches 400; Conservative 18; Mismatches 31; Indels 9; Gaps 3;

QY 20 QVQLQESGPGLVKPSVETLSITCAVSGSISGGYGMWIRPPGKGLWIGSFYSSSGNT 78
Db 1 QVTLRESGPAVKPTQTLTCTCFSGFSLSPGMSVGVIRPPGKALEWLAIDW-WDGKK 59

QY 79 YNPGLSKQVITSTDTSKNQPSLKLNSMTAADTAVYICVDRDLFSVGMVYNNWFDVWGP 138
Db 60 HYNPLSKDLRLTISKDTSKNQVVLKTNMDPADTATYICARD-----MIFNWIYEDVWGO 112

QY 139 GVLVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
Db 113 GTTVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 172

QY 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKPSNTKVDKABPKSCDKTHTCPPC 258
Db 173 FPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKPSNTKVDKABPKSCDKTHTCPPC 232

QY 259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 233 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 292

QY 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db 293 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 352

QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYISK 438
Db 353 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYISK 412

QY 439 LTVDKSRWQOGNVPFSCSVMEALHNNHYTQKSLSLSPGK 476
Db 413 LTVDKSRWQOGNVPFSCSVMEALHNNHYTQKSLSLSPGK 450

Search completed: March 29, 2003, 09:38:44
Job time : 19.2478 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:05 ; Search time 4490.25 Seconds
(without alignments)
9274.790 Million cell updates/sec

Title: US-09-758-173-11
Perfect score: 1431
Sequence: 1 ATGAACACCTGTGTTCTT.....CCTGTCTCGGTAATGA 1431

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1431	100.0	1431	6	AR108867	AR108867 Sequence
2	1315.8	91.9	1431	6	AR108863	AR108863 Sequence
3	1276.4	89.2	1567	6	AR135359	AR135359 Sequence
4	1261.2	88.1	1431	6	E10697	E10697 cDNA encodi
5	1256.8	87.8	1594	9	AK057754	AK057754 Homo sapi
6	1251.6	87.5	1596	9	AK098516	AK098516 Homo sapi
7	1236.8	86.4	1589	9	AK057775	AK057775 Homo sapi
8	1224.8	85.6	1418	6	A49389	A49389 Sequence 7
9	1213.6	84.8	1418	6	AR176296	AR176296 Sequence
10	1182.8	82.7	1566	9	AK097365	AK097365 Homo sapi
11	1181	82.5	1404	6	AR135375	AR135375 Sequence
12	1177.8	82.3	1404	6	AR135377	AR135377 Sequence
13	1176.2	82.2	1404	6	AR135376	AR135376 Sequence
14	1142.6	79.8	1630	9	BC024289	BC024289 Homo sapi
15	1134.8	79.3	1428	6	AR031184	AR031184 Sequence
16	1134.8	79.3	1428	6	AR042589	AR042589 Sequence
17	1134.8	79.3	1428	6	AR059282	AR059282 Sequence
18	1134.8	79.3	1428	6	AR076260	AR076260 Sequence
19	1134	79.2	1430	6	AX419496	AX419496 Sequence
20	1134	79.2	1673	9	HSIGGLH	Y14737 Homo sapien
21	1133.8	79.2	1507	9	BD000501	BD000501 Process f
22	1131.8	79.1	1679	9	BC018747	BC018747 Homo sapi
23	1130.6	79.0	1633	9	AK097859	AK097859 Homo sapi
24	1125.2	78.6	1428	6	AR031186	AR031186 Sequence
25	1125.2	78.6	1428	6	AR042591	AR042591 Sequence
26	1125.2	78.6	1428	6	AR059284	AR059284 Sequence
27	1125.2	78.6	1428	6	AR076262	AR076262 Sequence
28	1122.8	78.5	1599	6	AX330501	AX330501 Sequence
29	1122.8	78.5	1599	6	AX333307	AX333307 Sequence
30	1122.8	78.5	1599	6	AX334122	AX334122 Sequence
31	1122.8	78.5	1599	9	HUMIGHPEAH	MB7789 Human (hybr
32	1122.8	78.5	3143	9	BC019046	BC019046 Homo sapi
33	1122	78.4	1990	9	AK098817	AK098817 Homo sapi
34	1121.2	78.4	1549	6	A21385	A21385 Plasmid DNA
35	1121.2	78.4	1617	6	A29585	A29585 H.sapiens c
36	1116.2	78.0	1624	9	HSIGGLKH	Y14735 Homo sapien
37	1115.6	78.0	1359	9	MACIGHVCDR	L13307 Macaca fasc
38	1114	77.8	1631	9	AK097010	AK097010 Homo sapi
39	1112.4	77.7	1437	6	AR108865	AR108865 Sequence
40	1112	77.7	1656	9	BC006402	BC006402 Homo sapi
41	1108.2	77.4	1628	9	AK097361	AK097361 Homo sapi
42	1107.6	77.4	1633	9	AK097367	AK097367 Homo sapi
43	1106.2	77.3	1341	6	A07562	A07562 DNA sequenc
44	1103.8	77.1	1668	9	BC026038	BC026038 Homo sapi
45	1102.2	77.0	6557	6	I26929	I26929 Sequence 3

ALIGNMENTS

RESULT 1	AR108867	Sequence 11 from patent US 6113898.	1431 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR108867	Sequence 11 from patent US 6113898.				
DEFINITION	AR108867					
ACCESSION	AR108867					
VERSION	AR108867.1	GI:12825143				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1431)					
AUTHORS	Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.					
TITLE	Human B7.1-specific primatized antibodies and transfectomas					
JOURNAL	Patent: US 6113898-A 11 05-SEP-2000;					

FEATURES		Location/Qualifiers	
source	1..1431		
BASE COUNT	319 a 462 c 385 g 265 t		
ORIGIN			
Query Match	100.0%;	Score 1431;	DB 6; Length 1431;
Best Local Similarity	100.0%;	Pred. No. 4.5e-279;	
Matches 1431;	Conservative 0;	Mismatches 0;	Indels 0; Gaps
Qy	1	ATGAACACCTGTGGTCTCTCCCTCCTCGTGGCAGCTCCAGATGGTCTGCTGCCAG	60
Db	1	ATGAACAACCTGTGGTCTCTCCCTCCTCGTGGCAGCTCCAGATGGTCTGCTGCCAG	60
Qy	61	GTGCAGCTCAGAGATCGGGCCAGGACTTGTGAAGCCTTCGGAGACCTGTGCTCCCTCAC	120
Db	61	GTGCAGCTCAGAGATCGGGCCAGGACTTGTGAAGCCTTCGGAGACCTGTGCTCCCTCAC	120
Qy	121	TGCGGTGTCCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCGCCAGGCC	180
Db	121	TGCGGTGTCCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCGCCAGGCC	180
Qy	181	CCAGGGAAGGGCTGAGTGGATGGAGATTCTATAGTAGTAGTGGGAACCACTTACTAC	240
Db	181	CCAGGGAAGGGCTGAGTGGATGGAGATTCTATAGTAGTAGTGGGAACCACTTACTAC	240
Qy	241	AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAAGAACAGATTCTCC	300
Db	241	AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAAGAACAGATTCTCC	300
Qy	301	CTGAAGCTGAACCTCTATACCGCGCGGACACGGCCGCTGTATTACTGTGTGAGAGATCGT	360
Db	301	CTGAAGCTGAACCTCTATACCGCGCGGACACGGCCGCTGTATTACTGTGTGAGAGATCGT	360
Qy	361	CTTTTTCAGTTGTTGGAAATGGTTTACAACTGGTTCGATGTCTGGGGCCGGGAGTC	420
Db	361	CTTTTTCAGTTGTTGGAAATGGTTTACAACTGGTTCGATGTCTGGGGCCGGGAGTC	420
Qy	421	CTGGTCACCGTCTCCTCAGCTAGCACCAAGGCCCATCGGTCCTCCCTCGSCACCTCC	480
Db	421	CTGGTCACCGTCTCCTCAGCTAGCACCAAGGCCCATCGGTCCTCCCTCGSCACCTCC	480
Qy	481	TCCAAAGACACCTCTGGGGACACAGCGCCCTGGGCTGCCCTGCTCAAGACTACTTCCCC	540
Db	481	TCCAAAGACACCTCTGGGGACACAGCGCCCTGGGCTGCCCTGCTCAAGACTACTTCCCC	540
Qy	541	GAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACACAGGGCGTGGACACCTTCCCG	600
Db	541	GAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACACAGGGCGTGGACACCTTCCCG	600
Qy	601	GCTGTCTCAGTTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTTCCACG	660
Db	601	GCTGTCTCAGTTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTTCCACG	660
Qy	661	AGCTTGGGACCCAGACCTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTG	720
Db	661	AGCTTGGGACCCAGACCTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTG	720
Qy	721	GACAGAAAGCAGAGCCCCAAATCTTTGTGACAAAACCTCACATGCCACCGTGCCAGCA	780
Db	721	GACAGAAAGCAGAGCCCCAAATCTTTGTGACAAAACCTCACATGCCACCGTGCCAGCA	780
Qy	781	CCTGAATCTCTGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCTTC	840
Db	781	CCTGAATCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCTTC	840
Qy	841	ATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTT	900
Db	841	ATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTT	900
Qy	901	GAGGTCAAGTTCAACTGGTACCTGGGACCGGTGGAGTGCATAATGCCAAGAACGCG	960
Db	901	GAGGTCAAGTTCAACTGGTACCTGGGACCGGTGGAGTGCATAATGCCAAGAACGCG	960

QY	961	CGGGAGGACAGTACAAACAGCAGCTACCGTGTGGTACCGTCTCTACCGTCTGTGCACAG	1020
Db	961	CGGGAGGACAGTACAAACAGCAGCTACCGTGTGGTACCGTCTCTACCGTCTGTGCACAG	1020
QY	1021	GACTGCTGAATCGCAAGGAGTCAAGTGCAGGCTCTCCAAACAAAGCCCTCCAGAGCCCC	1080
Db	1021	GACTGCTGAATCGCAAGGAGTCAAGTGCAGGCTCTCCAAACAAAGCCCTCCAGAGCCCC	1080
QY	1081	ATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAAACACAGGTGTACACCGTG	1140
Db	1081	ATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAGAACACAGGTGTACACCGTG	1140
QY	1141	CCCCATCCCGGATGAGCTGACAAAGAACAGGTACAGCTGACCTGCTGTGTTCAAGGC	1200
Db	1141	CCCCCATCCCGGATGAGCTGACCAAGAACAGGTACAGCTGACCTGCTGTGTTCAAGGC	1200
QY	1201	TTCTATCCAGCAGCATCGCGTGGAGTGGGAGAGCAATGGGAGCCCGAGAAACACTAC	1260
Db	1201	TTCTATCCAGCAGCATCGCGTGGAGTGGGAGAGCAATGGGAGCCCGAGAGAACACTAC	1260
QY	1261	AAGACACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCAC	1320
Db	1261	AAGACACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCAC	1320
QY	1321	GTGGACAAGAGAGTGGGAGAGGAGCACTTCTCTATGCTCCGTGATGATGAGGCT	1380
Db	1321	GTGGACAAGAGAGTGGGAGAGGAGCACTTCTCTATGCTCCGTGATGATGAGGCT	1380
QY	1381	CTGCACAACCACTACACGAGAGAGCTCTCCCTGTCTCCGGTAAATGA	1431
Db	1381	CTGCACAACCACTACACGAGAGAGCTCTCCCTGTCTCCGGTAAATGA	1431
RESULT 2			
LOCUS	AR108863	1431 bp	DNA linear PAT 14-FEB-2001
DEFINITION	Sequence 3 from patent US 6113898.		
ACCESSION	AR108863		
VERSION	AR108863.1	GI:12825139	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1431)		
AUTHORS	Anderson, D.R., Brams, P., Hanna, N., Shetowsky, W.S. and Heard, C.		
TITLE	Human B7.1-specific primatized antibodies and antibodies and transfectomas		
JOURNAL	expressing said antibodies		
FEATURES	Patent: US 6113898-A 3 05-SEP-2000;		
source	Location/Qualifiers		
BASE COUNT	322 a 469 c 380 g 260 t		
ORIGIN	/organism="unknown"		
Query Match	91.9%; Score 1315.8; DB 6; Length 1431;		
Best Local Similarity	95.0%; Pred. No. 8.5e-256;		
Matches 1359;	Conservative 0; Mismatches 72; Indels 0; Gaps 0;		
QY	1	ATGAACACCTGTGGTTCTTCTCTCTCTGTGGGAGCTCCAGATGGGTCTGTGCCAG	60
Db	1	ATGAACACCTGTGGTTCTTCTCTCTCTGTGGGAGCTCCAGATGGGTCTGTGCCAG	60
QY	61	GTGAGCTGAGGAGTCGGGCCAGGACTGTGAAGCTTCGGAGACCTGTCCCTCAC	120
Db	61	GTGAGCTGAGGAGTCGGGCCAGGACTTCGAGCCCTTCGAGACCTGTCCGAC	120
QY	121	TGCGCTGTCTGTGGCTCCATCAGCGGTGTTATGCTGGGCTGGATCCGCCAGCC	180
Db	121	TGCGTGTCTGTGGCTCCATCAGCGGTACTACTGACCTGGATCCGCCAGCC	180
QY	181	CCAGGGAAGGGGCTGGAGTGGATGGAGTTTCTATAGTAGTGGGAACACTACTAC	240

Db	181	CTAGGAGGGAGCTGGAGTGGAATGGCCATATTTATGGTAAATGGTGCAGCACCAACTAC	241
Qy	241	AACCCCTCCCTCAAGAGTCAAGTCACCAATTTCAACAGACAGTCCAAAGAACAGATTCTCC	300
Db	241	AATCCCTCCCTCAAGAGTCGAGTCACCAATTTCAAAGACAGTCCAAAGAACAGATTCTTC	300
Qy	301	CTGAGCTGAATCTATGAACCGCCCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT	360
Db	301	CTGAATTTGAATTTCTGTACCGACCGGACACGGCCGTCTATTACTGTGTGAGAGGCCCT	360
Qy	361	CTTTTTTCAGTTGTTGGAATGGTTTCAACAACATCTGGTTCGATGTCGTGGGCCCGGAGTC	420
Db	361	CGCCCTGATTGCAACAACATTTGATGCGCGCTGGGTTCGATGTCGTGGGCCCGGAGAC	420
Qy	421	CTGGTCAACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCTG3CACCTCC	480
Db	421	CTGGTCAACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCTG3CACCTCC	480
Qy	481	TCCAAGAGCACCTCTGGGGGACAGCGGCCCTTGGGCTGCTGGTCAAGGACTACTTCCCC	540
Db	481	TCCAAGAGCACCTCTGGGGGACAGCGGCCCTTGGGCTGCTGGTCAAGGACTACTTCCCC	540
Qy	541	GAACCGGTACGGTGTCTGCGAACTCAGGCGCCCTGACCGGGGTGCACACCTTCCCG	600
Db	541	GAACCGGTACGGTGTCTGCGAACTCAGGCGCCCTGACCGGGGTGCACACCTTCCCG	600
Qy	601	GCTGTCTCAGTCTCAGGACTCTACTCCCTCAGACGCTGGTGACCGTCCCTCCAGC	660
Db	601	GCTGTCTCAGTCTCAGGACTCTACTCCCTCAGACGCTGGTGACCGTCCCTCCAGC	660
Qy	661	AGCTTGGGACCCAGACCTACATCTGCAACGTTGAATCACAAGCCAGCAACCAAGGTG	720
Db	661	AGCTTGGGACCCAGACCTACATCTGCAACGTTGAATCACAAGCCAGCAACCAAGGTG	720
Qy	721	GACAAGAAAGCAGAGCCCAATCTGTGACAAACTCACAATGCCACCGTGCCACGCA	780
Db	721	GACAAGAAAGCAGAGCCCAATCTGTGACAAACTCACAATGCCACCGTGCCACGCA	780
Qy	781	CTGAACTCTCTGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTC	840
Db	781	CCTGAACTCTCTGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTC	840
Qy	841	ATGATCTCCGGACCCCTGAGTCAATGCGTGGTGGTGAAGTGCACGACGACACCT	900
Db	841	ATGATCTCCGGACCCCTGAGTCAATGCGTGGTGGTGAAGTGCACGACGACACCT	900
Qy	901	GAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGTGCATTAATGCCAAGACAAAGCCG	960
Db	901	GAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGTGCATTAATGCCAAGACAAAGCCG	960
Qy	961	CGGAGGAGCAGTACAAAGCAGTACCGTGTGGTGGTGGTGAAGTGCACGACGAC	1020
Db	961	CGGAGGAGCAGTACAAAGCAGTACCGTGTGGTGGTGGTGAAGTGCACGACGAC	1020
Qy	1021	GACTGGCTGAATGGCAGAGTACAAGTGAAGGTCTTCAAAGAGCCCTCCAGACCCC	1080
Db	1021	GACTGGCTGAATGGCAGAGTACAAGTGAAGGTCTTCAAAGAGCCCTCCAGACCCC	1080
Qy	1081	ATCGAGAAAACCATCTCCAAAGCAAAAGGCGACCCCGAGAACCAAGTGTATACCCCTG	1140
Db	1081	ATCGAGAAAACCATCTCCAAAGCAAAAGGCGACCCCGAGAACCAAGTGTATACCCCTG	1140
Qy	1141	CCCCATCCCGGATGAGTGACCAAGAACAGGTGAGCTGACCTGACCTGGTCAAGGC	1200
Db	1141	CCCCATCCCGGATGAGTGACCAAGAACAGGTGAGCTGACCTGACCTGGTCAAGGC	1200
Qy	1201	TTCTATCCAGCGCATCGCCGTGGAGTGGGAGCAATGGGAGCCGGAGAACACTAC	1260
Db	1201	TTCTATCCAGCGCATCGCCGTGGAGTGGGAGCAATGGGAGCCGGAGAACACTAC	1260
Qy	1261	AAGACACGCTCCCGTGTGACTCCGAGCTCCTTCTTCTTACAGCAAGCTCACC	1320
Db	1261	AAGACACGCTCCCGTGTGACTCCGAGCTCCTTCTTCTTACAGCAAGCTCACC	1320

QY	1321	GTGACAAGACGACGGTGCACAGCGGAACGCTCTTCATGCTCCGTCATGAGGCT	1380
Db	1321	GTGACAAGACGACGGTGCACAGCGGAACGCTCTTCATGCTCCGTCATGAGGCT	1380
QY	1381	CTGCACAACCACTACACGACAGAAGCCTCTCCCTGTCTCCGGGTAATGA	1431
Db	1381	CTGCACAACCACTACACGACAGAAGCCTCTCCCTGTCTCCGGGTAATGA	1431
 RESULT 3 ARL135359			
LOCUS ARL135359 1567 bp DNA linear PAT 16-JUN-2001			
DEFINITION Sequence 17 from patent US 6135941.			
ACCESSION ARL135359			
VERSION ARL135359.1 GI:14476031			
KEYWORDS Unknown.			
SOURCE Unknown.			
ORGANISM Unknown.			
Unclassified.			
1 (bases 1 to 1567)			
REFERENCE Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,H., Au-Young,J.,			
AUTHORS Corley,N.C., Guegler,K.J. and Baughn,M.R.			
TITLE Human immune system associated molecules			
JOURNAL Patent: US 6135941-A 17 24-OCT-2000;			
FEATURES Location/Qualifiers			
source 1..1567			
BASE COUNT 346 a 503 c 428 g 289 t 1 others			
ORIGIN /organism="unknown"			
Query Match 89.2%; Score 1276.4; DB 6; Length 1567;			
Best Local Similarity 94.7%; Pred. No. 7.8e-248;			
Matches 1358; Conservative 0; Mismatches 61; Indels 15; Gaps 3;			
QY	1	ATGAACACCTGTGGTTCTTCTCCTCCTCTGTGTGGCAGCTCCCAGATGGCTCCTGTGCCAG	60
Db	78	ATGAACACCTGTGGTTCTTCTCCTCCTGTGTGGCAGCTCCCAGATGGCTCCTGTGCCAG	137
QY	61	GTCGAGCTCAGAGTGCGGCCACGACTGCTGAAGCCTTCGGAGACCCTGTCCCTCAC	120
Db	138	GTCGAGCTCAGAGTGCGGCCACGACTGCTGAAGCCTTCGGAGACCCTGTCCCTCAC	197
QY	121	TSCGCTGTCTCTGTGGCTCCATC---AGCGGTGGTTATGGCTGGGCTGGATCCGCCAG	177
Db	198	TGCGTGTCTCTGTGGCTCCATCAGTAGTGGTGGTTACTACTGGAGCTGGATCCGCCAG	257
QY	178	CCCCAGGAAGGGGCTGGAGTGGATTGGAGATTTCTATAGTAGTGGGAACACCTAC	237
Db	258	CCCCAGGAAGGGGCTGGAGTGGATTGGGTACATCTA--TTACAGTGGGAGACCCCTC	314
QY	238	TACAAACCTCCCTCAAGAGTCAAGTCAACATTTCAAACAGACAGTCCAAGAACCATGTC	297
Db	315	TACAAACCTCCCTCAAGAGTCAAGTCAACATATCAGTAGACACGTCCTCAAGAACCATGTC	374
QY	298	TCCCTGAAGCTCAACTCTATGACCGCGCGAGACGCGCGGTATTACTGTGTGAGAGAT	357
Db	375	TCCCTGAAGCTGAGCTCTGTGACTGCGCGAGACACGCGCGGTATTACTGTGTGAGAGAT	433
QY	358	CGTCTTTTTTCAAGTTGTTGGAAATGGTTTACAACAACTGGTTTCGATGTCTGGGGCCCGGGA	417
Db	434	-----TGACCTAGGTTTAAAGGGGGGGAACCTACGATATGGAGCTCTGGGCCACGGA	485
QY	418	GTCCTGGTCAACGCTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCTGGACCC	477
Db	486	ACCTCTGGTCAACGCTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCTGGACCC	545
QY	478	TCCTCCAAAGACACCTCTGGGGGACAGCGGCCCTTGGGCTGCCTGAGGACTACTTTC	537
Db	546	TCCTCCAAAGACACCTCTGGGGGACAGCGGCCCTTGGGCTGCCTGAGGACTACTTTC	605
QY	538	CCCGAAACCGGTGACGGTGTGTGGAACTCAGGCGCCCTGACACAGCGCGGTGCACACCTTC	597

```
Db 606 CCGAACCGGTGACGTGTCTGTGAACCTCAGGCGCCCTGACAGCGGGTGCACACCTTC 665
Qy 598 CCGGTGTCTCTACAGTCTCTCAGGACTTACTCTCTCAGCAGCGTGTGACCGTGCCTCC 657
Db 666 CCGGTGTCTCTACAGTCTCTCAGGACTTACTCTCTCAGCAGCGTGTGACCGTGCCTCC 725
Qy 658 AGCAGTTGGGACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAACCAAG 717
Db 726 AGCAGTTGGGACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAACCAAG 785
Qy 718 GTGGACAAGAACAGAGCCCAATCTGTGACAAAACCTCAACATGCCACCGTGCCTCA 777
Db 786 GTGGACAAGAGTTGAGCCCAATCTGTGACAAAACCTCAACATGCCACCGTGCCTCA 845
Qy 778 GCACCTGAACCTCTGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 837
Db 846 GCACCTGAACCTCTGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 905
Qy 838 CTCATGATCTCCGGACCCCTGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 897
Db 906 CTCATGATCTCCGGACCCCTGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 965
Qy 898 CTGAGGTCAAGTTCAACTGCTGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 957
Db 966 CTGAGGTCAAGTTCAACTGCTGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1025
Qy 958 CCGCGGAGGAGCAGTACACAGCAGTACCGTGTGTGAGTTCAGTTCAGTTCAGTTCAGT 1017
Db 1026 CCGCGGAGGAGCAGTACACAGCAGTACCGTGTGTGAGTTCAGTTCAGTTCAGTTCAGT 1085
Qy 1018 CAGGACTGGTGAATGCGAAGGAGTACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1077
Db 1086 CAGGACTGGTGAATGCGAAGGAGTACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1145
Qy 1078 CCATGAGAAACCATCTCAAGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1137
Db 1146 CCATGAGAAACCATCTCAAGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1205
Qy 1138 CTGCCCCCATCCCGGATGAGTCAAGCAAGAACAGGTCAGGTCAGGTCAGGTCAGGTCAGG 1197
Db 1206 CTGCCCCCATCCCGGAGGAGTCAAGCAAGAACAGGTCAGGTCAGGTCAGGTCAGGTCAGG 1265
Qy 1198 GGTCTTATCCAGCAGCATCGCGTGTGAGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1257
Db 1266 GGTCTTATCCAGCAGCATCGCGTGTGAGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1325
Qy 1258 TACAAGCACCGCTCCCGTGTGAGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1317
Db 1326 TACAAGCACCGCTCCCGTGTGAGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1385
Qy 1318 ACCGTGGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377
Db 1386 ACCGTGGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1445
Qy 1378 GCTCTGCAACACCACTACACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1431
Db 1446 GCTCTGCAACACCACTACACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1499

RESULT 4
LOCUS E10697
DEFINITION cDNA encoding heavy chain of human monoclonal antibody against
human cytomegalovirus 65KD antigen.
ACCESSION E10697
VERSION E10697.1 GI:22027790
KEYWORDS JP 1996038178-A/20.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Tanaka,S., Niwa,H. and Tanaka,H.
```

```
TITLE HUMAN MONOCLONAL ANTIBODY AND PRODUCTION THEREOF, AND PRIMER FOR
JOURNAL CLONING OF GENE THEREOF
COMMENT Patent: JP 1996038178-A 20 13-FEB-1996;
TANAKA HIDEYUKI, NISSHINBO IND INC
OS Homo sapiens (human)
PN JP 1996038178-A/20
PD 13-FEB-1996
PF 20-FEB-1995 JP 1995030742
PR 18-FEB-1994 JP 94P 21628
PI TANAKA SHIGEKI, NIWA HIRONUKI, TANAKA HIDEYUKI PC
C12N15/09,C07K16/08,C12N1/21,C12N15/02,C12P21/08,C12Q1/68,PC
G01N33/53,
PC G01N33/531,G01N33/577,(C12N1/21,C12R1:19),(C12P21/08,PC
C12R1:19);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1..1431
/organism="Homo sapiens"
/contig="B cell"
FT sig_peptide 1..57
/product="signal peptide of heavy chain of FT
human monoclonal
antibody against human cytomegalovirus 65kd
antigen"
FT mat_peptide 58..1425
/product="heavy chain of human monoclonal FT
antibody against
human cytomegalovirus 65kd antigen" FT CDS
FT 1..1428
/product="heavy chain of human monoclonal FT
antibody against
human cytomegalovirus 65kd antigen" FT 3'UTR
FEATURES
source
1429..>1431.
Location/Qualifiers
1..1431
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 314 a 475 c 379 g 263 t
ORIGIN
Query Match 88.1%; Score 1261.2; DB 6; Length 1431;
Best Local Similarity 93.9%; Pred. No. 9.2e-245;
Matches 1347; Conservative 0; Mismatches 78; Indels 9; Gaps 3;
Qy 1 ATGAACACCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60
Db 1 ATGAAGCATCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60
Qy 61 GTCAGCTGCAGGAGTCCGGCCAGGAGTGTGAAGCTTCGGAGACCTTCGGAGACCTTCCTCTCACC 120
Db 61 CTCAGCTGCAGGAGTCCGGCCAGGAGTGTGAAGCTTCGGAGACCTTCCTCTCACC 120
Qy 121 TGGCTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 177
Db 121 TGCACCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Qy 178 CCCCCAGGGAAGGGCTTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 237
Db 181 CCCCCAGGGAAGGGCTTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 237
Qy 238 TACAACCCCTCTCTCAAGAGTCAAGTCAACATTTTCAACAGACACACGCTCCNAGAACCAAGTTC 297
Db 238 TACAACCCCTCTCTCAAGAGTCAAGTCAACATTTTCAACAGACACACGCTCCNAGAACCAAGTTC 297
Qy 298 TCCTCAAGCTGAACCTCTATGACCGCCGAGACACGCGCGTGTATTACTGTGTGAGAGAT 357
Db 298 TCCTCAAGCTGAACCTCTATGACCGCCGAGACACGCGCGTGTATTACTGTGTGAGAGAT 357
Qy 358 CGTCTTTTTCAGTGTGTGGAAATGGTTTACAACAACTCGGTTCGATGTCTGGGGGCCCGGGA 417
```

Db	358	TCGCCGCAGTATTACGATCTTTTGGCTT---CCCTTCCTCATATCGGGCCAGGGA	414
Qy	418	GTCTGTGTACCGTCTCCTCAGCTAGCACCAAGGCCCATCGTGTTCCTCCCTTGCAACC	477
Db	415		
Qy	478	TCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGAGCTACTTC	537
Db	475	TCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCCTGGTCAAGAGCTACTTC	534
Qy	538	CCCGAACCGGTGACGGTGTGCTGGAATCTAGCGCCCTGTACCAAGCGCGTGCACACCTTC	597
Db	535	CCCGAACCGGTGACGGTGTGCTGGAATCTAGCGCCCTGTACCAAGCGCGTGCACACCTTC	594
Qy	598	CCGGCTGTCTACAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTGCCTCC	657
Db	595	CCGGCTGTCTACAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTGCCTCC	654
Qy	658	AGCAGCTTGGGCAACCCAGACTTACATCTGCAACGTGTAATCAACGCCACGCAACCAAG	717
Db	655	AGCAGCTTGGGCAACCCAGACTTACATCTGCAACGTGTAATCAACGCCACGCAACCAAG	714
Qy	718	GTGGACAAGAAAGCAGAGCCCAATCTGTGACAAAATCACAACATGCCACCGTGCCTCA	777
Db	715	GTGGACAAGAAATTTGAGCCCAATCTGTGACAAAATCACAACATGCCACCGTGCCTCA	774
Qy	778	GCACCTGAACTCTCTGGGGGACCGTCACTTCTCTTCTCCCCCAAAACCCAGGACACC	837
Db	775	GCACCTGAACTCTCTGGGGGACCGTCACTTCTCTTCTCCCCCAAAACCCAGGACACC	834
Qy	838	CTCATGATCTCCGGACCCCTGAGGTCAATGCGTGTGTGTGACGTGAGCCACGAAAGAC	897
Db	835	CTCATGATCTCCGGACCCCTGAGGTCAATGCGTGTGTGTGACGTGAGCCACGAAAGAC	894
Qy	898	CCTGAGGTCAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATATGCCAAGACAAG	957
Db	895	CCTGAGGTCAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATATGCCAAGACAAG	954
Qy	958	CCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGTGTGACGTCTCAACCGTCTGCAC	1017
Db	955	CCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGTGTGACGTCTCAACCGTCTGCAC	1014
Qy	1018	CAGGACTGTGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCAACAAAGCCCTCCAGCC	1077
Db	1015	CAGGACTGTGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCAACAAAGCCCTCCAGCC	1074
Qy	1078	CCCATCGAGAAAACCATCTCCAAAGCCAAAGGCAGCCCGCAGAACCCACAGGTGTACAC	1137
Db	1075	CCCATCGAGAAAACCATCTCCAAAGCCAAAGGCAGCCCGCAGAACCCACAGGTGTACAC	1134
Qy	1138	CTGCCCCCATCCCGGATCAGCTGACCAAGAACAGGTGACCTGTGCTGCTGCTGCTCAAA	1197
Db	1135	CTGCCCCCATCCCGGATCAGCTGACCAAGAACAGGTGACCTGTGCTGCTGCTGCTCAAA	1194
Qy	1198	GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACCAAC	1257
Db	1195	GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGAGCGGAGAACCAAC	1254
Qy	1258	TACAGACCAACCGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGAAAGCTC	1317
Db	1255	TACAGACCAACCGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGAAAGCTC	1314
Qy	1318	ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGTGATGCATGAG	1377
Db	1315	ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGTGATGCATGAG	1374
Qy	1378	GCTCTGCACAACCATCTACAGCAGAAAGCCTCTCCCTGTCTCCGGTAAATGA	1431
Db	1375	GCTCTGCACAACCATCTACAGCAGAAAGCCTCTCCCTGTCTCCGGTAAATGA	1428

RESULT 5

AK057754
LOCUS
DEFINITION Homo sapiens cDNA FLJ25025 fis, clone CBL01928, highly similar to
Ig gamma immunoglobulin heavy chain.
ACCESSION AK057754
VERSION GI:16553681
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL01928.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Moxinaga, M.,
Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
Sugano, S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1594)
AUTHORS Sugano, S. and Suzuki, Y.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; Clone selection for
full insert sequencing: RAB and Helix Research Institute.
FEATURES
source
location/Qualifiers
1..1594
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBL01928"
/tissue_type="cerebellum"
/clone_lib="CBL"
/note="cloning vector: pME18SFL3"
15..1460
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB71560.1"
/db_xref="GI:16553682"
/db_xref="IMG/IMG:AK057754"
/translation="MDVMCKMKHLWFFLLLVAAPRWLQAQLQESGPKVLPKPSBTL
TLTCSVGSIGSIATPTGFWCFROPQPGKGLQFIGSVYVTGAHNPISLKRVTISADTS
KAQFLTITSVTAADTAVYVCARHWPVRLGVDAFDPWGPGILTVASASATKGSVFL
VLAPSSKTSGGTAAALGCLVKDYFPEPTVWSNGASCTGHTTFAVLAQSSGLYSLLS
VTPVSSSLGTITRTTCVNVNHPKSNTKVDKKEPKSCDKHTKCPPELGLGQSPVFL
FPFKPRLMTISRTPEVTQVVDVSHEDPEVKFNWYVDGVENHNAKTPKPREQYNSTY
RVSYLTVLHQDLNGKEYCKYSNKALPAPIETKISKAGQPREPQVYTLPPSRDEL
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDLSDGSEFFLYSKLTIVDKSR
WQQGNVFCFSVMHEALHNHYTQKSLSLSPGK"
338 a 532 c 437 g 287 t
BASE COUNT
ORIGIN
Query Match 87.8%; Score 1256.8; DB 9; Length 1594;
Best Local Similarity 93.8%; Pred. No. 7.le-244;
Matches 1345; Conservative 0; Mismatches 77; Indels 12; Gaps 3;
Qy 1 ATGAACACCTGTGTTCTTCCTCCTCGTGTGACGCTCCACAGATGGTCTGTGCCAG 60
|||||
Db 36 ATGAAGCACCTGTGTTCTTCCTCCTCGTGTGACGCTTCGGAGACCTGTCCCTCAC 120
|||||
Qy 61 GTGACAGTGCAGAGTCGGGCCCGACGACTGGTGAAGCTTCGGAGACCTGTCCCTCAC 120
|||||
Db 96 TTGACAGTGCAGAGTCGGGCCCGACGACTGGTGAAGCTTCGGAGACCTGTCCCTCAC 155
|||||
Qy 121 TCGCGTGTCTCTGGTGGCTCCAT---CAGCGGTGGTTATGGCTGGCGGTGGATCCGCAG 177
|||||

Query Match	87.8%	Score 1256.8;	DB 9;	Length 1594;
Best Local Similarity	93.8%	Pred. NO. 7.1e-244;		
Matches 1345; Conservative	0;	Mismatches 77;	Indels 12;	Gaps 3;

1 ATGAACACCTGTGGTTCTTCTCCTCCTGTGGCAGTCCAGATGGGTCCTGTCCAG 60
36 ATGAACACCTGTGGTTCTTCTCCTCCTGTGGCGGTCCAGATGGGTCCTGGCCAG 95
61 GTGAGCTCAGAGTCTGGGCCCAGGACTTGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
96 TTGACGCTCAGAGTCTGGGCCCAGGACTTGTGAAGCCTTCGGAGACCCTGACCCCTCACG 155
121 TCGCGTGTCTGTGGTGCTCCAT---CAGCGGTGTTATGCTTGGGGCTGGATCCGCCAG 177

D	b	96	GTGACACCTGCAGGAGTCCGGCTCAGGACTGGTGAGGCCCTTCACAGACTCTGTCCCTCACG	155
Q	y	121	TGCGCTGTCTCTGTGGTTCAT--CAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAG	177
D	b	156	TGCGCTGTCTCTGTGTACTCATCACAGTGGTCTCACTCTCGAGCTGGATTCGGCGAG	215
Q	y	178	CCCCCAGGGAAGGGCTGGAGTGGAGTTTCTATAGTAGTAGTGGGAACACTTAC	237
D	b	216	CCACCAGGGAAGGGCTGGAGTGGATTGGCTACGTCTA---TCTCAGTGGGACCACTCT	272
Q	y	238	TACAACCCCTCCCTCMAGAGTCAAGTCAACATTCAACAGACAGTCCAGAACCAAGTTC	297
D	b	273	TACAATCCGTCCCTCAAGAGTCSACTCACATGTCATAAGACAGGTCCAACACCAAGTTC	332
Q	y	298	TCCCTGAAGCTGAACCTCTATGACCCCGCGGACAGGGCCGTGTATTACTGTGTGAGAGAT	357
D	b	333	TCCCTGAGTTGACCTCTGTGACCGCCGCGACAGGCCGTGTATTACTGTGCCAGAGGG	392
Q	y	358	CGTCTTTTTTCAGTTGTTGGAAATGGTTTACAAACAATGGTTTCATGTCTGGGGCCCGGA	417
D	b	393	CCTGTTCAATCCCAAGGAT---TTGATACCAACGTTCTCGTTTGACTACTGGGGCCAGGA	449
Q	y	418	GTCCTGTGCACGGTCTCTCAGCTAGCACCAAGGGCCCATCGTCTTCCCCTTGGGACCC	477
D	b	450	ACCTGTGTCAACGGCTCTCAGCCCTCACCAAGGGCCCATCGGTCTTCCCCTTGGGACCC	509
Q	y	478	TCTCCAAGACACCTCTGGGGGCACAGCGGCCCTGGGCTGCTGTCAAGACACTACTTC	537
D	b	510	TCCTCCAAGACACCTCTGGGGGCACAGCGGCCCTGGGCTGCTGTCAAGACACTACTTC	569
Q	y	538	CCCGAAACCGGTGACGGTGTCTGTGAACTCAGGGGCCCTCAGACGGCGCTGCACACTTTC	597
D	b	570	CCCGAAACCGGTGACGGTGTCTGTGAACTCAGGGGCCCTGACACGGCGCTGCACACTTTC	629
Q	y	598	CCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCC	657
D	b	630	CCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCC	689
Q	y	658	AGCAGCTTGGGCAACCCAGACCTCATCTGCAAGCTGAATCACAAGGCCACGCAACACCAAG	717
D	b	690	AGCAGCTTGGGCAACCCAGACCTCATCTGCAAGCTGAATCACAAGGCCACGCAACACCAAG	749
Q	y	718	GTGACAAGAAGACAGAGCCCAACTTTGTGACAAAACCTCACACATGCCACCGTSCCCA	777
D	b	750	GTGACAAGAAGATTGAGCCCAACTTTGTGACAAAACCTCACACATGCCACCGTSCCCA	809
Q	y	778	GCACCTGAATCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAGAACCCCAAGGACAC	837
D	b	810	GCACCTGAATCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAGAACCCCAAGGACAC	869
Q	y	838	CTCATGTATCTCCCGGACCCCTGAGGTCAATATGGTGGTGGAGTGAAGTGAAGCAGAAC	897
D	b	870	CTCATGTATCTCCCGGACCCCTGAGGTCAATATGGTGGTGGAGTGAAGTGAAGCAGAAC	929
Q	y	898	CCTGAGTCAAGTTCAACTCGTTGAGCGCGTGGAGGTGCATAATGCCAAGACAAAG	957
D	b	930	CCTGAGTCAAGTTCAACTCGTTGAGCGCGTGGAGGTGCATAATGCCAAGACAAAG	989
Q	y	958	CCGGGAGGAGGAGTACACACGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTAAC	1017
D	b	990	CCGGGAGGAGGAGTACACACGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTAAC	1049
Q	y	1018	CAGSACTGGCTGAATGGCAAGGAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGCC	1077
D	b	1050	CAGSACTGGCTGAATGGCAAGGAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGCC	1109
Q	y	1078	CCCATCAGAAAAACCATCTCTCCAAAGCCAAAGGGCAGCCCCCGAGAACCAAGGTGTACAC	1137
D	b	1110	CCCATCAGAAAAACCATCACCAAAGCCAAAGGGCAGCCCCCGAGAACCAAGGTGTACAC	1169
Q	y	1138	CTGCCCCATCCCGGGATGAGCTGACCAAGAACCAAGTCAAGCTCAGCTGAGCTGGTCAAA	1197

Db	1170	CTGCCCCCATCCCGGATGAGTGACCAAGAACCAAGTCAGCCTCAGCTGCTGGTCAA	1229
Qy	1198	GGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGACAATGGCGACCGGAGAACAC	1257
Db	1230	GGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGACAATGGCGACCGGAGAACAC	1289
Qy	1258	TACAAGACACGCTCCCGTCTGTGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTC	1317
Db	1290	TACAAGACACGCTCCCGTCTGTGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTC	1349
Qy	1318	ACCGTGGACAGAGCAGGTGGCGACAGGGGAACGTCTTCTCATGCTCCGTGATGATGAG	1377
Db	1350	ACCGTGGACAGAGCAGGTGGCGACAGGGGAACGTCTTCTCATGCTCCGTGATGATGAG	1409
Qy	1378	GCTCTGCACAACTACTACACGAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1410	GGTCTGCACAACTACTACACGAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1463
RESULT 7			
AK057775			
LOCUS			
DEFINITION	Homo sapiens CDNA FLJ25046 fis, clone CBL03624, highly similar to I9 gamma immunoglobulin heavy chain.	1589 bp mRNA linear PRI 26-MAR-2002	
ACCESSION	AK057775		
VERSION	AK057775.1	GI:165533709	
KEYWORDS	oligo capping; fis (full insert sequence)		
SOURCE	Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL03624		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1589)		
AUTHORS	Sugano, S. and Suzuki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)		
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.		

```

null insert sequencing: K&B and Helix Research Institute.
FEATURES
    source
        1. .1589
            /organism="Homo sapiens"
            /db_xref="IMG/IMG:AK057775"
            /db_xref="taxon:9606"
            /clone="CBL03624"
            /issue_type="cerebellum"
            /clone_lib="CBL"
            /notes="cloning vector: pME18SFL3"
BASE COUNT      338 a   532 c   430 g   289 t
ORIGIN
Query Match      86.4%;   Score 1236.8;   DB 9;   Length 1589;
Best Local Similarity 93.0%;   Pred. No. 7.8e-240;
Matches 1334;   Conservative 0;   Mismatches 82;   Indels 18;   Gaps 3;
Qy 1 ATGAACACCTGTGGTTCTTCCTCCTCGTGGCGAGCTCCAGATGGGTCTCTGCCAG 60
    |||||
Db 38 ATGAAGCAGATGTGGTTCTTCCTCCTCGTGGCGGCTCCAGATGGGTCTCTGCCAG 97

```

Qy	61	GTGCAGCTGCAGGAGTCGGGCCACGACTGTGTGAAGCTTCGGAGACCCCTGTCCCTCACC	120
Db	98	CTGCAGCTGCAGAGTCTGGGCCACGAGCTCTCTGAAGCTTCGGAGACCCCTGTCCCTCACC	157
Qy	121	TGGCTGTCTCTGTGGTGCTCCAT--CAGCGGTTGGTTATGCTGTGGGCTGGATTCGCGCAG	177
Db	158	TGGCTGTGTCTGTGGTCCATTACCAGCAATGATTACTGCTGGAATTGGATTCGCCCAG	217
Qy	178	CCCCAGGGAAGGGCTGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACTAC	237
Db	218	CCCCAGGGAAGAGACTGAGTGGTTGGATGTCTC-----AATGACGGGCGCACCTAC	271
Qy	238	TACAACCCCTCCCTCAAGAGTCAAGTCAACATTTTCAACAGACAGTCCCAAGAACCAAGTTTC	297
Db	272	TACGAGCCGTCCTTCGGGAGTCTGAGTCAACCATATCCGACAGAGCTCCAAAGAACCAATTC	331
Qy	298	TCCCTGAAGCTGAACCTTATGACCCGCGGACACGGCCGTTGTTATTACTGTGTGAGAGAT	357
Db	332	TCCCTGAGGCTGACCTCTCGTCCCCCGCAGACACGGCTGTTATTATTGTGGAGTCTC	391
Qy	358	CGTCTTTTTTCACTGTTGGATGGTTTACAACAACACTGGTTTCGATGTCCTGGGCCCCGGA	417
Db	392	CGTGTTCAGGGTTCGGGAGTCCCTTTTC-----TTTGACTTCTGGGGCCAGGGG	442
Qy	418	GTCCTGTGTCAACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTTGGCACCC	477
Db	443	ACCTGTGTCAACCGTCTCTCAGCTCCCAAGGGCCCATCGGTCTTCCCCTTGGCACCC	502
Qy	478	TCCTTCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTCAAGGACTACTTC	537
Db	503	TCCTTCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTCAAGGACTACTTC	562
Qy	538	CCCGAACCGGTGACGGTGTCTGTGGAACCTCAGCGGCCCTGACAGCGGCTGCACACCTTC	597
Db	563	CCCGAACCGGTGACGGTGTCTGTGGAACCTCAGCGGCCCTGACAGCGGCTGCACACCTTC	622
Qy	598	CCGGGTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGGTCCCTCC	657
Db	623	CCGGGTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGGTCCCTCC	682
Qy	658	AGCAGCTTGGGACCCAGACCTACATCTCGACGCTGATCAGCAGCCAGCAACACCAAG	717
Db	683	AGCAGCTTGGGACCCAGACCTACATCTCGACGCTGATCAGCAGCCAGCAACACCAAG	742
Qy	718	GTGACAAGAAAGCAGAGGCCAAATCTTGTGACAAAATCTCACATGCCCCACCGTGCCCA	777
Db	743	GTGNCAGAAAGTTGAGCCCCAANTCTTGTGACAAAATCTCACATGCCCCACCGTGCCCA	802
Qy	778	GCACCTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCTTCCCCCMAAACCCCAAGGACCC	837
Db	803	GCACCTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCTTCCCCCMAAACCCCAAGGACCC	862
Qy	838	CTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCAGCAAGAC	897
Db	863	CTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCAGCAAGAC	922
Qy	898	CCTGAGGTCAAAGTTCAAATCTGTGACGTGGACCGGCTGGAGGTGCATAATGCCAAGACAAAG	957
Db	923	CCTGAGGTCAAAGTTCAAATCTGTGACGTGGACCGGCTGGAGGTGCATAATGCCAAGACAAAG	982
Qy	958	CCGCGGGAGGACGATGACACAGACGTTACCGTGTGGTGTGGTCTTCCACCGTCTCTGCAC	1017
Db	983	CCGCGGGAGGACGATGACACAGACGTTACCGTGTGGTGTGGTCTTCCACCGTCTCTGCAC	1042
Qy	1018	CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCCGACC	1077
Db	1043	CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCCGACC	1102
Qy	1078	CCCATCGAAAAACATCTCCAAAGCCAAAGGGGACGCCCGGAGAACCAAGGTGTACACC	1137
Db	1103	CCCATCGAAAAACATCTCCAAAGCCAAAGGGGACGCCCGGAGAACCAAGGTGTACACC	1162

Qy	1138	CTGCCCCCATCCGGGATGAGCTGACCAAGAACACAGGTGAGCTGACCTGACCTGCGTGGTCAAA	1197
Db	1163	CTGCCCCCATCCGGGATGAGTGAACCAAGAACACAGGTGAGCTGACCTGACCTGCGTGGTCAAA	1222
Qy	1198	GGCTTCTATCCACGACATCGCCGCTGGAGTGGAGAGCAATGGGAGCCGGAGAACAAAC	1257
Db	1223	GGCTTCTATCCACGACATCGCCGCTGGAGTGGAGAGCAATGGGAGCCGGAGAACAAAC	1282
Qy	1258	TACAAGACCAAGCGCTCCCGTGTGGACTTCGAGCGGTCTCTTCTTCTTCTACAGCAAGCTC	1317
Db	1283	TACAAGACCAAGCGCTCCCGTGTGGACTTCGAGCGGTCTCTTCTTCTTCTACAGCAAGCTC	1342
Qy	1318	ACCGTGACAGACGAGGTGGCAGCAGGGGAAAGCTTCTTCATGCTCCGATGCATGAG	1377
Db	1343	ACCGTGACAGACGAGGTGGCAGCAGGGGAAAGCTTCTTCATGCTCCGATGCATGAG	1402
Qy	1378	GCTCTGCACAAACACTACACGACAGAGAGCTCTCCCTGTCTCCGGTAAATGA	1431
Db	1403	GCTCTGCACAAACACTACACGACAGAGAGCTCTCCCTGTCTCCGGTAAATGA	1456
RESULT 8			
A49389			
LOCUS	A49389	Sequence 7 from Patent WO9607740.	DNA 1418 bp linear PAT 07-MAR-1997
DEFINITION	A49389		
ACCESSION	A49389		
VERSION	A49389.1	GI:2302866	
KEYWORDS		unidentified.	
SOURCE		unidentified	
ORGANISM		unclassified.	
REFERENCE		1 (bases 1 to 1418)	
AUTHORS		Edelman,D., Margaritha,C., Kaczorek,M. and Chaabihi,H.	
TITLE		MONOCLONAL RECOMBINANT ANTI-RHESUS D (D7C2) ANTIBODY	
JOURNAL		Patent: WO 9607740-A 7 14-MAR-1996;	
COMMENT		PASTEUR INSTITUT (FR)	
FEATURES		Other publication FR 2724182 960308.	
source		Location/Qualifiers	
		1..1418	
		/organism="unidentified"	
		/db_xref="taxon:32644"	
CDS		1..1418	
		/notes="unnamed protein product"	
		/codon_start=1	
		/protein_id="CAA03180.1"	
		/db_xref="GI:2302866"	
		/translation="MGMSCHLLFLVATGTVHSGVQLQOMGAGLLKPSSETLSLTCTVTV	
		GGSGFYGYSWIRKQPPKGLWEIGNEHSGTSINFLSKRVTISVDTSKNQPSLKLNL	
		SVTAADTAVYICARPEYKWKYHGFDPMGQGTTFVSSASTGSPSVFLPAPSSKTS	
		SGGTAAALGLVKDYFPEPTVTVSNAGALTSGVHTTFVAVLQSSGLYSLSVTVVPSSSL	
		GTQTYICNVNHNKSVNTHVDKKAAPKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTL	
		MISTPTPTCVVDVSDHEDPEFENMVDVGTGKAKGQPREPQVTLPPSRDELTKNOVSLTC	
		HQWLINGKEFKCKSVKNALPAPIETKISKAKGQPREPQVTLPPSRDELTKNOVSLTC	
		LVKGFPYSDTAVENESNGQDENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVPSFC	
		SVMEALHNHYTQKSLSLSPGK"	
sig_peptide		1..57	
mat_peptide		58..1418	
		/product="IMMUNOGLOBULIN, HEAVY CHAIN"	
BASE COUNT	333 a	458 c	378 g 249 t
ORIGIN			
Query Match		85.6%	Score 1224.8; DB 6; Length 1418;
Best Local Similarity		93.0%	Prod. No. 2.1e-237;
Matches 119.		0.	Mismatches 287;
Conservative			Indels 12; Gaps 3

	Query Match	85.6%	Score 1224.8	DB 6	Length 1418
	Best Local Similarity	93.0%	Pred. No. 2.1e-237		
	Matches 1319	Conservative 0	Mismatches 27	Indels 12	Gaps 3
QY	13	TGTTTCTTCTCTCTCTGGTGGCAGCTCCAGATGGGTCTGTGCCAGGTGCAGTGCAG	72		
Db	13	TGTATCATCTCTTCTTGTGTAGCAACAGCTACAGGTGTCCACTCCGAGGTCCAACTGCAG	72		
QY	73	GAGTGGGGCCGAGGACTGTGTGAAGCCTTTCGGAGACCTGTCCCTTCACCTGGCGTGTCTCT	132		
Db	73	CTCTGGGGCCGAGGACTGTGTGAAGCCTTTCGGAGACCTGTCCCTTCACCTGGCACTGTCTAT	132		

Query Match	84.8%	Score 1213.6	DB 6	Length 1418
Best Local Similarity	92.5%	Prod. No. 3.8e-235		
Matches 1312	Conservative	0	Mismatches 94	Indels 12
QY	13	TGGTTCCTCCTCCTCGTGGCAGCTCCACATGGGTCTGTCCAGGTGGCTGTCCAGGTGCAGCTGCAG	72	
Db	13	TGTATCATCCTCTCTTGGTAGCAACAGCTACAGGTGCCATCTCCAGGTCCAACTGGAG	72	
QY	73	GAGTCGGGCCCGACGACTGGTGAAGCCCTTCGGAGACCTGTCCCTCACTCGCGTGTCTCT	132	
Db	73	CAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCCCTCACTCGCTGTCTAT	132	
QY	133	GGTGGCTCCATACAGCGTGGTATGGCTGGGGCTGGATCGCCAGCGCCCCCAGGGAAAGGG	192	
Db	133	GGTGGTCTCTCA--GTGGTTACTTGGAGCTGGATCGCCAGCCCCCAGGGAAAGGG	189	
QY	193	CTGGAGTGGATTTGGAGTCTTCTATAGTAGTAGTGGGAACACTACTAAACCCCTCCCTC	252	
Db	190	CTGGAGTGGATTTGGGGAATC---AATCATAGTGGGAACACAACTAAACCCGTCCTC	246	
QY	253	AAGAGTCAAGTCAACCATTTCAACAGACACGTCCAAGAACCAAGTTCTCCCTGAAGCTGAAC	312	
Db	247	AAGAGTCGAGTCACCATATCAGTAGACAGCTCCAAGAACAGTTCTCCCTGAACCTGAAC	306	
QY	313	TCTATGACCGCGGGACACGCGCGTGTATATCTGTGTGAGAGATCGTCTTTTTTCAGTT	372	
Db	307	TCTGTGACCGCGCGGACACGCGTGTGTATCTGTGTGGAGGGCCCCAGAGATATAA---363		
QY	373	GTTGGATTTGGTTTACAACAACATGGTTTCGATGTCTGGGGCCCGGGAGTCTGTGGTCAACGTC	432	
Db	364	---TGAAGTATCATGGGNCCTGTTTCGACCCCTGGGGCCAAAGTACCACTGTCAACGTC	420	
QY	433	TCCTCAGCTAGCACCAAGGGCCCATCGGTTCTTCCCTCGGACCCCTCTCCAAAGAGACC	492	
Db	421	TCCTCAGCTCCCAAGGGGCCCATCGGTTCTTCCCTCGGACCCCTCTCCAAAGAGACC	480	
QY	493	CTGGGGSCACGCGGCCCTCGGCTGTGGTCAAGGACTACTTTCGCCGAACCGGTGAGC	552	

Db 210 CAGCCAGGAGGCGCTGGAGTGGATGGACATC---AATTCCTATGCCTACAAGTTC 266
Qy 238 TACAACCCCTCCCTCAAGAGTCAAGTCAACATTTCAACAGACACAGTCCCAAGAACCAAGTTC 297
Db 267 TACAATCAGTCCCTCGAGAGTCGACTTTCCATGTCAATGGACACATCTCGGAATCAGTTC 326
Qy 298 TCCCTGAAGCTGAACCTCTATAGCCGCGGGACACAGCCGCTGTATTAATCTGTGTGAGAT 357
Db 327 TCCCTGAAGATGACCTCTGTGATGACGTAGACACAGCCGCTGTATTTCTGTGCG----- 380
Qy 358 CGTCTTTTTTCAGTGTGTGAATGTTTACAACAACCTGGTTCGATGTCTGGGCGCGGA 417
Db 381 -----TTGTTTAAGTCTAAGTGTTCGACCCCTGGGCGCGGA 419
Qy 418 GTCTGTGTCACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 477
Db 420 ACACCTGGTCATCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 479
Qy 478 TCTTCCAAGGACACCTCTGGGGGACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTC 537
Db 480 TCTTCCAAGGACACCTCTGGGGGACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTC 539
Qy 538 CCGAACCCGCTGACGGTCTGTGGAACCTCAGCGCCCTGACAGCGGGGTGCACACCTTC 597
Db 540 CCGAACCCGCTGACGGTCTGTGGAACCTCAGCGCCCTGACAGCGGGGTGCACACCTTC 599
Qy 598 CCGGCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCC 657
Db 600 CCGGCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCC 659
Qy 658 AGCAGTTGGGACCCAGACCTACATCTGCAACGTGAATCAAGGCCAGCAACCAAG 717
Db 660 AGCAGTTGGGACCCAGACCTACATCTGCAACGTGAATCAAGGCCAGCAACCAAG 719
Qy 718 GTGGACAAGAAAGAGAGCCAAATCTTGTGACAAACTCAACATGCCACCGTGCCCA 777
Db 720 GTGGACAAGAAAGTGGAGCCAAATCTTGTGACAAACTCAACATGCCACCGTGCCCA 779
Qy 778 GCACCTGAATCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACC 837
Db 780 GCACCTGAATCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACC 839
Qy 838 CTCATGATCTCCGGACCCCTCAGGTACATGCTGTGTGTGGAGCGTGAGCCACGAAGAC 897
Db 840 CTCATGATCTCCGGACCCCTCAGGTACATGCTGTGTGTGGAGCGTGAGCCACGAAGAC 899
Qy 898 CCGTGAAGTCAAGTTCAACTGGTACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAG 957
Db 900 CCGTGAAGTCAAGTTCAACTGGTACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAG 959
Qy 958 CCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGTGTGAGCGTCTCACCCTCTGAC 1017
Db 960 CCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGTGTGAGCGTCTCACCCTCTGAC 1019
Qy 1018 CAGGACTGGCTGAATGGCAAGAGTACAAGTGCAGAGTCTCAACAAAGCCCTCCACGCC 1077
Db 1020 CAGGACTGGCTGAATGGCAAGAGTACAAGTGCAGAGTCTCAACAAAGCCCTCCACGCC 1079
Qy 1078 CCATCTGAGAAAACCATCTCCAAAGCCAAAGGACGCCCGAGAACCCAGAGTGTACACC 1137
Db 1080 CCATCTGAGAAAACCATCTCCAAAGCCAAAGGACGCCCGAGAACCCAGAGTGTACACC 1139
Qy 1138 CTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGACCTGACCTGCTGGTCAAA 1197
Db 1140 CTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGACCTGACCTGCTGGTCAAA 1199
Qy 1198 GCTTTCTATCCAGGACATGCGCGTGAAGTGGAGAGCAATGGGCGAGCCGAGAAAC 1257
Db 1200 GCTTTCTATCCAGGACATGCGCGTGAAGTGGAGAGCAATGGGCGAGCCGAGAAAC 1259
Qy 1258 TACAAGACACGCTCCCGTGTGAGTCCGACGCGCTCTTCTCTCTACAGCAAGCTC 1317

Db 1260 TACAAGACCAAGCCTCCCGTCTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTC 1319
Qy 1318 ACCGTGGACAGACAGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATCATGAG 1377
Db 1320 ACCGTGGACAGACAGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATCATGAG 1379
Qy 1378 GCTCTGCACCAACTACAGCAGAGAGGCTCTTCCCTGTCTCCGGGTAAATGA 1431
Db 1380 GCTCTGCACCAACTACAGCAGAGAGGCTCTTCCCTGTCTCCGGGTAAATGA 1433
RESULT 11
ARI135375
LOCUS ARI135375 1404 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 7 from patent US 6136310.
ACCESSION ARI135375
VERSION ARI135375.1 GI:14476047
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Hanna,N., Newman,R.,Anthony. and Reff,M.,Elliot.
TITLE Recombinant anti-CD4 antibodies for human therapy
JOURNAL Patent: US 6136310-A 7 24-OCT-2000;
FEATURES
Location/Qualifiers
source 1..1404
BASE COUNT 312 a 448 c 377 g 267 t
ORIGIN
Query Match 82.5%; Score 1181; DB 6; Length 1404;
Best Local Similarity 90.4%; Pred. No 1.5e-228;
Matches 1294; Conservative 0; Mismatches 110; Indels 27; Gaps 2;
Qy 1 ATGAAACACCTGTGGTTCCTCTCCTGGTGGCAGCTCCAGATGGGTCTGTGCCAG 60
Db 1 ATGAAACACCTGTGGTTCCTCTCCTGGTGGCAGCCCCAGATGGGTCTGTGCCAG 60
Qy 61 GTCAGCTGCAGAGTCCGGCCCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 61 GTCAGCTGCAGAGTCCGGCCCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Qy 121 TGGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC 180
Db 121 TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATATTTGGTCTGGATCCGCCAGTCC 180
Qy 181 CCAGGAAGGGGTGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC 240
Db 181 CCAGGAAGGGACTGGAGTGGATCGGTACATCTATGGCAGTGGTGGGGGACCAATTAC 240
Qy 241 AACCCCTCCCTCAAGATCAAGTCAACCATTTCAACAGACACGTCCCAAGAACCAAGTTCCTCC 300
Db 241 AATCCCTCCCTCAACAAATCGAGTCTCCATTTCAATAGACACGTCCCAAGAACCTTCTCTCC 300
Qy 301 CTGAAGCTGAACCTCTATGACCGCGCGGACACGCGCGTGTATTACTGTGTGAGAGATCGT 360
Db 301 CTGAAGCTGAGGTCTGTGACCGCGCGGACACGCGCGTCTATTACTGTGTGAGAGTAATA-- 358
Qy 361 CTTTTTTCAGTTGTTGGAATGGTTTACAACAATGGTTCGATGTCTGGGGCCCGGGAGTTC 420
Db 359 -----TATTGAAATATCTTCACTGGTTATTACTGGGGCCAGGGAGTTC 402
Qy 421 CTGGTCAACCGTCTCCTCAGCTAGCACCAAGGCCCATCGGTCTTCCCTCCCTGGACCCCTCC 480
Db 403 CTGGTCAACCGTCTCCTCAGCTAGCACCAAGGCCCATCGGTCTTCCCTCCCTGGGGCCCTGC 462
Qy 481 TCAAGAGACACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTCTCAAGGACTACTTCCCTCC 540
Db 463 TCCAGAGACACCTCCGAGAGACACAGCGGCCCTGGGCTGCTGTCTCAAGGACTACTTCCCTCC 522
Qy 541 GAACCGGTGACGGTGTGTTGGAACCTAGCGCCCTGACAGCGCGGTGCACACCTTCCCG 600

Db 523 GAACCGGTGACGGTGTCTGGAACTCAGCGGCCCTGACACAGCGCGGTGACACACTTCCCG 582
 Qy 601 GCTGTCTCAGACTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTTCCAGC 660
 Db 583 GCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTTCCAGC 642
 Qy 661 AGCTTGGGACCCAGACCTACATCTGCAAGTGAATCAACAAGCCAGCAACACCAAGTG 720
 Db 643 AGCTTGGGACCCAGGACCTACACCTCAACGCTAGATCAACAAGCCAGCAACACCAAGTG 702
 Qy 721 GACAAGAAAGACAGAGCCCAAAATCTGTGACAAAACTCAACATGCCACCGTGCACGCA 780
 Db 703 GACAAGAGAGTGTGATCCAAATATGG-----TCCCCCATGCCATCATGCCAGCA 753
 Qy 781 CTGTAACTCTCTGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 Db 754 CTGTAGTTCCTGGGGGACCATCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 813
 Qy 841 ATGATCTCCCGGACCCCTGAGGTACATCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 900
 Db 814 ATGATCTCCCGGACCCCTGAGGTACATCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 873
 Qy 901 GAGGTCAAGTTCAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTA 960
 Db 874 GAGGTCAAGTTCAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTA 933
 Qy 961 CGGAGGACGATACACAGCAGTACCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1020
 Db 934 CGGAGGACGATACACAGCAGTACCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 993
 Qy 1021 GACTGGCTGAATGGCAAGGAGTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1080
 Db 994 GACTGGCTGAATGGCAAGGAGTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1053
 Qy 1081 ATGAGAAACCATCTCCAAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
 Db 1054 ATGAGAAACCATCTCCAAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1113
 Qy 1141 CCCCCATCCCGGATGAGTGTGACCAAGAACAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAG 1200
 Db 1114 CCCCCATCCAGAGAGATGACCAAGAACAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAG 1173
 Qy 1201 TTCTATCCAGAGACATCCGCTGTGAGTGGAGAGCAATGGGACCCGAGAAACAACTAC 1260
 Db 1174 TTCTATCCAGAGACATCCGCTGTGAGTGGAGAGCAATGGGACCCGAGAAACAACTAC 1233
 Qy 1261 AAGACACGCTCCGCTGTGACTCCGAGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
 Db 1234 AAGACACGCTCCGCTGTGACTCCGAGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1293
 Qy 1321 GTGGAACAAGAGAGTGGCAGAGGGGAAAGCTCTTCTCATGCTCCGTCATGATGAGGCT 1380
 Db 1294 GTGGAACAAGAGAGTGGCAGAGGGGAAAGCTCTTCTCATGCTCCGTCATGATGAGGCT 1353
 Qy 1381 CTCGACAAACCTACACGAGAGAGGCTCTCCCTGTCTCCGGTAAATGA 1431
 Db 1354 CTGCAACCACTACACAGAGAGGCTCTCCCTGTCTCTGGGTAATGA 1404

RESULT 12

AR135377

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PAT 16-JUN-2001

1404 bp DNA linear

Sequence 11 from patent US 6136310.

AR135377.1 GI:14476049

Unknown.

Unclassified.

*1 (bases 1 to 1404)

Hanna, N., Newman, R. Anthony, and Reff, M. Elliot.

Recombinant anti-CD4 antibodies for human therapy

Patent: US 6136310-A 11 24-OCT-2000;

FEATURES

Source

1. 1404

/organism="unknown"

BASE COUNT 313 a 447 c 379 g 265 t

ORIGIN

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Query Match

Best Local Similarity

Matches 1292; Conservative

0; Mismatches 112; Indels 27; Gaps 2;

Qy	961	CGGAGGAGCAGTATCAACACAGCACGTGACCGTGTGGTACGGTCTCTACCGTCTGTGCACGAC	1020
Db	934	CGGAGGAGCAGTATCAACACAGCACGTGACCGTGTGGTACGGTCTCTACCGTCTGTGCACGAC	993
Qy	1021	GACTGGCTGAATGCAAGGAGTACAAGTGCAAGGTCTCCAAACAAGCCCTCCACGACCC	1080
Db	994	GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAAACAAGGCTCCGTCCTCC	1053
Qy	1081	ATCGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCCGTG	1140
Db	1054	ATCGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCCGTG	1113
Qy	1141	CCCCCATCCCGGGATGAGCTACCAAGNACACAGTCCAGCTGACCTGCTGGTCAAAGGC	1200
Db	1114	CCCCCATCCCGAGGAGATGACCAAGAACACAGTCCAGCTGACCTGCTGGTCAAAGGC	1173
Qy	1201	TTCTATCCACGGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTTAC	1260
Db	1174	TTCTATCCACGGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTTAC	1233
Qy	1261	AAGACCAAGCCTCCCGTCTGGATCCGACCGGCTCTTCTTCTCTTACAGCAAGCTCACC	1320
Db	1234	AAGACCAAGCCTCCCGTCTGGATCCGACCGGCTCTTCTTCTCTTACAGCAAGCTCACC	1293
Qy	1321	GTGCACAAGCAGGTGCGACAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT	1380
Db	1294	GTGCACAAGCAGGTGCGACAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT	1353
Qy	1381	CTGCACAACCACTACACGACAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1354	CTGCACAACCACTACACAGAGAGCCCTCTCCCTGTCTCTGGGTAAATGA	1404
RESULT 13			
AR135376			
LOCUS			
DEFINITION			
TITLE			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 1291, Conservative			
0; Mismatches 113; Indels 27; Gaps 2;			
Qy	1	ATGAAACACCTGTGGTCTTCTCTCTGTGGCAGCTCCCGAGATGGGTCTGTGCCAG	60
Db	1	ATGAAACACCTGTGGTCTTCTCTCTGTGGCAGCTCCCGAGATGGGTCTTGTGCCAG	60
Qy	61	GTGCAGCTGCAGGAGTCGGGCCACGAGCTGTGAAGCCTTCGGAGACCTGTCCCTCACC	120
Db	61	GTGCAGCTGCAGGAGTCGGGCCACGAGCTGTGAAGCCTTCGGAGACCTGTCCCTCACC	120
Qy	121	TGCGTGTCTCTGTGGTCTCCATCAGCGGTGGTATTGGCTGGGGCTGGATCCGCCAGGCC	180
Db	121	TGCAGTGTCTCTGTGGTCTCCATCAGCGGTGACTATTATTGGTCTGGATCCGCCAGTCC	180
Qy	181	CCAGGAAAGGGCTGGAGTGGATGGGAGTTTCTATAGTAGTAGTGGGAACACTTACTAC	240
Db	181	CCAGGAAAGGCACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGACCAATTAC	240

Qy	241	A	A	C	C	C	T	C	C	C	T	C	A	A	G	A	G	T	C	A	A	G	T	C	A	A	G	A	C	A	G	T	C	A	A	G	A	C	A	G	T	C	C	300							
Db	241	A	A	T	C	C	C	T	C	A	A	C	A	A	T	C	G	A	G	T	C	C	A	A	T	A	G	A	C	A	G	T	C	A	A	G	A	C	T	C	T	C	300								
Qy	301	C	T	C	A	A	G	C	T	G	N	A	C	T	C	T	A	T	A	G	C	C	G	C	G	A	C	A	G	C	G	C	G	T	A	T	A	C	T	G	T	G	A	G	A	T	C	G	T	360	
Db	301	C	T	G	A	A	A	C	T	G	A	C	C	C	C	G	C	G	A	C	A	G	C	G	C	T	A	T	A	C	T	A	T	G	T	G	C	G	A	G	A	T	A	-	-	358					
Qy	361	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	420								
Db	359	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	402									
Qy	421	C	T	G	G	T	C	A	C	C	G	T	C	T	C	T	A	G	C	T	A	G	C	A	C	A	A	G	G	C	C	A	T	C	G	T	C	T	T	C	C	C	T	G	G	C	A	C	T	C	480
Db	403	C	T	G	G	T	C	A	C	C	G	T	C	T	C	T	C	A	G	C	T	A	G	C	A	A	G	G	G	C	C	A	T	C	C	G	T	C	T	T	C	C	C	C	T	G	C	462			
Qy	481	T	C	C	A	A	G	A	C	A	C	T	C	T	G	G	G	G	C	A	C	A	G	G	C	C	T	G	G	C	T	G	C	T	G	C	T	A	G	G	A	T	C	T	C	C	540				
Db	463	T	C	C	A	G	A	G	A	C	A	C	T	C	G	A	G	A	C	A	G	C	C	C	C	T	G	G	C	T	G	C	T	G	C	T	G	C	T	A	G	G	A	T	C	C	522				
Qy	541	G	A	A	C	C	G	T	G	C	T	G	G	A	A	C	T	C	A	G	C	G	C	C	T	G	A	C	C	A	G	C	G	G	T	G	C	A	C	A	C	T	C	C	G	600					
Db	523	G	A	A	C	C	G	T	G	A	C	T	G	C	T	A	G	C	C	C	T	A	G	C	G	C	C	T	G	A	C	C	A	G	C	G	G	T	G	C	A	C	T	C	C	G	582				
Qy	601	G	C	T	G	T	C	C	T	A	G	C	T	C	T	A	G	C	A	C	T	A	C	C	T	C	A	G	C	A	G	C	T	G	T	G	A	C	G	T	G	C	C	C	T	C	A	G	660		
Db	583	G	C	T	G	T	C	C	T	C	A	G	C	T	C	T	A	G	C	T	A	C	C	T	C	A	G	C	G	T	G	T	G	A	C	G	T	G	A	C	G	T	C	C	C	C	A	G	642		
Qy	661	A	G	C	T	T	G	G	C	A	C	C	T	A	C	T	G	C	A	A	C	T	G	A	A	C	T	C	A	A	G	C	C	C	A	G	C	C	A	C	A	C	A	A	G	T	G	720			
Db	643	A	G	C	T	T	G	G	C	A	C	C	T	A	C	C	T	G	C	A	A	C	T	G	A	A	C	T	C	A	A	G	C	C	C	A	G	C	C	A	C	A	C	A	A	G	T	G	702		
Qy	721	G	A	C	A	A	A	G	A	G	A	G	C	C	A	A	A	C	T	C	A	C	A	A	A	C	T	C	A	C	A	T	G	C	C	A	A	A	C	C	C	A	C	C	A	G	780				
Db	703	G	A	C	A	A	G	A	G	T	G	A	G	T	C	C	A	A	A	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	753						
Qy	781	C	C	T	G	A	A	C	T	C	T	G	G	G	G	A	C	C	G	T	C	A	G	T	C	T	T	C	T	C	C	C	C	C	A	A	A	C	C	A	A	G	A	C	A	C	C	T	C	840	
Db	754	C	C	T	G	A	G	T	C	G	A	G	G	G	G	A	C	C	A	G	T	C	T	C	T	G	T	T	C	C	C	C	C	C	A	A	A	C	C	A	A	G	A	C	A	C	T	C	813		
Qy	841	A	T	G	A	T	C	C	C	G	A	C	C	C	T	G	A	G	T	C	A	C	T	G	T	G	T	G	T	G	G	A	C	T	G	A	C	C	A	A	G	A	C	C	T	900					
Db	814	A	T	G	A	T	C	C	C	G	A	C	C	C	T	G	A	G	T	C	A	C	T	G	T	G	T	G	T	G	T	G	A	C	T	G	A	C	C	A	A	G	A	C	C	C	873				
Qy	901	G	A	G	T	C	A	A	G	T	C	A	A	C	T	G	T	G	A	C	T	G	A	C	G	C	G	T	G	A	G	T	G	C	A	T	A	T	C	C	A	A	G	A	A	C	G	960			
Db	874	G	A	G	T	C	A	A	G	T	C	A	A	C	T	G	T	G	A	C	T	G	A	C	G	T	G	A	G	T	G	A	G	T	G	C	A	T	A	T	C	C	A	A	G	A	A	C	G	933	
Qy	961	C	G	G	A	G	A	G	C	A	G	T	C	A	A	C	A	G	C	A	G	T	A	C	C	G	T	G	T	G	T	G	C	A	C	C	G	T	C	C	A	A	A	G	C	C	C	1020			
Db	934	C	G	G	A	G	A	G	C	A	G	T	T	C	A	A	C	A	G	C	A	G	T	A	C	C	G	T	G	T	G	T	G	C	A	C	C	G	T	C	C	A	C	C	A	G	993				
Qy	1021	G	A	C	T	G	G	T	G	A	T	G	G	A	G	A	G	T	C	A	A	G	T	C	T	C	A	A	A	A	G	C	C	T	C	C	A	A	A	G	C	C	C	C	1080						
Db	994	G	A	C	T	G	G	T	G	A	T	G	G	A	G	A	G	T	C	A	A	G	T	C	T	C	A	A	A	A	G	C	C	C	C	A	A	A	G	C	C	C	C	1053							
Qy	1081	A	T	C	G	A	A	A	C	A	T	C	C	A	A	G	C	C	A	A	G	G	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	1140							
Db	1054	A	T	C	G	A	A	A	C	A	T	C	C	A	A	G	C	C	A	A	G	G	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	1113								
Qy	1141	C	C	C	C	A	T	C	C	C	G	A	T	G	A	T	G	A	C	C	A	A	G	T	C	A	A	G	T	C	A	A	G	T	C	A	A	G	T	C	A	A	G	T	C	1200					
Db	1114	C	C	C	C	A	T	C	C	C	A	G	A	T	G	A	T	G	A	C	C	A	A	G	T	C	A	A	G	T	C	A	A	G	T	C	A	A	G	T	C	A	A	G	T	1173					
Qy	1201	T	T	C	T	A	T	C	C	C	A	G	C	A	T	C	G	C	T	G	G	A	G	C	A	T	T	G	G	A	G	C	A	T	T	G	G	A	G	C	A	T	T	1260							
Db	1174	T	T	C	T	A	C	C	C	A	G	C	A	T	C	G	C	T	G	A	T	G	G	A	G	C	A	T	T	G	G	A	G	C	A	T	T	G	G	A	G	C	A	T	1233						
Qy	1261	A	A	G	A	C	A	C	G	C	T	C	C	G	T	G	A	C	T	C	C	G	A	C	G	C	T	C	T	T	C	T	C	T	A	C	A	G	A	G	T	C	A	C	1320						
Db	1234	A	A	G	A	C	A	C	G	C	T	C	C	G	T	G	A	C	T	C	C	A	G	C	T	C	T	T	C	T	C	T	C	T	A	C	A	G	A	G	T	A	C	1293							

Qy	1321	GTGACAAAGACAGGTGGCAGCAGGGAGAACTCTTCTCATCTCTCCGTGATGCATGAGGCT	1380
Db	1294	GTGACAAAGACAGGTGGCAGCAGGGAGAACTCTTCTCATCTCTCCGTGATGCATGAGGCT	1353
Qy	1381	CTGCACAAACCACTACACGACGAGAGGCTCTCCCTGTCTCCGGGTAATGA	1431
Db	1354	CTGCACAAACCACTACACGACGAGAGGCTCTCCCTGTCTCTGGGTAATGA	1404
RESULT	14		
BC024289			
LOCUS	BC024289	Homo sapiens, clone MGC:39273 IMAGE:5440834, mRNA	linear PRI 28-FEB-2002
DEFINITION	BC024289	Homo sapiens, clone MGC:39273 IMAGE:5440834, mRNA, complete cds.	
ACCESSION	BC024289		
VERSION	BC024289.1	GI:18999464	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1630)		
TITLE	Strausberg,R.		
JOURNAL	Direct Submission		
REMARK	Submitted (26-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	Contact: MGC help desk		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: Dr. Mark Watson		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Genome Sequence Centre,		
	BC Cancer Agency, Vancouver, BC, Canada		
	info@cgsc.bc.ca		
	Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeeidi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Series: IRAL Plate: 42 Row: 0 Column: 20		
	This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.		
FEATURES	Location/Qualifiers		
source	1..1630		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="MGC:39273 IMAGE:5440834"		
	/tissue_type="Spleen"		
	/clone_lib="NIH_MGC_113"		
	/lab_host="DH10B-R"		
	/notes="Vector: pOTB7"		
	64..1479		
	/codon_start=1		
	/product="Unknown (protein for MGC:39273)"		
	/protein_id="AAH24289.1"		
	/db_xref="GI:18999465"		
	/translation="MBLGLRNVFLVAILEGVQCEVOLVBSGGGLVPGGSLRLSCAAS GFTFSSYMNWVRQAQKGLWEVSSSSSIYYADSVKGRFTIISDNKAKNSLYLQM NSLRADLTAVYICARDLRQLTSTWYFDLMGRGLTLTVSSASTKGPSVFLPSSKSTGSGTAAIGCLVKDIFPEPTVTVSMNSGALTSGVHTFPAVLQSSGLYISUUVTVPSKSLTQTQIICNVNHNKPTVDKVRPEPKSCDKTHTCPPELLEGGLGFSVFLPPPKPKDTLM ISRLPEVTQCVVDVSHEDPEVKFNATGVEVHNAKTKPREQYNSTYRVVSLTFLH QDWLNKGVKCYKSNKALPAIKETISKAGQPREQVITLPPSRDELTKNQVSLTFLH		
CDS			

BASE COUNT		374 a	518 c	442 g	296 t		
ORIGIN							
Query Match		79.8%; Score 1142.6; DB 9; Length 1630;					
Best Local Similarity		88.5%; Pred. No. 8.4e-221;					
Matches 1267; Conservative		0; Mismatches 149; Indels 15; Gaps 2;					
QY	1	ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCACAGATGGGTGCTGTGCCAG	60				
DB	64	ATGGAACCTGGGGCTCCGCTGGGTTTCCTTGTGCTATTTTAGAAGGTGTCAGGTGTGAG	123				
QY	61	GTCCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTCAC	120				
DB	124	GTGCAGCTGGTGGAGTCTGGGGAGGCTGGTCAAGCCTGGGGGTCCCTGAGACTCTCC	183				
QY	121	TGGCTGTCTCTGGTGGCTCCATCAGGGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC	180				
DB	184	TGTGCAGCCTCTGGATTCACTCTCA---GTAGCTATAGCATGAACATGGGTCCGCCAGGCT	240				
QY	181	CCAGGGAAGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACTACTAC	240				
DB	241	CCAGGGAAGGGCTGGAGTGGGTCTCATCATGATGATGATAGTAGTACATATACTAC	300				
QY	241	AACCCCTCCCTCAAGAGTCAAGTCAACATTTCAACAGACACGTCCCAAGAACCAAGTTCTCC	300				
DB	301	GCAGACTCAGTGAAGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTAT	360				
QY	301	CTGAAGCTGAACCTATGACCGCGGGGACACGGCGGTATTACTGTGTGAGAGATCGT	360				
DB	361	CTGCAATGAACACGCTGAGAGCGGAGGACCGGCTGTGATTACTGTGGGAGAGATCTC	420				
QY	361	CTTTTTCAGTTGTGGAATGTTTTACAAACAATGGTTTCGATGTCTGGGGCCCGGGAGTC	420				
DB	421	CGCCAGC-----TAACTTCTACTGTGACTTTCGATCTCTGGGGCCGTGGCACC	468				
QY	421	CTGTGTACCGTCTCTCAGCTAGGACCAAGGGGCCATTCGGTCTTTCCTCCCTGGGACCCCTCC	480				
DB	469	CTGTGTACTGTCTCTCAGCCTCCACCAAGGGGCCATTCGGTCTTTCCTCCCTGGGACCCCTCC	528				
QY	481	TCCAAGAGCACTCTGGGGGACAGCGGCCCTGGGTGCTCTGGTGTCAAGGACTACTTCCCC	540				
DB	529	TCCAAGAGCACTCTGGGGGACAGCGGCCCTGGGTGCTCTGGTGTCAAGGACTACTTCCCC	588				
QY	541	GAACCGGTGACGGTGTGCTGGAACTCAGGCGCCCTGACACGAGCGCGTGCAACCTTCCCG	600				
DB	589	GAACCGGTGACGGTGTGCTGGAACTCAGGCGCCCTGACACGAGCGCGTGCAACCTTCCCG	648				
QY	601	GCTGTCTCAGTCTCAGGACTCTACTTCCCTCAGCAGCGTGTGTACCGTGCCTCCAGC	660				
DB	649	GCTGTCTCAGTCTCAGGACTCTACTTCCCTCAGCAGCGTGTGTACCGTGCCTCCAGC	708				
QY	661	AGCTTGGGCAACCAGACCTACATCTGCAAGTGAATCACAAGCCCAAGCAACCAAGGTG	720				
DB	709	AGCTTGGGCAACCAGACCTACATCTGCAAGTGAATCACAAGCCCAAGCAACCAAGGTG	768				
QY	721	GACAAGAAAGCAGAGCCCAAACTTTGTGACAAAACCTCACATGCCCCACCGTCCCAAGCA	780				
DB	769	GACAAGAAAGTTGAGGCCAAATCTTTGTGACAAAACCTCACATGCCCCACCGTCCCAAGCA	828				
QY	781	CCTGAACCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAAACCAAGGACACCCCTC	840				
DB	829	CCTGAACCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAAACCAAGGACACCCCTC	888				
QY	841	ATGATCTCCCGGACCCCTGAGGTCAATATGGTGGTGGAGCTGAGCCACGAAGACCTT	900				
DB	889	ATGATCTCCCGGACCCCTGAGGTCAATATGGTGGTGGAGCTGAGCCACGAAGACCTT	948				
QY	901	GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATTAATGCCAAGACAAGCCG	960				
DB	949	GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATTAATGCCAAGACAAGCCG	1008				

QY 961 CGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTGTGAGCGTCTCACCGTCTGCACCG 1020
Db 1009 CGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTGTGAGCGTCTCACCGTCTGCACCG 1068
QY 1021 GACTGGCTGAATGGCAGGAGTACAAAGTGCAGAGTGTCCAAACAAAGCCCTCCAGCCCC 1080
Db 1069 GACTGGCTGAATGGCAGGAGTACAAAGTGCAGAGTGTCCAAACAAAGCCCTCCAGCCCC 1128
QY 1081 ATCGAGAAACCATCTCCAAAGCCAAAGGAGCGCCCGAGAACACACAGGTTGACACCGTG 1140
Db 1129 ATCGAGAAACCATCTCCAAAGCCAAAGGAGCGCCCGAGAACACACAGGTTGACACCGTG 1188
QY 1141 CCCCATCCCGGATGAGTACCAAGAACACAGGTGAGCTGACCTGCTGGTCAAAAGGC 1200
Db 1189 CCCCATCCCGGATGAGTACCAAGAACACAGGTGAGCTGACCTGCTGGTCAAAAGGC 1248
QY 1201 TTCTATCCAGCGCATCGCGTGTGAGTGGAGAGCAATGGCGAGCGCGGAGAAACAATAC 1260
Db 1249 TTCTATCCAGCGCATCGCGTGTGAGTGGAGAGCAATGGCGAGCGCGGAGAAACAATAC 1308
QY 1261 AGACACGCTCCCGTGTGAGTCCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1309 AAGACACGCTCCCGTGTGAGTCCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1368
QY 1321 GTGGACAAGAGCAGGTGGCAGCGGGAACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1369 GTGGACAAGAGCAGGTGGCAGCGGGAACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1428
QY 1381 GTGGACAACCATACACGAGAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1431
Db 1429 GTGGACAACCATACACGAGAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1479

RESULT 15
AR031184 LOCUS AR031184 1428 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5866125.
ACCESSION AR031184
VERSION AR031184.1 GI:5945473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1428)
AUTHORS Brans, P., Chamat, S., Salim., Pan, L.-Z., Walsh, E.E., Heard, C. Janne.
TITLE Neutralizing high affinity human monoclonal antibodies specific to RSV F-protein and methods for their manufacture and therapeutic use thereof
JOURNAL Patent: US 5866125-A 17 02-FEB-1999;
FEATURES
source Location/Qualifiers
BASE COUNT 326 a 464 c 373 g 265 t
ORIGIN

Query Match 79.3%; Score 1134.8; DB 6; Length 1428;
Best Local Similarity 89.0%; Pred. No. 3.2e-219;
Matches 1262; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

QY 17 TCCTTCCT 76
Db 17 TCCTTCCT 76
QY 77 CGGCGCCAGAGCTGTGAAGCCCTCCGAGACCTGCTCCCTCACCTCGGTGTCTCTCTCTCT 136
Db 77 CTGGTCT 136
QY 137 GCTC---CATCAGCGGTGGTATGGCTGGGGCTGGATCCGCCAGCCGCCAGGGAAGGGCC 193
Db 137 TCTCACTCAGCAACCTTAGAATGGGTGTGACCTGGATCCGTGACGCCGCCCGGGAAGGCC 196
QY 194 TGGAGTGGATTGGAGGTTTCTATAGTAGTAGTGGGAACACCTACTACAAACCCCTCTCTCA 253

Db 197 TAGAATGGCTTGGAAACAATTTTTCGAGTGCAGAA---GTCCTTCAGTCTCTCTCTGA 253
QY 254 AGAGTCAAGTCACTACCAATTTTCAACAGACAGTCCCAAGAACCCAGTTCCTCCCTGAAGCTGAAC 313
Db 254 AGAGAGAGTCACTACCACTCCAGAGACACTCCAGAGCCAGGTGGTCTTACGTTGACCA 313
QY 314 CTATGACCCCGCGGACAGCGCGTGTATTAATCTGTGTGAGAGATCGTCTTTTTCAGTTG 373
Db 314 ACGTGGACCTGTGGACACAGCCACATATTAATGTGTGACGGGTAGGACTGTATGACATCA 373
QY 374 TTGGAATGGTTTACAAACAAGTGTGTCTGGGGCCCGGAGTCTCTGTGTCAAGCTCT 433
Db 374 ATGCTT---ATTACCTATATCTACCTGGATTATTGGGGGAGGGAACCCCTGGTCAACGCTCT 430
QY 434 CCTCAGCTAGCACCAAGGCGCCATCGGTCTTCCCTGTGCACCTCTCTCTCAAGAGCACCT 493
Db 431 CCTCAGCTAGCACCAAGGCGCCATCGGTCTTCCCTGTGCACCTCTCTCTCAAGAGCACCT 490
QY 494 CTGGGGGCAAGCGGCGCTGGTGTCAAGAGTACTTTCCCGGAAACCGGTGACGG 553
Db 491 CTGGGGGCAAGCGGCGCTGGTGTCAAGAGTACTTTCCCGGAAACCGGTGACGG 550
QY 554 TGTCTGTGAACTCAGCGGCGCTGACAGCGGGTGCACACCTTCCCGGCTGTCTCTACAGT 613
Db 551 TGTCTGTGAACTCAGCGGCGCTGACAGCGGGTGCACACCTTCCCGGCTGTCTCTACAGT 610
QY 614 CCTCAGGACTTACTCTCTCAGCAGCGTGTGACCGTGGCTCTCCAGCAGCTTTGGGCACCC 673
Db 611 CCTCAGGACTTACTCTCTCAGCAGCGTGTGACCGTGGCTCTCCAGCAGCTTTGGGCACCC 670
QY 674 AGACCTACATCTGCAACGTAATCAAAAGCCCAAGCAACCAAGGTGGACAAAGAGCAG 733
Db 671 AGACCTACATCTGCAACGTAATCAAAAGCCCAAGCAACCAAGGTGGACAAAGAGCAG 730
QY 734 AGCCCAATCTGTGACAAACTCACACATGCCACCGTSCCCAGCACCTGAACTCTCTGG 793
Db 731 AGCCCAATCTGTGACAAACTCACACATGCCACCGTSCCCAGCACCTGAACTCTCTGG 790
QY 794 GGGGACCGTCAAGTCTCTCTCTTCCCGGCAAAACCAAGGACACCTCATGATCTCCCGGA 853
Db 791 GGGGACCGTCAAGTCTCTCTCTTCCCGGCAAAACCAAGGACACCTCATGATCTCCCGGA 850
QY 854 CCCCTGAGGTCAATGCGTGTGTGTGAGTGCACGACGACGACGACCTGAGGTCAAGTTCA 913
Db 851 CCCCTGAGGTCAATGCGTGTGTGTGAGTGCACGACGACGACCTGAGGTCAAGTTCA 910
QY 914 ACTGTAAGTGGAGCGGTGAGTGCATTAATGCCAAGACAAAGCCCGGAGGAGCAGT 973
Db 911 ACTGTAAGTGGAGCGGTGAGTGCATTAATGCCAAGACAAAGCCCGGAGGAGCAGT 970
QY 974 ACAACAGCAGTACCGTGTGTGTGAGTGCATCTACCGTCTCTGCAACAGGACTGGCTGAATG 1033
Db 971 ACAACAGCAGTACCGTGTGTGTGAGTGCATCTACCGTCTCTGCAACAGGACTGGCTGAATG 1030
QY 1034 GCAAGGAGTCAAGTGCAGGTCTTCCAAAGCCCTCCAGCGCCCATCGAAGAAACCA 1093
Db 1031 GCAAGGAGTCAAGTGCAGGTCTTCCAAAGCCCTCCAGCGCCCATCGAAGAAACCA 1090
QY 1094 TCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACACCTCTCCCGGCTTCCCGGG 1153
Db 1091 TCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACACCTCTCCCGGCTTCCCGGG 1150
QY 1154 ATGAGTGCACAAAGAACCGAGTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1213
Db 1151 ATGAGTGCACAAAGAACCGAGTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1210
QY 1214 ACATCGCGGTGGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAGACCAAGCCTC 1273
Db 1211 ACATCGCGGTGGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAGACCAAGCCTC 1270
QY 1274 CCGTCTCTGAGTCTCCGACCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1333

Db 1271 CCGTGTGGACTCCGACGGCTCCTTCTCTACAGCAAGCTCACCGTGGACAAGACA 1330
QY 1334 GGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACACCACT 1393
|||
Db 1331 GGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACACCACT 1390
|||
QY 1394 ACACGCAGAAGAGCCTTCTCCCTGTCTCCGGTAAATGA 1431
|||
Db 1391 ACACGCAGAAGAGCCTTCTCCCTGTCTCCGGTAAATGA 1428
|||

Search completed: April 6, 2003, 01:56:18
Job time : 4493.25 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 65.1566 Seconds
(without alignments)
6735.375 Million cell updates/sec

Title: US-09-758-173-11

Perfect score: 1431

Sequence: 1 ATGAACACCTGTGTTCTT.....CCCTGTCCTCCGGTAATGA 1431

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	3	US-08-487-550-11
2	1315.8	91.9	1431	3	US-08-487-550-3
3	1276.4	89.2	1567	3	US-09-049-672A-17
4	1213.6	84.8	1418	4	US-08-793-450-7
5	1181	82.5	1404	3	US-08-523-894-7
6	1177.8	82.3	1404	3	US-08-523-894-11
7	1176.2	82.2	1404	3	US-08-523-894-9
8	1134.8	79.3	1428	1	US-08-488-376-17
9	1134.8	79.3	1428	2	US-08-634-223-17
10	1134.8	79.3	1428	2	US-08-634-224-17
11	1134.8	79.3	1428	2	US-08-634-400-17
12	1134.8	79.3	1428	2	US-08-635-878-17
13	1134.8	79.3	1428	2	US-08-770-057-17
14	1134.8	79.3	1428	2	US-09-335-697B-17
15	1134.8	79.3	1428	4	US-09-335-697B-17
16	1125.2	78.6	1428	1	US-08-488-376-19
17	1125.2	78.6	1428	2	US-08-634-223-19
18	1125.2	78.6	1428	2	US-08-634-224-19
19	1125.2	78.6	1428	2	US-08-634-400-19
20	1125.2	78.6	1428	2	US-08-635-878-19
21	1125.2	78.6	1428	2	US-08-770-057-19
22	1125.2	78.6	1428	4	US-09-335-697B-19
23	1125.2	78.6	1428	4	US-09-335-697B-19
24	1121.2	78.4	1617	2	US-08-378-939-9
25	1118	78.1	19040	4	US-09-343-485A-3
26	1112.4	77.7	1437	3	US-08-487-550-7
27	1107.8	77.4	1576	1	US-08-157-101A-6

28	1102.2	77.0	6557	1	US-08-286-740-3	Sequence 3, Appli
29	1102.2	77.0	6557	5	PCT-US95-09576-3	Sequence 3, Appli
30	1097.8	76.7	1350	1	US-08-157-101A-9	Sequence 9, Appli
31	1096.6	76.6	9209	1	US-08-149-099C-3	Sequence 3, Appli
32	1096.6	76.6	9209	1	US-08-476-275-2	Sequence 2, Appli
33	1096.6	76.6	9209	2	US-08-478-967A-3	Sequence 3, Appli
34	1096.6	76.6	9209	4	US-08-475-815B-3	Sequence 2, Appli
35	1096.6	76.6	18986	2	US-08-819-866-2	Sequence 2, Appli
36	1096.6	76.6	18986	2	US-09-023-715-2	Sequence 2, Appli
37	1096.6	76.6	18986	4	US-09-343-485A-2	Sequence 2, Appli
38	1093.8	76.4	8120	3	US-09-027-449-68	Sequence 68, Appli
39	1093.8	76.4	8120	3	US-09-026-985-68	Sequence 68, Appli
40	1093.8	76.4	8120	4	US-09-121-952A-68	Sequence 68, Appli
41	1093.8	76.4	8120	4	US-09-234-340A-68	Sequence 21, Appli
42	1069	74.7	1655	3	US-09-049-672A-21	Sequence 21, Appli
43	1051.2	73.5	6285	1	US-08-467-420A-49	Sequence 49, Appli
44	1051.2	73.5	6285	1	US-08-470-110A-49	Sequence 49, Appli
45	1051.2	73.5	6285	1	US-08-667-769A-49	Sequence 49, Appli

ALIGNMENTS

RESULT 1

US-08-487-550-11

; Sequence 11, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1431 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1431

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 1..1431

US-08-487-550-11

Query Match

100.0%; Score 1431; DB 3; Length 1431;

[illegible]

Db	961	CGGAGAGCAGGTACAAACGACGACGTACCGTGTGGTCAAGCTCTCAACCGTCTCTCAACG	1020
Qy	1021	GACTGGCTGAATGGCAAGGAGTACAAGTCAAGTCTCCAAACAAAGAGCCCTCCCAAGCCCCC	1080
Db	1021	GACTGGCTGAATGGCAAGGAGTACAAGTCAAGTCTCCAAACAAAGAGCCCTCCCAAGCCCCC	1080
Qy	1081	ATCGAGAAACCATCTCCAAAGCCAAAGGGAGCCCGAGAACACACAGGTGTACACCCCTG	1140
Db	1081	ATCGAGAAACCATCTCCAAAGCCAAAGGGAGCCCGAGAACACACAGGTGTACACCCCTG	1140
Qy	1141	CCCCCATCCGGGATGAGTGCACCAAGAACACAGGTTCAGCTGCCTGGTCAAAAGGC	1200
Db	1141	CCCCCATCCGGGATGAGTGCACCAAGAACACAGGTTCAGCTGCCTGGTCAAAAGGC	1200
Qy	1201	TTCTATCCAGCGACATCCGCTGGAGTGGGAGAGCANTGGCAGCCGGAGAACAACTAC	1260
Db	1201	TTCTATCCAGCGACATCCGCTGGAGTGGGAGAGCANTGGCAGCCGGAGAACAACTAC	1260
Qy	1261	AAGACCAACGCTCCCGTGTGAGCTCCGACCCGAGCGCTCCTTCTCTACAGCAAGCTCACC	1320
Db	1261	AAGACCAACGCTCCCGTGTGAGCTCCGACCCGAGCGCTCCTTCTCTACAGCAAGCTCACC	1320
Qy	1321	GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTCTCATCTCCGTGATGCATGAGGCT	1380
Db	1321	GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTCTCATCTCCGTGATGCATGAGGCT	1380
Qy	1381	CTGCACAAACACTACACGACAGAGACCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1381	CTGCACAAACACTACACGACAGAGACCTCTCCCTGTCTCCGGGTAAATGA	1431
RESULT 3			
US-09-049-672A-17			
; Sequence 17, Application US/09049672A			
; Patent No. 6135941			
; GENERAL INFORMATION:			
; APPLICANT: Hillman, Jennifer L.			
; APPLICANT: Lal, Preeti			
; APPLICANT: Tang, Y. Tom			
; APPLICANT: Yue, Henry			
; APPLICANT: Au-Young, Janice			
; APPLICANT: Corley, Neil C.			
; APPLICANT: Guegler, Karl J.			
; APPLICANT: Baughn, Mariah R.			
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS			
; NUMBER OF SEQUENCES: 28			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Incyte Pharmaceuticals, Inc.			
; STREET: 3174 Porter Drive			
; CITY: Palo Alto			
; STATE: CA			
; COUNTRY: USA			
; ZIP: 94304			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: Fast-SEQ for Windows Version 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/049,672A			
; FILING DATE: HEREWITH			
; CLASSIFICATION: 536			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER:			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Cerrone, Michael C			
; REGISTRATION NUMBER: 39,132			
; REFERENCE/DOCKET NUMBER: PF-0497 US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 650-855-0555			
; TELEFAX: 650-845-4166			
; TELEX:			

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTUT01
; CLONE: 1513264
US-09-049-672A-17

Query Match 89.2%; Score 1276.4; DB 3; Length 1567;

Best Local Similarity 94.7%; Pred. No. 1.4e-298; Mismatches 61; Indels 15; Gaps 3;

Qy 1 ATGAAACACCTGTGTTCTTCTCTCTCTGTTGGGAGCTCCAGATGGTCTCTGTCACG 60
Db 78 ATGAAACACCTGTGTTCTTCTCTCTCTGTTGGGAGCTCCAGATGGTCTCTGTCACG 137
Qy 61 GTGAGCTGAGGAGTGGGGCCAGAGCTGGTGAAGCTTCGGAGACCTGTCTCTGACC 120
Db 138 GTGAGCTGAGGAGTGGGGCCAGAGCTGGTGAAGCTTCGGAGACCTGTCTCTGACC 197
Qy 121 TGCGCTGTCTGTGTGCTCATC---AGCGGTGGTATAGGCTGGGGCTGGATCCGCCAG 177
Db 198 TGCGCTGTCTGTGTGCTCATCAGTGTGTGTGTTACTGTGAGCTGGATCCGCCAG 257
Qy 178 CCCCAGGAGGGCTGGAGTGGAGTTCATATAGTAGTAGTGGGAGACCTTAC 237
Db 258 CCCCAGGAGGGCTGGAGTGGAGTTCATATAGTAGTAGTGGGAGACCTTAC 314
Qy 238 TACAACCCCTCCCTCAAGAGTCAAGTCAACATTTCAACAGACAGCTCCAAAGAACCACTTC 297
Db 315 TACAACCCCTCCCTCAAGAGTCAAGTCAACATTTCAACAGACAGCTCCAAAGAACCACTTC 374
Qy 298 TCCCTGAAGCTGAATCTATGACCGCGCGGACACCGCGGTGTATCTGTGTGAGAT 357
Db 375 TCCCTGAAGCTGAATCTATGACCGCGCGGACACCGCGGTGTATCTGTGTGAGAT 433
Qy 358 CGTCTTTTTCAGTTGTTGAATGGTTTAAACAACATGGTTCGATGTCTGTGGGGCCCGGA 417
Db 434 -----TGACGTAGTGTAAAGGGGGGAACTACGGGTATGAGCTGTGGGGCCCGGA 485
Qy 418 GTCTGTGTCACCGTCTCTCAGCTAGACCAAGGGGCGCATCGTCTTCCCTCTGACCC 477
Db 486 ACCCTGTGTCACCGTCTCTCAGCTAGACCAAGGGGCGCATCGTCTTCCCTCTGACCC 545
Qy 478 TCCTCCAGAGCACCTCTGGGGGACAGCGGGCCCTGGGCTGTCTGTCTCAAGGACTACTTC 537
Db 546 TCCTCCAGAGCACCTCTGGGGGACAGCGGGCCCTGGGCTGTCTGTCTCAAGGACTACTTC 605
Qy 538 CCGAAACGGGTGAGGTGCTGTGAATCTAGGCGCCCTGACAGCGGGGTGACACCTTC 597
Db 606 CCGAAACGGGTGAGGTGCTGTGAATCTAGGCGCCCTGACAGCGGGGTGACACCTTC 665
Qy 598 CCGGCTGTCTTACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGGTGTGACCGTGCCTTC 657
Db 666 CCGGCTGTCTTACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGGTGTGACCGTGCCTTC 725
Qy 658 AGCAGCTTGGCACCAGCTTACATCTGAAGTGAATCAAGCCCGAGCAACCAAG 717
Db 726 AGCAGCTTGGCACCAGCTTACATCTGAAGTGAATCAAGCCCGAGCAACCAAG 785
Qy 718 GTGACAAGAAAGCAGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTGCCCA 777
Db 786 GTGACAAGAGAGTTGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTGCCCA 845
Qy 778 GCACCTGAATCTCTGGGGGACGTGATCTTCTTCTTCCCGCCCAAAACCAAGGACAC 837
Db 846 GCACCTGAATCTCTGGGGGACGTGATCTTCTTCTTCCCGCCCAAAACCAAGGACAC 905
Qy 838 CTCATGATCTCCCGGACCCCTGAGGTCAATGCTGGTGTGAGCTGTGAGCCCAAGAC 897

Db 906 CTCATGATCTCCCGACCCCTGAGGTCAATGCTGTGTGGACGTGAGCCACGAAGAC 965
Qy 898 CTTGAGGTCAAGTTCAACTGTGTGACGCGCTGGAGGTGCATAATGCCAACACAAG 957
Db 966 CTTGAGGTCAAGTTCAACTGTGTGACGCGCTGGAGGTGCATAATGCCAACACAAG 1025
Qy 958 CCGGGGAGGAGCAGTACAACAGACAGTACCGTGTGTGAGCTCTTCAACGCTCTCCAC 1017
Db 1026 CCGGGGAGGAGCAGTACAACAGACAGTACCGTGTGTGAGCTCTTCAACGCTCTCCAC 1085
Qy 1018 CAGGACTGCTCAATGGCAAGGAGTACAAGTGAAGGTCTTCAACAAAGCCCTCCACGCC 1077
Db 1086 CAGGACTGCTCAATGGCAAGGAGTACAAGTGAAGGTCTTCAACAAAGCCCTCCACGCC 1145
Qy 1078 CCATCGAGAAACCATCTTCAAGCCAAAGGAGGAGCCCGGAGAACCCACAGGTGTACAC 1137
Db 1146 CCATCGAGAAACCATCTTCAAGCCAAAGGAGGAGCCCGGAGAACCCACAGGTGTACAC 1205
Qy 1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTGAGCTGCTGTGTTCAAA 1197
Db 1206 CTGCCCCCATCCCGGGAGGAGTGAACCAAGAACCAAGGTGAGCTGCTGTGTTCAAA 1265
Qy 1198 GGCTTCTATCCAGCGACATCGCGTGGAGTGGAGCAATGGCAGCGGAGAACCAAC 1257
Db 1266 GGCTTCTATCCAGCGACATCGCGTGGAGTGGAGCAATGGCAGCGGAGAACCAAC 1325
Qy 1258 TACAAGACACGCTCCCGTGTGAGCTCCGAGCGCTCTTCTTCTTCTTCTTCTTCTTCT 1317
Db 1326 TACAAGACACGCTCCCGTGTGAGCTCCGAGCGCTCTTCTTCTTCTTCTTCTTCTTCT 1385
Qy 1318 ACCGTGGACAAGCAGGTGGCAGCGAGCGAGGAACTGTTCTCATGCTCCGTGATGATGAG 1377
Db 1386 ACCGTGGACAAGCAGGTGGCAGCGAGGAACTGTTCTCATGCTCCGTGATGATGAG 1445
Qy 1378 GCTCTGCACCACTTACACGACAGAGACCTCTCCCTGCTCCCGGTGAATGA 1431
Db 1446 GCTCTGCACCACTTACACAGAGAGACCTCTCCCTGCTCCCGGTGAATGA 1499

RESULT 4

US-08-793-450-7

; Sequence 7, Application US/08793450

; Patent No. 6312690

; GENERAL INFORMATION:

; APPLICANT: EDELMAN, LENA

; APPLICANT: MARGARITTE, CHRISTEL

; APPLICANT: KACZOREK, MICHEL

; APPLICANT: CHAABIHI, HASSAN

; TITLE OF INVENTION:

; MONOCLONAL RECOMBINANT ANTI-RHESUS D

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

; ADDRESS: P.C.

; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,450

; FILING DATE: 03-MAR-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 94/10566

; FILING DATE: 02-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1418
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..57
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..1418
OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY"
OTHER INFORMATION: CHAIN"

US-08-793-450-7

Query Match 84.8%; Score 1213.6; DB 4; Length 1418;
Best Local Similarity 92.5%; Pred. No. 1.8e-283;
Matches 1312; Conservative 0; Mismatches 94; Indels 12; Gaps 3;

Qy	13	TGGTTCCTCTCTCTGTTGGGAGCTCCAGATGGTCTCTGTCACAGTCCAGCTGAG	72
Db	13	TGTATCATCTCTCTCTGTTGGTAGCAACAGCTACAGGTGTCCACTCCAGGTCCAACTGGAG	72
Qy	73	GAGTCGGGCGCCAGAGCTGTGTAGGCTTCGGAGACCTGTCCCTCACCTGCGCTGTCT	132
Db	73	CAGTGGGCGCCAGAGCTGTGTAGGCTTCGGAGACCTGTCTCCCTCACCTGCTGTCT	132
Qy	133	GGTGGCTCCATCAGCGGTGTATGCTGGGCTGGATCCGACCGCCCGCCAGGGAAGGGG	192
Db	133	GGTGGGTCCTTCA---GTGGTTACTACTGGAGCTGGATCCGACCGCCCGCCAGGGAAGGGG	189
Qy	193	CTGGAGTGGATGGGAGTTTCTATAGTACTAGTGGACACCTACTACACCCCTCCCTC	252
Db	190	CTGGAGTGGATGGGGAATC---AATCATGTGGAGCACCACCTACTCCCTGAACTGAAC	246
Qy	253	AAGAGTCAAGTCAACATTTCAACAGACACGTCCAGAACCAAGTTCCTCCCTGAAGCTGAAC	312
Db	247	AAGAGTCAAGTCAACATATCAGTAGACACGTCCAGAACCAAGTTCCTCCCTGAACTGAAC	306
Qy	313	TCTATGACCGCGGACACCGCGGTGTATTACTGTGTGAGAGATCGTCTTTTTCAGTT	372
Db	307	TCTGTGACCGCGGACACCGCGGTGTATTACTGTGTGAGAGGCGCCAGAGTATAAA---	363
Qy	373	GTTGGAAATGGTTTACAACTGGTTTCGATGTCTGGGGCGCGGGAGTCTGTGTCAACGTC	432
Db	364	---TGGAAATGATCATGGGACTGGTTTCGACCCCTGGGCGCAAGGTACCACTGTCAACGTC	420
Qy	433	TCCTCAGTACGACCAAGGCGCCATCGTCTTCCCGCTGGGACACCTCTCCCAAGAGCAC	492
Db	421	TCCTCAGCGCTCCCAAGGCGCCATCGTCTTCCCGCTGGGACACCTCTCCCAAGAGCAC	480
Qy	493	TCGGGGGACACGCGGCTTGGGCTCCCTGGTTCAGGACTACTTCCCGGAAACCGGTGACG	552
Db	481	TCGGGGGACACGCGGCTTGGGCTTGGTTCAGGACTACTTCCCGGAAACCGGTGACG	540
Qy	553	GTGTGTGGAATCAGCGCGCTTGACAGCGGCTGCAACCTTCCCGGCTGTCTTACAG	612
Db	541	GTGTGTGGAATCAGCGCGCTTGACAGCGGCTGCAACCTTCCCGGCTGTCTTACAG	600
Qy	613	TCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGCGCTCCCTCCAGCAGCTTGGGCACC	672
Db	601	TCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGCGCTCCCTCCAGCAGCTTGGGCACC	660

Qy	673	CAGACCTACATCTGTCAACGTTGAATCAAGCCCGAGCAACCAAGGTGGAAGAAGCA	732
Db	661	CAGACCTACATCTGTCAACGTTGAATCAAGCCCGAGCAACCAAGGTGGAAGAAGCA	720
Qy	733	GAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGGCCAGCAGCTGAATCTCTG	792
Db	721	GAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGGCCAGCAGCTGAATCTCTG	780
Qy	793	GGGGACCGTCAAGTCTTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGG	852
Db	781	GGGGACCGTCAAGTCTTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGG	840
Qy	853	ACCCCTGAGTCAATCGGTGGTGGAGCTGAGCAGCAAGACCTCTGAGTCAAGTTC	912
Db	841	ACCCCTGAGTCAATCGGTGGTGGAGCTGAGCAGCAAGACCTCTGAGTCAAGTTC	900
Qy	913	AACTGGTACGTGGAGCGGTGGAGGTGTCATAATGCCAAGACAAAGCCGCGGAGGAGCAG	972
Db	901	AACTGGTACGTGGAGCGGTGGAGGTGTCATAATGCCAAGACAAAGCCGCGGAGGAGCAG	960
Qy	973	TACAACAGCAGTACCTGTTGGTCCAGGTCTCTACCGTCTGTGACAGGACTGGCTGAAT	1032
Db	961	TACAACAGCAGTACCTGTTGGTCCAGGTCTCTACCGTCTGTGACAGGACTGGCTGAAT	1020
Qy	1033	GGCAGGAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCC	1092
Db	1021	GGCAGGAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCC	1080
Qy	1093	ATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGG	1152
Db	1081	ATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGG	1140
Qy	1153	GATGAGCTGACCAAGAACCAAGGTGAGTCAAGTGTGACACCTGCTTCAAGGCTTCTATCCCAGC	1212
Db	1141	GATGAGCTGACCAAGAACCAAGGTGAGTCAAGTGTGACACCTGCTTCAAGGCTTCTATCCCAGC	1200
Qy	1213	GACATCCCGTGGAGTGGAGAGCAATGGGAGCGAGCAATGGGAGCGGAGAACCAACTACAAAGACACGCT	1272
Db	1201	GACATCCCGTGGAGTGGAGAGCAATGGGAGCGGAGCAATGGGAGCGGAGAACCAACTACAAAGACACGCT	1260
Qy	1273	CCCGTGTGGACTCCGAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGC	1332
Db	1261	CCCGTGTGGACTCCGAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGC	1320
Qy	1333	AGGTGGCAGCAGGAGGAACTCTTCTCATGCTCCGTCGATGATGAGGCTCTGCACAAACAC	1392
Db	1321	AGGTGGCAGCAGGAGGAACTCTTCTCATGCTCCGTCGATGATGAGGCTCTGCACAAACAC	1380
Qy	1393	TACAGCAGAGAGCCCTCTCCCTGTCTCCGGTAAATG	1430
Db	1381	TACAGCAGAGAGCCCTCTCCCTGTCTCCGGTAAATG	1418

RESULT 5
US-08-523-894-7
Sequence 7, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Ref, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy

STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with th
CHROMOSOME/SEGMENT: mutation
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1404
US-08-523-894-11

Query Match	82.3%	Score 1177.8	DB 3	Length 1404
Best Local Similarity	90.3%	Pred. No. 7.8e-275		
Matches 1292	Conservative	0	Mismatches 112	Indels 27
Gaps				
QY	1	ATGAAACACCTGTGGTTCTTCCCTCCTCCTCGTGGCAGCTCCCAGATGGGTCTGTCTCCAG	60	
Db	1	ATGAAACACCTGTGGTTCTTCTCCTCCTCGTGGCAGCTCCCAGATGGGTCTGTCTCCAG	60	
QY	61	GTGCAGTGTGACGAGTCCGGCCACGAGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTCAC	120	
Db	61	GTGCAGTGTGACGAGTCCGGCCACGAGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTCAC	120	
QY	121	TGCGCTGTCTGTGGTGCCTCCATCAGCGGTGTATGGCTGGGGCTGGATCGCCAGGCC	180	
Db	121	TGCAGTGTCTGTGGTGCCTCCATCAGCGGTGACTATTATTGGTTCTGGATCGCCAGTCC	180	
QY	181	CCAGGGAAGGGCTGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGGAACACTACTAC	240	
Db	181	CCAGGGAAGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGCCACCAATTAC	240	
QY	241	AACCCCTCCCTCAAGAGTCAAGTCCACATTTCAACAGACACGTCCAAGAACAGATTCTCC	300	
Db	241	ATATCCCTCCCTCAACAAATCAGATCTCCATTTCAATAGACACGTCCTCAAGAACCTTTCTCC	300	
QY	301	CTGAAGCTGAACCTCTATGACCGCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT	360	
Db	301	CTGAAGACTGAGGCTGTGACCGCGCGGACACGGCCGTCTATTACTGTGCGAGTAATA---	358	
QY	361	CTTTTTTCAGTTGTTGGAATGTTTACAACTGTTTCGATGTCTGGGGCCCGGAGTGC	420	
Db	359	-----TATTGAAATATCTTCACTGGTTATTATCTGGGGCCAGGAGTGC	402	

Qy	421	CTGTGTCACCGCTCTCTCAGCTAGCACCAAGGGCCATCGGTCTTCCCTCCCTGGCACCCCTCC	480
Db	403	CTGTGTACCGGTCTCTCAGCTAGCACCAAGGGCCATCGGTCTTCCCTCCCTGGGGCCCTGC	462
Qy	481	TCCAAGAGCACTCTGGGGGCACAGCGGCCCTTGGGTGCTTGGTCAAGACTACTTTCCTCC	540
Db	463	TCCAGAGCACTCTCGAGAGCACAGCGGCCCTGGGTGCTTGGTCAAGACTACTTTCCTCC	522
Qy	541	GAAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTCAGCAGCGGGGTGCACACCTTCCCG	600
Db	523	GAAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTCAGCAGCGGGGTGCACACCTTCCCG	582
Qy	601	GCTGTCTTACAGTCTCAGACTCTACTTCTCAGCAGCGTGGTGAACCGTGCCTCCAGC	660
Db	583	GCTGTCTTACAGTCTCAGACTCTACTTCTCAGCAGCGTGGTGAACCGTGCCTCCAGC	642
Qy	661	AGCTTGGGCACCCAGACTACATCTGCAAGCTGAATCAACGCCAGCAACACCAAGGTG	720
Db	643	AGCTTGGGCACGAAGACTACACTGCAAGCTAGATCAACGCCAGCAACACCAAGGTG	702
Qy	721	GACAAGAAAGCAGAGCCCAATCTTGTGACAAACTCACAATGCCACCGTGCCTCCAGCA	780
Db	703	GACAAGAGGTGAGTCCAAATATGG-----TCCCCCATGCCCCACCTGCCCCAGCA	753
Qy	781	CCTGAACTCTTGGGGGACCGTCAGTCTTCTTCTTCCCCCAAAACCCAGAGACCTC	840
Db	754	CCTGAGTTCAGGGGGAGCATCAGTCTTCTTCTTCCCCCAAAACCCAGAGACTCTC	813
Qy	841	ATGATCTCCCGGACCCCTGAGGTCAATCGCTGGTGGAGCTCAGGCACGAGACCCCT	900
Db	814	ATGATCTCCCGGACCCCTGAGGTCACTGCTGGTGGAGCTGAGCCAGAGACCCCT	873
Qy	901	GAGTCAAGTTCAACTGTGACGTGGACGGCTGGAGGTGCATAATGCCAAGCAAAAGCG	960
Db	874	GAGTCCAGTTCAACTGGTACGTGGATGCGTGGAGGTGCATAATGCCAAGCAAAAGCG	933
Qy	961	CGGAGAGCAGTACAACAGCAGTACCGTGGTGGTCAACCGTCTCACCGTCTCTGCACAG	1020
Db	934	CGGAGAGCAGTTCAAACAGCAGTACCGTGGTGGTCAACCGTCTCACCGTCTCTGCACAG	993
Qy	1021	GACTGGCTGAATGGCAAGGATCAAGTGCAAAGTCTCCAAACAAAGCCCTCCCAAGCCCC	1080
Db	994	GACTGGCTGAACGGCAAGGATCAAGTGCAAAGTCTCCAAACAAAGCCCTCCCGTCTCTCC	1053
Qy	1081	ATCGAGAAACCACTTCCAAAGCCAAAGGGACGCCCGCAGAAACCAAGGTGTACACCTGT	1140
Db	1054	ATCGAGAAACCACTTCCAAAGCCAAAGGGACGCCCGCAGAGCCACAGGTGTACACCTGT	1113
Qy	1141	CCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTCAAGCTGACTGCTGGTCAAAAGGC	1200
Db	1114	CCCCCATCCAGGAGAGATGACCAAGAAACCAAGTCAAGCTGACTGCTGGTCAAAAGGC	1173
Qy	1201	TTCTATCCAGCGACATCCCGCTGGAGTGGGAGAGCAATGGCGAGCCGGAGAAACAATAC	1260
Db	1174	TTCTATCCAGCGACATCCCGCTGGAGTGGGAGAGCAATGGCGAGCCGGAGAAACAATAC	1233
Qy	1261	AAGACCAAGCCTCCCGTGTGACTCCGACGGCTCTTCTTCTCATGCTCCGTGATGACATGAGCT	1320
Db	1234	AAGACCAAGCCTCCCGTGTGACTCCGACGGCTCTTCTTCTCATGCTCCGTGATGACATGAGCT	1293
Qy	1321	GTGGACAAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGACATGAGCT	1380
Db	1294	GTGGACAAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGACATGAGCT	1353
Qy	1381	CTGCACCAACTACACCGCAGAGACCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1354	CTGCACCAACTACACAGAAAGACCTCTCCCTGTCTCTGGGTAAATGA	1404

RESULT 7
US-08-523-894-9
; Sequence 9, Application US/08523894
; Patent No. 6136310

GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1404
PS-08-523-894-9

	Query Match	82.2%;	Score 1176.2;	DB 3;	Length 1404;
	Best Local Similarity	90.2%;	Pred. No. 1.9e-274;		
	Matches 1291;	Conservative	0;	Mismatches 113;	Indels 27; Gaps
QY	1	ATGAAACACCTGTGGTTCCTTCCTCCTGGTGGCAGCTCCAGATGGGTCTGTGCCAG	60		
DB	1	ATGAAACACCTGTGGTTCCTTCCTCCTGGTGGCAGCCCCAGATGGGTCTGTGCCAG	60		
QY	61	GTGCAGTGCAGAGTGGGCCCCAGACACTGGGTGAAGCCTTCGGAGACCTGTGCTTCACC	120		
DB	61	GTGCAGTGCAGAGTGGGCCCCAGACTGGTGAAGCCTTCGGAGACCTGTGCTTCACC	120		
QY	121	TGGGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGGCC	180		
DB	121	TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTTGGATCCGCCAGTCC	180		
QY	181	CCAGGGAAGGGCTGGAGTGGATTGGGAGTTCTTATAGTAGTAGTGGGAACCACTTACTAC	240		
DB	181	CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCCCAATATAC	240		
QY	241	AACCCCTCCCTCAAGAGTCAAGTCAACATTTCAACAGACACGTCCCAAGAACCAAGTTCTCC	300		
DB	241	AATCCCTCCCTCAACATCGAGTCTCCATTTCATATGACACGTCCCAAGAACCTTCTCTCC	300		

QY	301	CTGAAGCTGAACTCTATGA	CGCGCGCGGACA	CGCGCGTGTATTACTGTGTGACAGATCGT	360
Db	301	CTGAAACTGAGTCTGTGAC	CGCGCGCGGACA	CGCGCGTCTATTACTGTGCGAGTAATA--	358
QY	361	CTTTTTTCAGTTGTTGNAATGGTTTACAA	CAACTGGTTCGATGCTCTGGGGCCCGGAGTC	420	
Db	359	-----TATTGAATAATCTTC	ACTGGTTATTATCTATCTGGGGCCAGGAGTC	402	
QY	421	CTGGTCACCGTCTCTCAGCTAGCACCA	AGGGGCCCATCGTCTTTCCTCCCTGGCACCCCTCC	480	
Db	403	CTGGTCACCGTCTCTCAGCTAGCACCA	AGGGGCCCATCGTCTTTCCTCCCTGGCGCCCTGC	462	
QY	481	TGCAAGAGCACCTCTGGGGGCA	CAGCGGCCCTGGGTGCTGTGTCGAAGGACTACTTCCCC	540	
Db	463	TCCAGGAGCACCTCCGAGAGCA	CAGCGGCCCTGGGTGCTGTGTCGAAGGACTACTTCCCC	522	
QY	541	GAAACCGGTGACGGTGTCTGTGAACT	CAAGGCGCCCTGACAGCGGCGTGCACACCTTCCCG	600	
Db	523	GAAACCGGTGACGGTGTCTGTGAACT	CAAGGCGCCCTGACAGCGGCGTGCACACCTTCCCG	582	
QY	601	GCTGTCTTACAGTCTCTCAGGACTCT	TACTTCCCTCAGCAGCGTGTGACCGTGCCTCCAGC	660	
Db	583	GCTGTCTTACAGTCTCTCAGGACTCT	ATCTCCCTCAGCAGCGTGTGACCGTGCCTCCAGC	642	
QY	661	AGCTTTGGGCACCCAGACCTTACAT	CTGCAAGCTGTAATCAAAAGCCCAAGCAACCAAGGTG	720	
Db	643	AGCTTTGGGCACGAAGACCTTAC	ACTGCAAGCTGTAATCAAAAGCCCAAGCAACCAAGGTG	702	
QY	721	GACAAGAAAGCAGGCCCAATCTTGT	GACAAAACCTCACACATGCCCCAGCGTGCCTCCAGCA	780	
Db	703	GACAAGAGAGTTGAGTGC	CAAAATATGG-----TCCCCCATGCCCATCATGCCCAGCA	753	
QY	781	CTGTAACTCTCGGGGACCGTCA	GTCTTCTTCTTCCCCCAAAACCAAGGACACCCCTC	840	
Db	754	CTGTAGTTTGAAGGGGGACCAT	CAGTCTTCTTCTTCCCCCAAAACCAAGGACACTCTC	813	
QY	841	ATGATCTCCCGGACCCCTGAGTGC	ACATGCGTGTGTGTGACGTGAGCGACGACGAAGACCT	900	
Db	814	ATGATCTCCCGGACCCCTGAGTGC	ACATGCGTGTGTGACGTGAGCGACGACGAAGACCT	873	
QY	901	GAGGTCAAGTTTCAACTGTGTA	CGTGAACCGCGTGGAGTGCATATGTCACCAAGACAAAGCCG	960	
Db	874	GAGGTCCAGTTTCAACTGTGTA	CGTGTGATCGGTGAGGTGTCATATGTCACCAAGACAAAGCCG	933	
QY	961	CGGGAGGACAGTACAAACAGCAGT	ACCGTGTGTGTGTCAGCGTCTCTCACCGTCTCTGCACCCAG	1020	
Db	934	CGGGAGGACAGTTCACACAGCAGT	ACCGTGTGTGTGTCAGCGTCTCTCACCGTCTCTGCACCCAG	993	
QY	1021	GACTGGCTGAATGGCAAGGATCA	AGGTGCAAGGTCTCCAAAGGCCCTCCAGACCCCC	1080	
Db	994	GACTGGCTGAACGGCAAGGATCA	AGGTGCAAGGTCTCCAAAGGCCCTCCAGACCCCC	1053	
QY	1081	ATCGAGAAAAACCATCTTCA	AGGCAAGGCCCGCCCGAGAACCAACAGGTGTACACCCCTG	1140	
Db	1054	ATCGAGAAAAACCATCTTCA	AGGCAAGGCCCGCCCGAGAACCAACAGGTGTACACCCCTG	1113	
QY	1141	CCCCCATCCCGGATGAGCTG	ACCAAGAACAGGTTCAGCTTGA	1200	
Db	1114	CCCCCATCCCGGATGAGCTG	ACCAAGAACAGGTTCAGCTTGA	1173	
QY	1201	TTCTATCCCAAGCAGCATCG	CCGTGGAGTGGGAGACAAATGGGACGCGGAGAACCACTAC	1260	
Db	1174	TTCTATCCCAAGCAGCATCG	CCGTGGAGTGGGAGACAAATGGGACGCGGAGAACCACTAC	1233	
QY	1261	AAGACACCGCTCCCGTGTG	AGATCCCGAGCGCTCTTCTTCTTCTTACAGCAAGCTCAC	1320	
Db	1234	AAGACACCGCTCCCGTGTG	AGATCCCGAGCGCTCTTCTTCTTCTTACAGCAAGCTCAC	1293	
QY	1321	GTGACCAAGAGCAGGTGG	CAGCAGGGGAACGTCTTCTCATGTCCGTGATCATGAGGCT	1380	
Db	1294	GTGACCAAGAGCAGGTGG	CAGCAGGGGAATGTCTTCTCATGTCCGTGATCATGAGGCT	1353	
QY	1381	CTGCACCAACCATAC	ACGCAGAAAGCCCTCTCCCTGTCTCCGGGTAAATGTATGAT	1431	

Db 1354 CTGCACACCACTACACACAGAAGCCCTCTCCCTGTCTCTGGGTAAATGA 1404

RESULT 8

```

US-08-488-376-17
; Sequence 17, Application US/08488376
; Patent No. 5811524
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
; US-08-488-376-17

Query Match 79.3%; Score 1134.8; DB 1; Length 1428;
Best Local Similarity 89.0%; Pred. No. 1.8e-264;
Matches 1262; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

Qy 17 TCTTCCCTCCTCGTGGCGAGCTCCAGATGGGTCTGTCTCCAGGTGCGAGTGCAGAGT 76
Db 17 TCTTGCTCTTCTTGTCGCTGTTGCTACGCGTGTCTGTCTCCAGGTGCGAGTGCAGAGT 76

Qy 77 CGGCCCCAGGACTGGTGAAGCTTCGGAGACCTGTGTCCTCACCTGGGCTGTCTCTGGTG 136
Db 77 CTGGTCTCTGTGGTGGTGAACCCACAGAGACCCCTCAGCTTGACCTGCACCGTCTCTGGGT 136

Qy 137 GCTC---CATCAGCGGTGGTATTATGGCTGGGGCTTGGATCCGCCAGCCCCCAGAGGAGGGGC 193
Db 137 TCTCACTCAGCAACCTTAGAATGGGTGTGACCTGGATCCGTGAGCCCCCGGGAAGGCC 196

Qy 194 TGGAGTGGATTGGAGGTTTCTATAGTAGTAGTGGGAACACTACTACAACCCCTCCCTCA 253
Db 197 TAGAATGGCTTGGAAACATTTTTCGAGTCGACGAGAA---GTCTTCAGTCCCTTCCTGA 253

```

QY 1334 GGTGGCAGCGGGAAAGCTCTTTCATGCTCCGTCATGTCATGAGGCTCTGCACAAACACT 1393
Db 1331 GGTGGCAGCGGGAAAGCTCTTTCATGCTCCGTCATGTCATGAGGCTCTGCACAAACACT 1390
QY 1394 ACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAATGA 1431
Db 1391 ACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAATGA 1428

RESULT 9

US-08-634-223-17
; Sequence 17, Application US/08634223
; Patent No. 5840298
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAWAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P. O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
; US-08-634-223-17

Query Match 79.3%; Score 1134.8; DB 2; Length 1428;
Best Local Similarity 89.0%; Pred. No. 1.8e-264;
Matches 1262; Conservative 0; Mismatches 147; Indels 9; Gaps 3;
QY 17 TCTTCTCTCTCGTGGCAGCTCCAGATGGGTCTGTCTCCAGGTGCAGTGCAGGAGT 76
Db 17 TCTTCTCTCTCTCGTGGTGTCTACGGGTGTCTCTCCAGGTGCAGTGCAGGAGT 76
QY 77 CGGCCCCAGGACTGGTGAAGCTTCGAGACCTGTCCTCAGCTGGGTCTCTGGTG 136
Db 77 CTGGTCTCTGTGGTGAAGACCCACAGAGACCTCAGCTGACCTGACCGTCTCTGGGT 136

QY 137 GCTC---CATCAGCGGTGGTTATGCTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGCC 193
Db 137 TCTCACTCAGCAACCTTAGAATGGGTGTGACCTGGATCCGTCAGCCCCCGGGAAGGGCC 196
QY 194 TGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTACAACCCCTCCCTCA 253
Db 197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAA---GTCCTTCAGTCTCTCTGA 253
QY 254 AGAGTCAAGTCAACATTTTCAACAGACAGCTCCAAGAACCAAGTTCTCCCTGAAGCTGAAC 313
Db 254 AGAGCAGACTCACCACCTCCAGGACACCTCCAGAAGCCAGGTGGTCTTAAGCTTGACCA 313
QY 314 CTATGACCGCGCGACACCGCGCTGTATTACTGTGTGAGAGATCGTCTTTTTCAGTTG 373
Db 314 AGTGGACCTGTGTGACACACCATATTACTGTGACGGGTAGGACTGTATGACATCA 373
QY 374 TTGGAATGGTTTACAACAACCTGGTTTCGATGTCTGGGGCCCGGGAGTCTCTGTCAACCGTCT 433
Db 374 ATGCTT---ATTACCTATACTACCTGGATTATTGGGGGCAGGGAACCTTGGTCAACCGTCT 430
QY 434 CTTAGCTAGACACCAAGGGCCCATCGGTCTTCCCTCTGGGACACCTCTCTCAAGAGCACT 493
Db 431 COTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCTGGCACCCTCTCTCAAGAGCACT 490
QY 494 CTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCCGGTGACGG 553
Db 491 CTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCCGGTGACGG 550
QY 554 TGTGTGGAACCTCAGGGCCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTTACAGT 613
Db 551 TGTGTGGAACCTCAGGGCCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTTACAGT 610
QY 614 CTTAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCTCAGCAGCTTGGGGACCC 673
Db 611 COTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCTCAGCAGCTTGGGGACCC 670
QY 674 AGACCTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGCAACAAGAACGAG 733
Db 671 AGACCTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGCAACAAGAACGAG 730
QY 734 AGCCCAAACTTTGTGACAAAACTCACACATGCCACCGTGCACAGCACTGAACTCTCTGG 793
Db 731 AGCCCAAACTTTGTGACAAAACTCACACATGCCACCGTGCACAGCACTGAACTCTCTGG 790
QY 794 GGGACCGTCACTCTTCTTCTTCCCGCAAAACCAAGGACACCTCATGATCTCCCGGA 853
Db 791 GGGACCGTCACTCTTCTTCTTCCCGCAAAACCAAGGACACCTCATGATCTCTCCCGGA 850
QY 854 CCCCTGAGGTCAACATGCTGTGTGGACGTGAGCCAGGACCAAGACCTTGAGTCAAGTTCA 913
Db 851 CCCCTGAGGTCAACATGCTGTGTGGACGTGAGCCAGGACCAAGACCTTGAGTCAAGTTCA 910
QY 914 ACTGTACGTGACCGGTGGAGTGCATAATGCCAAGACAAAGCCCGGAGGAGAGCAGT 973
Db 911 ACTGTACGTGACCGGTGGAGTGCATAATGCCAAGACAAAGCCCGGAGGAGCAGT 970
QY 974 ACAACAGCAGTACCGTGTGTGACCGTCTCAGCTCTGACCGTCTGTCACCGAGTCTGATG 1033
Db 971 ACAACAGCAGTACCGTGTGTGACCGTCTCAGCTCTGACCGTCTGTCACCGAGTGTGATG 1030
QY 1034 GCAAGGAGTACAAGTGAAGGTCTTCCAACAAAGCCCTCCAGACCCCATCGAGAAAAACCA 1093
Db 1031 GCAAGGAGTACAAGTGAAGGTCTTCCAACAAAGCCCTCCAGACCCCATCGAGAAAAACCA 1090
QY 1094 TCTCAAAGCAAAAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCCGCCATCCCGGG 1153
Db 1091 TCTCAAAGCAAAAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCCGCCATCCCGGG 1150
QY 1154 ATGAGCTGACCAAGAACAGGTGACCTGACCTGCTGCTGCTCAAGGCTTCTATCCCAAGC 1213
Db 1151 ATGAGCTGACCAAGAACAGGTGACCTGACCTGCTGCTGCTCAAGGCTTCTATCCCAAGC 1210

Query Match	79.3%	Score 1134.8	DB 4	Length 1428
Best Local Similarity	89.0%	Pred. No. 1.8e-264		
Matches 1262	Conservative 0	Mismatches 147	Indels 9	Gaps
QY	17	TCCTCTCTCTCTGGCGAGCTCCACAGATGGGTCTCTCTCCAGGTGCAGTGCAGAGT 76		
Db	17			
QY	77	CGGGCCCAAGCACTGGTGAAGCCCTTCCGAGACCCCTCTCCCTCACTCGCGCTGTCTCTGGTG 136		
Db	77			
QY	137	GTCTC---CATCAGCGGTGGTATATGGCTGGGGTGGATCGCGACGCCGCCAGGGAAGGGGC 193		
Db	137			
QY	194	TGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTCTATCAAAACCTCTCCCTCA 253		
Db	197	TAGAATGGCTTGGAAACATTTTTTTCGAGTGCAGAGAA---GTCTCTTCAGTCTCTCTCTGA 253		
QY	254	AGAGTCAAGTCAACCATTTTCAACAGACACGTCCAAGAACAGTCTTCCCTCGAAGCTGAAT 313		
Db	254			
QY	314	CTATGACCGCCGGGACACGGCCGTGTATTACTGTGTGAGAGATCGTCTTTTTTTCAGTTG 373		
Db	314			
QY	374	TTGGAAATGGTTTACAACAACTGGTTCGATGTCTGGGGGCCGGGGAGTCTCGGTCAACGTCT 433		
Db	374			
QY	434	CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCGCACCTCTCTCCAAAGAGCACCT 493		
Db	431	CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCGCACCTCTCTCCAAAGAGCACCT 490		

Qy	254	AGAGTCAAGTACCAATTTCAACAGACAGCTCCAGAAACAGTTCTCCCTCGAGGTGACCT	313
Db	254	AGAGCAGAGACTCACCACCTCCAGGACACTCCAGAAAGCAGGTGGTCTTAAGCTTGACCA	313
Qy	314	CTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGTCTTTTTCAGTTG	373
Db	314	ACGTGGACCCCTGTGGACACAGCCACATATTCTGTGCACGGGTAGGACTGTATGACATCA	373
Qy	374	TTGGGAATGTTTACAAACAATGGTTCATGTCTGGGGGCCGGGAGTCTCGTCAACGGTCT	433
Db	374	ATGCCTT---ATTACTATACCTACCTGGATTATGGGGCAGGGAACCTCGTCAACGGTCT	430
Qy	434	CTCTAGCTAGCACCAAGGGGCCATCGGTCTTCCCTCTGGCAACCTCTCTCAAGAGACCT	493
Db	431	CTCTAGCTAGCACCAAGGGGCCATCGGTCTTCCCTCTGGCAACCTCTCTCAAGAGACCT	490

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 48.9575 Seconds
(without alignments)
1295.559 Million cell updates/sec

Title: US-09-758-173-12

Perfect score: 2549

Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHHYTKSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A: Geneseq_101002.*
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2549	100.0	476	AAW01822	Primitised anti-hu
2	2549	100.0	476	AAW63765	Macaque primitized
3	2549	100.0	476	AAU11646	Protein sequence o
4	2342.5	91.9	473	AA336206	Human immune syste
5	2309	90.6	476	AAW01818	Primitised anti-hu
6	2309	90.6	476	AAW63761	Macaque primitized
7	2309	90.6	476	AAU11539	Protein sequence o
8	2296.5	90.1	475	AA933553	Monoclonal antibod
9	2278	89.4	470	AA44721	Human immune syste
10	2217	87.0	472	AA93166	Anti-rhesus D reco

11	2162.5	84.8	467	13	AA222759	Reshaped CD4 antib
12	2159.5	84.7	467	13	AA222758	Reshaped CD4 antib
13	2148	84.3	470	13	AA222757	Reshaped CAMPATH-1
14	2145.5	84.2	467	18	AAW14927	Human gamma-4PE he
15	2144.5	84.1	467	18	AAW14925	Human gamma-4 heav
16	2138.5	83.9	446	17	AAW05829	Humanized ID10 ant
17	2137.5	83.9	467	18	AAW14926	Human gamma-4E hea
18	2134.5	83.7	581	22	AA881972	Ganglioside GD2 sp
19	2126.5	83.4	475	18	AAW11639	Human anti-RSV mon
20	2126.5	83.4	475	22	AA653640	Amino acid sequenc
21	2126	83.4	451	20	AA50031	Human E27 anti-IgE
22	2126	83.4	451	20	AAW95863	Mus musculus anti-
23	2126	83.4	451	21	AAW07473	Amino acid sequenc
24	2126	83.4	451	22	AAW74212	E27 anti-IgE antib
25	2126	83.4	451	22	AAW76952	Full length heavy
26	2124	83.3	451	20	AAW95659	Mus musculus anti-
27	2124	83.3	451	20	AAW95661	Mus musculus anti-
28	2124	83.3	451	21	AAW85201	Light chain amino
29	2124	83.3	451	22	AAW47088	Anti-IgE antibody,
30	2124	83.3	451	22	AAW76948	Full length heavy
31	2124	83.3	451	22	AAW76950	Full length heavy
32	2122.5	83.3	450	22	AAE10515	Humanized high pot
33	2121	83.2	462	21	AAW26884	Human immunoglobul
34	2120.5	83.2	450	22	AAE10521	Humanized high pot
35	2119.5	83.2	450	22	AAE10511	Humanized high pot
36	2119.5	83.2	450	22	AAE10513	Humanized high pot
37	2118.5	83.1	450	22	AAE10509	Humanized high pot
38	2117.5	83.1	450	22	AAE10517	Humanized high pot
39	2115.5	83.0	450	22	AAE10523	Humanized high pot
40	2115.5	83.0	450	22	AAE10525	Humanized high pot
41	2114.5	83.0	450	22	AAE10519	Humanized high pot
42	2094.5	82.2	475	18	AAW11641	Human anti-RSV mon
43	2094.5	82.2	477	22	AAU14288	Human novel protei
44	2094	82.1	476	22	AAW49243	Chimeric 4H6 anti-
45	2093	82.1	453	14	AAW33311	Humanized Mab11 Ve

ALIGNMENTS

RESULT 1
AAW01822
ID AAW01822 standard; Protein; 476 AA.
XX AAW01822;
XX AC
XX DT 25-MAY-1997 (first entry)
XX DE Primitised anti-human B7.1 antigen antibody 16C10 heavy chain.
XX DE Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW Primitised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX WO9640878-A1.
XX PD 19-DEC-1996.
XX PF 06-JUN-1996; 96WO-US10053.
XX PR 07-JUN-1995; 95US-0487550.
XX PA (IDEC-) IDEC PHARM CORP.
XX PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX WPI; 1997-108638/10.

```
DR N-PSDB; AAT62513.
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
XX
XX Claim 14; Fig 10B; 81pp; English.
XX
CC 2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
CC heavy variable genes (see also AAT62512 and AAT62513) are inserted into
CC an expression vector (pref. NEOSPLA) which contains human light and
CC heavy chain constant region genes to allow prodn. of the primatised
CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC antibodies have also been produced (see also AAW01817-20). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.
XX
SQ Sequence 476 AA;
Query Match 100.0%; Score 2549; DB 18; Length 476;
Best Local Similarity 100.0%; Pred. No. 6e-149;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKHLWFFLLVAAAPRWLSQVLOESGPGLVKPSSETLSLTCVSGSGISGGYGMWIRQP 60
Db 1 MKHLWFFLLVAAAPRWLSQVLOESGPGLVKPSSETLSLTCVSGSGISGGYGMWIRQP 60
Qy 61 PGKLEWIGSFYSSSGNTYNNPSLKSQVTTSTDTSKNQFSLKLSMTAADTAVYVCVRDR 120
Db 61 PGKLEWIGSFYSSSGNTYNNPSLKSQVTTSTDTSKNQFSLKLSMTAADTAVYVCVRDR 120
Qy 121 LFSVVGMYNNWFDWGPGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
Db 121 LFSVVGMYNNWFDWGPGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
Qy 181 EPVTVMNSGALTSQVHTFPVAVLQSSGLYSLSVSVTVVPSSSLGTTQYICNVNHPKSNTKV 240
Db 181 EPVTVMNSGALTSQVHTFPVAVLQSSGLYSLSVSVTVVPSSSLGTTQYICNVNHPKSNTKV 240
Qy 241 DKAEPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Db 241 DKAEPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Qy 301 EVKFNWYVDGVEVHNAKTPREBQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 301 EVKFNWYVDGVEVHNAKTPREBQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Qy 361 LEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
Db 361 LEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
Qy 421 KTTTPVLDSGDFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSLSPGK 476
Db 421 KTTTPVLDSGDFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSLSPGK 476
RESULT 2
AAW63765
ID AAW63765 standard; Protein; 476 AA.
XX
XX AAW63765;
AC
AC
DE 29-SEP-1998 (first entry)
XX
XX Macaque primatised 16C10 heavy chain protein.
XX
XX Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
XX CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
XX T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
XX immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
XX T cell proliferation.
```

```
XX OS Macaca fascicularis.
XX
XX PN W09819706-A1.
XX
XX PD 14-MAY-1998.
XX
XX PF 29-OCT-1997; 97MO-US19906.
XX
XX PR 08-NOV-1996; 96US-0746361.
XX
XX PA (IDEC-) IDEC PHARM CORP.
XX
XX PI Anderson DR, Brams P, Hanna N;
XX WPI; 1998-286601/25.
XX DR N-PSDB; AAV35489.
XX
XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
XX inhibiting binding to CD28 - useful as specific immunosuppressants
XX for treating diseases that involve interactions between T and B
XX cells, e.g. graft rejection or tumours
XX
XX Example 7; Fig 5b; 87pp; English.
XX
XX This sequence represents a primatised form of the antibody 16C10 heavy
XX chain from macaque. This sequence is used in a method which studies new
XX monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
XX B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
XX Mab's are specific immunosuppressants for treatment of diseases involving
XX T cell/B cell interactions, particularly autoimmune disease, specifically
XX idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
XX I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
XX inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
XX host diseases, B cell lymphoma, infections (including by human immune
XX deficiency virus) or inflammatory disease and tumours. Optionally the
XX Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
XX also be used as imaging agents and as vaccines or immunogens to develop
XX anti-idiotypic reagents. Mab's are optionally combined with other proteins
XX or small molecule immunosuppressants. Blocking B7/CD28 interactions
XX induces long-term, antigen-specific immunosuppression, i.e. it inhibits
XX production of interleukin-2 (IL-2), T cell proliferation and
XX antigen-specific immunoglobulin G (IgG) responses.
XX
XX Sequence 476 AA;
Query Match 100.0%; Score 2549; DB 19; Length 476;
Best Local Similarity 100.0%; Pred. No. 6e-149;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKHLWFFLLVAAAPRWLSQVLOESGPGLVKPSSETLSLTCVSGSGISGGYGMWIRQP 60
Db 1 MKHLWFFLLVAAAPRWLSQVLOESGPGLVKPSSETLSLTCVSGSGISGGYGMWIRQP 60
Qy 61 PGKLEWIGSFYSSSGNTYNNPSLKSQVTTSTDTSKNQFSLKLSMTAADTAVYVCVRDR 120
Db 61 PGKLEWIGSFYSSSGNTYNNPSLKSQVTTSTDTSKNQFSLKLSMTAADTAVYVCVRDR 120
Qy 121 LFSVVGMYNNWFDWGPGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
Db 121 LFSVVGMYNNWFDWGPGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
Qy 181 EPVTVMNSGALTSQVHTFPVAVLQSSGLYSLSVSVTVVPSSSLGTTQYICNVNHPKSNTKV 240
Db 181 EPVTVMNSGALTSQVHTFPVAVLQSSGLYSLSVSVTVVPSSSLGTTQYICNVNHPKSNTKV 240
Qy 241 DKAEPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Db 241 DKAEPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Qy 301 EVKFNWYVDGVEVHNAKTPREBQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 301 EVKFNWYVDGVEVHNAKTPREBQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
```

QY 361 IEKTSKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 Db 361 IEKTSKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 QY 421 KTTTPVLDSDGSGFLLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 476
 Db 421 KTTTPVLDSDGSGFLLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 476

RESULT 3
 AAU11646
 ID AAU11646 standard; Protein; 476 AA.
 AC AAU11646;
 DT 12-MAR-2002 (first entry)
 XX Protein sequence of primatised form of the heavy chain of 16C10 antibody.

DE Human; macaque monkey; light chain; primatised antibody; 16C10 antibody.
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; mutein.

OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX WO200189567-A1.
 PN 29-NOV-2001.
 PD 22-MAY-2001; 2001WO-US16364.
 XX 22-MAY-2000; 2000US-0576424.
 PF (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Hanna N, Brams P;
 PI WPI; 2002-089895/12.
 DR N-PSDB; AAS17247.
 XX Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease such as
 PT allergy -
 XX Example 8; Fig 5b; 89pp; English.

XX The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present protein
 CC sequence represents the heavy chain of 16C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).

SQ Sequence 476 AA;
 Query Match 100.0%; Score 2549; DB 23; Length 476;
 Best Local Similarity 100.0%; Pred. No. 6e-149;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSISSGYGHWIRQP 60
 Db 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSISSGYGHWIRQP 60
 QY 61 PKGLEWIGSFYSSGNTYYNPISKQVTTISDTSKNQFSLKLSMTAADTAVYVCVRDR 120
 Db 61 PKGLEWIGSFYSSGNTYYNPISKQVTTISDTSKNQFSLKLSMTAADTAVYVCVRDR 120
 QY 121 LFSVVGMYNNWFDVWGPGVLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFP 180
 Db 121 LFSVVGMYNNWFDVWGPGVLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFP 180
 QY 181 EPTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTQYICNVNHPKSNTKV 240
 Db 181 EPTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTQYICNVNHPKSNTKV 240
 QY 241 DKKAEPKSCDKTHTCPGPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
 Db 241 DKKAEPKSCDKTHTCPGPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
 QY 301 EVKENWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVKSNKALPAP 360
 Db 301 EVKENWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVKSNKALPAP 360
 QY 361 IEKTSKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 Db 361 IEKTSKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 QY 421 KTTTPVLDSDGSGFLLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 476
 Db 421 KTTTPVLDSDGSGFLLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 476

RESULT 4
 AAB36206
 ID AAB36206 standard; protein; 473 AA.
 XX AAB36206;
 AC AAB36206;
 XX 15-FEB-2001 (first entry)
 DT Human immune system associated protein HISAP-4.
 DE Human; immune system associated protein; HISAP-4; immune disorder;
 XX infection; autoimmune disease; cancer.
 KW Homo sapiens.
 OS US6135941-A.
 XX 24-OCT-2000.
 PD 27-MAR-1998; 98US-0049672.
 PF 27-MAR-1998; 98US-0049672.
 PR (INCY-) INCYTE PHARM INC.
 XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
 PI Hillman JL, Au-Young J;
 XX WPI; 2001-030926/04.
 DR N-PSDB; AAC66522.
 XX New human immune system associated proteins (HISAP) and polynucleotides
 PT encoding the HISAP, useful for diagnosing, treating or preventing
 PT immune or cell proliferative disorders or infections -

AAW63761;
 29-SEP-1998 (first entry)
 Macaque primatized 7C10 heavy chain DNA.
 Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
 CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
 T cell proliferation; ss.
 Macaca fascicularis.
 WO9819706-A1.
 14-MAY-1998.
 29-OCT-1997; 97WO-US19906.
 08-NOV-1996; 96US-0746361.
 (IDEC-) IDEC PHARM CORP.
 Anderson DR, Brams P, Hanna N;
 WPI; 1998-286601/25.
 N-PSDB; AAV35485.
 New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 inhibiting binding to CD28 - useful as specific immunosuppressants
 for treating diseases that involve interactions between T and B
 cells, e.g. graft rejection or tumours
 Example 7; Fig 3b; 87pp; English.
 This sequence represents a primatized form of the antibody 7C10 heavy
 chain from macaque. This sequence is used in a method which studies new
 monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 Mab's are specific immunosuppressants for treatment of diseases involving
 T cell/B cell interactions, particularly autoimmune disease, specifically
 idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 host diseases, B cell lymphoma, infections (including by human immune
 deficiency virus) or inflammatory disease and tumours. Optionally the
 Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 also be used as imaging agents and as vaccines or immunogens to develop
 anti-idiotype reagents. Mab's are optionally combined with other proteins
 or small molecule immunosuppressants. Blocking B7/CD28 interactions
 induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 production of interleukin-2 (IL-2), T cell proliferation and
 antigen-specific immunoglobulin G (IgG) responses.

Query Match 90.6%; Score 2309; DB 19; Length 476;
 Best Local Similarity 91.2%; Pred. No. 3.5e-134;
 Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRVLSQVLQSGGLVLPKPSFTLTLCAVSGGSISSGYSYGMWIRQP 60
 DB 1 MKHLWFFLLVAAPRVLSQVLQSGGLVLPKPSFTLTLCAVSGGSISSGYSYGMWIRQT 60
 QY 61 PGKGLWIGSYSSGNTYNSLSKQVITSDTSKNQFSLKLSMTAATVAVYCVDR 120
 DB 61 PGKGLWIGHYNGATYNSLSKSRVITSKDTSKNQFFLNLNSVTADTAVYCARGP 120
 QY 121 LFSVGMVNNVWPGVGLVTVSSASTKGPSVPLAPSSKTSGGTAALGCLVKDYFP 180
 DB 121 RPDCTICGGWVWPGDGLTVSSASTKGPSVPLAPSSKTSGGTAALGCLVKDYFP 180

QY 181 EPTVTVSNWNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKV 240
 DB 181 EPTVTVSNWNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKV 240
 QY 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
 DB 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
 QY 301 EVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
 DB 301 EVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
 QY 361 IEKTIKAKGQPREPOVYITLPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 DB 361 IEKTIKAKGQPREPOVYITLPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 QY 421 KTTTPVLDSGDSFLLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
 DB 421 KTTTPVLDSGDSFLLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476

RESULT 7
 AAU11539
 ID AAU11539 standard; Protein; 476 AA.
 AC AAU11539;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Protein sequence of primatized form of the heavy chain of 7C10 antibody.
 XX Human; macaque monkey; light chain; primatized antibody; 7C10 antibody;
 XX neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 XX B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 XX tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 XX graft-vs-host disease; immunosuppression; organ rejection;
 XX interleukin-2; IL-2; mutant; mutein.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX WO200189567-A1.
 XX 29-NOV-2001.
 XX 22-MAY-2001; 2001WO-US16364.
 XX 22-MAY-2000; 2000US-0576424.
 XX (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Hanna N, Brams P;
 XX WPI; 2002-089895/12.
 XX N-PSDB; AAS17243.
 XX Use of monoclonal antibody which specifically binds to B7.1 antigen
 CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, as
 treating cancer, graft-vs-host disease and autoimmune disease such as
 allergy -
 XX Example 8; Fig 3b; 89pp; English.
 XX The present invention relates to a new use of a monoclonal antibody
 which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 (CD86) for inducing the apoptosis of B7+ cells. The invention is
 useful for treating diseases such as B cell cancer, lymphoma, a
 cancer where B cells promote the growth and/or metastasis of tumours,
 B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 CC type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis

or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present protein sequence represents the heavy chain of 7c10, a primatised antibody used in the invention to induce apoptosis and inhibit production of interleukin-2 (IL-2).

XX Sequence 476 AA;

Query Match 90.6%; Score 2309; DB 23; Length 476;

Best Local Similarity 91.2%; Pred. No. 3.5e-134; Mismatches 33; Indels 0; Gaps 0;

Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MKHLWFFLLVAAPRWLSQVLOESGPGVLKPSSETLSLTCVAVSGSGISGGYGVGWIRQP 60
 Db 1 MKHLWFFLLVAAPRWLSQVLOESGPGVLKPSSETLSLTCVAVSGSGISGGYGVGWIRQT 60

Qy 61 PGKLEWIGSYSSGNTYNNPSLKSQVITSTDTSKNQFSLKLSMTAADTAVYVCVRDR 120
 Db 61 PGRGLEWIGHIYGNGATTNNPSLKSRTVTSKDTKNQFSLKLSMTAADTAVYVCARGP 120

Qy 121 LFSVVGMYNNWFDVNGPGVLTVSSASTKGPSVFLPAPSSKSTSGCTAALGCLVKDYFP 180
 Db 121 RPDCTTCYGGWVDVNGPGVLTVSSASTKGPSVFLPAPSSKSTSGCTAALGCLVKDYFP 180

Qy 181 EPTVSNWNSGALTSVGHVTPPAVLQSSGLYSLSVTVVPSSSLGTQYICNVNHNKPSNTKV 240
 Db 181 EPTVSNWNSGALTSVGHVTPPAVLQSSGLYSLSVTVVPSSSLGTQYICNVNHNKPSNTKV 240

Qy 241 DKAEKPSCKDTHTCPCPAPELLGGPSVFLPPPKDQTLMSRTPEVTCVVDVSHEDP 300
 Db 241 DKAEKPSCKDTHTCPCPAPELLGGPSVFLPPPKDQTLMSRTPEVTCVVDVSHEDP 300

Qy 301 EVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
 Db 301 EVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360

Qy 361 IEKTSKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 Db 361 IEKTSKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy 421 KTTTPPVLDSGSPFLYSKLTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 476
 Db 421 KTTTPPVLDSGSPFLYSKLTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 476

RESULT 8
 AAR93553
 ID AAR93553 standard; Protein; 475 AA.

XX AAR93553;
 XX 20-AUG-1996 (first entry)

XX Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.

DE Polymerase chain reaction; primer; amplify; PCR; light chain; Mab;
 KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.

XX Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "Signal peptide"
 FT Protein 20..475
 FT /note= "Mature heavy chain"

XX JP08038178-A.

PD 13-FEB-1996.
 XX
 PF 20-FEB-1995; 95JP-0030742.
 XX
 PR 18-FEB-1994; 94JP-0021628.
 XX
 PA (NISON) NISSHINO IND INC.
 PA (TANA) TANAKA H.
 XX
 DR WPI: 1996-154852/16.
 DR N-PSDB; AAT18059.
 XX
 PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
 PT produced by primer amplification, used in the diagnosis of hCMV
 PT infection
 XX
 PS Claim 4; Page 16-18; 22pp; Japanese.

XX The sequences given in AAR93553-54 represent the heavy and light chains
 CC respectively of a monoclonal antibody against a 65 kD antigen of human
 CC cytomegalovirus (hCMV). The DNA's encoding these sequences were
 CC amplified using the sequences given in AAT18040-58. The monoclonal
 CC antibody may be used in the diagnosis of hCMV.

XX Sequence 475 AA;

Query Match 90.1%; Score 2296.5; DB 17; Length 475;

Best Local Similarity 91.6%; Pred. No. 2e-133; Mismatches 437; Conservative 10; Mismatches 27; Indels 3; Gaps 3;

Qy 1 MKHLWFFLLVAAPRWLSQVLOESGPGVLKPSSETLSLTCVAVSGSGIS-GGYGVGWIRQ 59
 Db 1 MKHLWFFLLVAAPRWLSQVLOESGPGVLKPSSETLSLTCVSGDSISRSSYSWGCIRQ 60

Qy 60 PGKLEWIGSYSSGNTYNNPSLKSQVITSTDTSKNQFSLKLSMTAADTAVYVCVRD 119
 Db 61 PGKLEWIGITY-YSGSTYNNPSLKSRTVTSVDSANNQFSLKLSMTAADTAVYVCART 119

Qy 120 RLFVSVGVMYNNWFDVNGPGVLTVSSASTKGPSVFLPAPSSKSTSGCTAALGCLVKDYF 179
 Db 120 SP-QYDYDLTTCGSPSYNGQGLTVTVSSASTKGPSVFLPAPSSKSTSGCTAALGCLVKDYF 178

Qy 180 PEPVTVSNWNSGALTSVGHVTPPAVLQSSGLYSLSVTVVPSSSLGTQYICNVNHNKPSNTK 239
 Db 179 PEPVTVSNWNSGALTSVGHVTPPAVLQSSGLYSLSVTVVPSSSLGTQYICNVNHNKPSNTK 238

Qy 240 VDKAEKPSCKDTHTCPCPAPELLGGPSVFLPPPKDQTLMSRTPEVTCVVDVSHED 299
 Db 239 VDKAEKPSCKDTHTCPCPAPELLGGPSVFLPPPKDQTLMSRTPEVTCVVDVSHED 298

Qy 300 PEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPA 359
 Db 299 PEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPA 358

Qy 360 PIEKTSKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
 Db 359 PIEKTSKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 418

Qy 420 YKTTTPPVLDSGSPFLYSKLTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 476
 Db 419 YKTTTPPVLDSGSPFLYSKLTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 475

RESULT 9
 AAY44721
 ID AAY44721 standard; Protein; 470 AA.

XX AAY44721;

XX 25-APR-2000 (first entry)

XX Human immune system molecule, ISMO-2.

XX

KW Human: immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW treatment; prevention; cell proliferation; immune system disorder.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Signal_peptide
FT 20..470
FT /label= Mature_ISMO-2
FT 120
FT Modified-site /note= "N-glycosylated"
FT 320
FT Modified-site /note= "N-glycosylated"
FT 105
FT Modified-site /note= "Casein kinase II phosphorylation site"
FT 232
FT Modified-site /note= "Casein kinase II phosphorylation site"
FT 290
FT Modified-site /note= "Casein kinase II phosphorylation site"
FT 377
FT Modified-site /note= "Casein kinase II phosphorylation site"
FT 47
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 81
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 92
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 98
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 142
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 154
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 322
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 347
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 460
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT 69
FT Modified-site /note= "Tyrosine kinase phosphorylation site"
FT 319
FT Modified-site /note= "Tyrosine kinase phosphorylation site"
FT 387..409
FT Region /note= "conserved Ig/MHC protein block"
FT 446..463
FT Region /note= "conserved Ig/MHC protein block"
FT 34..116
FT Domain /note= "shows similarity to Ig superfamily protein domain"
FT 160..225
FT Domain /note= "shows similarity to Ig superfamily protein domain"
FT 383..450
FT Domain /note= "shows similarity to Ig superfamily protein domain"

XX WO200000608-A2.

XX 06-JAN-2000.

XX 21-JUN-1999; 99WO-US13995.

XX 30-JUN-1998; 98US-0107223.

XX (INCY-) INCYTE PHARM INC.

XX Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;
XX Baughn MR;

XX WPI; 2000-170916/15.

DR N-PSDB; AAZ50012.

XX Immune system molecules used in the diagnosis, treatment and prevention
PT of disorders associated with the immune system and cell proliferation
PT -
XX Claim 1; Pages 60-61; 69pp; English.

XX The present sequence is an immune system molecule,
CC ISMO-2 from an Incyte clone 2849752 isolated from the human breast
CC tumour cDNA library (BRSTU13). This sequence is expressed in several
CC libraries, generally those associated with cancer, cell
CC proliferation, immune response or trauma. It shows homology to
CC vertebrate immunoglobulin gamma heavy-chain.
CC The present sequence is useful in the diagnosis, treatment and
CC prevention of disorders associated with the immune system and
CC cell proliferation.

XX SQ Sequence 470 AA;

Query Match 89.4%; Score 2278; DB 21; Length 470;
Best Local Similarity 91.4%; Pred. No. 2.7e-132;
Matches 435; Conservative 9; Mismatches 26; Indels 6; Gaps 3;

QY 1 MKHLWPFLLLVAAAPRWVLSQVQLQESGPGLVKPSSETLSLTCAVSGSISGGYGWIRQP 60
DB 1 MKHLWPFLLLVAAAPRWVLSQVQLQESGPGLVKPSSETLSLTCTVSGSIR-SYYWNWIRLP 59
QY 61 PGKGLEWIGSYSSGNTYYPNLSKSOVTISTDTSKNPSLKLNSMTAADTAVYVCVRDR 120
DB 60 PGKGLEWIGYIY-TSGSTNYPNLSKSRVTMSVDTSKNPSLKLSSVTAADTAVYCARPP 118
QY 121 LFSVVGWVYNNWFDVMGPGVLVTVSSASTKGPVSFPLAPSSKSTSGTAAAGCLVKDYPP 180
DB 119 PNATTTTWTST----GAKGALVTVSSASTKGPVSFPLAPSSKSTSGTAAAGCLVKDYPP 174
QY 181 EPTVSWNSGALTSGVHTTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKV 240
DB 175 EPTVSWNSGALTSGVHTTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKV 234
QY 241 DKAEAPKSCDKTHTCPPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 235 DKAEAPKSCDKTHTCPPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDP 294
QY 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 295 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 355 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 414
QY 421 KTTTPPVLDSDGFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNNHYTKSLSPGK 476
DB 415 KTTTPPVLDSDGFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNNHYTKSLSPGK 470

RESULT 10

AAR93166

ID AAR93166 standard; Protein; 472 AA.

XX AC AAR93166;

XX 30-OCT-1996 (first entry)

XX Anti-rhesus D recombinant antibody D7C2 heavy chain.

XX Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;

XX rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain;

XX variable region; insect host cell; baculovirus; recombinant production.

XX Homo sapiens.

OS Synthetic.

XX

Key Location/Qualifiers
Peptide 1..19
/label= signal_peptide
/note= "mouse VH signal peptide sequence encoded by synthetic linker"
Protein 20..472
/label= heavy_chain
/note= "human_gamma 1 chain constant region and the variable region from anti-rhesus D antibody D7C2"
FR2724182-A1.
08-MAR-1996.
02-SEP-1994; 94FR-0010566.
02-SEP-1994; 94FR-0010566.
(INSP) INST PASTEUR.
(PROT-) PROTEINE PERFORMANCE.
Chaabihi H, Edelman L, Kaczorek M, Margaratte C;
WPI; 1996-162018/17.
N-PSDB; AAT26889.
Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies
Example 2; Page 35-37; 46pp; French.
The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies.
Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.

Query Match 87.0%; Score 2217; DB 17; Length 472;
Best Local Similarity 90.4%; Pred. No. 1.6e-128;
Matches 424; Conservative 9; Mismatches 32; Indels 4; Gaps 3;
8 LLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSGISGGYWGWIQQPPGKLEW 67
8 LFLVATATGVHSQVQLQWAGLGLKPSSETLSLTCTVYGGSFY-GYYWSWIRQPPGKLEW 66
68 IGSFYSSGNTYINPSPKLSQVITSTDSKQFSLKLSMTAADTAVYVCVDRDLFSVVG 127
67 IGEI-NHSGSTNYPSPKLSRVITSDTSKQFSLKLSMTAADTAVYVCARPEYK--WK 123
128 VYNNFDFVWGVLTVSSASTKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSW 187
124 YHGMDFDPWGQGTITVTVSSASTKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSW 183
188 NSGALTSGVTHFPAVLQSGGSLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKAEPK 247
184 NSGALTSGVTHFPAVLQSGGSLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKAEPK 243
248 SCDKTHTCPPCPAPPELLGSPSVFLPPPKDQTLMSRTPETVCVVDVSHEDPEVKENWY 307
244 SCDKTHTCPPCPAPPELLGSPSVFLPPPKDQTLMSRTPETVCVVDVSHEDPEVKENWY 303
308 VDGVEVHNAKTPREEQNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISK 367
304 VDGVEVHNAKTPREEQNSTYRVVSVLVKVLHODWLNKGYKCKVSNKALPAPIEKTISK 363

Qy 368 AKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 427
Db 364 AKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 423
Qy 428 DSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK 476
Db 424 DSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK 472
RESULT 11
AAR22759
ID AAR22759 standard; Protein; 467 AA.
XX
AC AAR22759;
DT 20-OCT-1992 (first entry)
DE Reshaped CD4 antibody heavy chain CD4VHNEW-Ser30.
KW Antigen; CDR; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy.
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "signal peptide"
FT Peptide 20..467
FT /note= "mature peptide"
FT Region 50..54
FT /note= "Complementarity determining region 1"
FT Region 69..85
FT /note= "Complementarity determining region 2"
FT Region 118..126
FT /note= "Complementarity determining region 3"
XX WO3205274-A.
XX 02-APR-1992.
XX 16-SEP-1991; 91WO-GB01578.
XX 17-SEP-1990; 90GB-0020282.
XX (GORM/) GORMAN S D.
XX Clark M R, Cobbold S P, Gorman S D, Waldmann H;
XX WPI; 1992-132139/16.
XX N-PSDB; AAO23581.
XX Humanisation of antibodies binding to human CD4 antigen - by mutation of framework-encoding regions of DNA encoding variable domain of rat or mouse antibody chain
XX Disclosure; Fig 7; 74pp; English.
XX The sequence is that of the reshaped CD4 antibody heavy chain CD4VHNEW-Ser30. Reshaped CD4 antibody can be used to induce tolerance against an antigen. It can also be used to alleviate autoimmune diseases such as rheumatoid arthritis, and to prevent graft rejection. Tolerance to a graft, e.g. an organ graft or a bone marrow transplantation can also be useful to alleviate allergies. Tolerance to allergens could also be achieved. See also AAR22753-R22763.
XX
SQ Sequence 467 AA;
Query Match 84.8%; Score 2162.5; DB 13; Length 467;
Best Local Similarity 87.6%; Pred. No. 3.4e-125;
Matches 411; Conservative 18; Mismatches 31; Indels 9; Gaps 3;
Qy 8 LLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSGISGGYWGWIQQPPGKLEW 67

Db 8 LFLVATATGVHSGVQLQESGPGVLVRSQTLSTCTVSGTFTS-NYGMWVRQPPGRGLEW 66
Qy 68 IGSFYSSGNTYNNPSLKSQVITSTDTSKNQFSLKLNMTAADTAVYYCVRDLFSVVG 127
Db 67 IGTISHDGSSTYFRDSVKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARQG--TIAGI 124
Qy 128 VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSW 187
Db 125 RH-----WGQGSLLTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSW 178
Qy 188 NSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKAEPK 247
Db 179 NSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKAEPK 238
Qy 248 SCDKTHTCPPCAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWY 307
Db 239 SCDKTHTCPPCAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWY 298
Qy 308 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 367
Db 299 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 358
Qy 368 AKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 427
Db 359 AKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 418
Qy 428 DSDGSFFLYSKLTVDKSRWQGNVFCSVMHEALHNHYTQKSLSLSPGK 476
Db 419 DSDGSFFLYSKLTVDKSRWQGNVFCSVMHEALHNHYTQKSLSLSPGK 467
RESULT 12
AAR22758
ID AAR22758 standard; Protein; 467 AA.
XX
AC AAR22758;
XX
DT 20-OCT-1992 (first entry)
XX
DE Reshaped CD4 antibody heavy chain CD4VHNEW-Thr30.
XX
KW Antigen; CDR; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS Rattus rattus.
FH Key
FT Peptide
FT 1..19 Location/Qualifiers
FT /note= "signal peptide"
FT 20..467
FT /note= "mature peptide"
FT 50..54
FT /note= "Complementarity determining region 1"
FT 69..85
FT /note= "Complementarity determining region 2"
FT 118..126
FT /note= "Complementarity determining region 3"
XX
PN W09205274-A.
XX
PD 02-APR-1992.
XX
PF 16-SEP-1991; 91WO-GB01578.
XX
PR 17-SEP-1990; 90GB-0020282.
XX
PA (GORM/) GORMAN S D.
XX
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H;
XX
DR WPI; 1992-132139/16.
DR N-PSDB; AAQ23571.
XX

PT Humanisation of antibodies binding to human CD4 antigen - by
PT mutation of framework-encoding regions of DNA encoding variable
XX domain of rat or mouse antibody chain
PS Disclosure; Fig 6; 74pp; English.
XX
CC The sequence is that of the reshaped CD4 antibody heavy chain
CC CD4VHNEW-Thr30. Reshaped CD4 antibody can be used to induce tolerance
CC against an antigen. It can also be used to alleviate autoimmune diseases
CC such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also AAR22753-R22763.
XX
SQ Sequence 467 AA;
Query Match 84.7%; Score 2159.5; DB 13; Length 467;
Best Local Similarity 87.4%; Pred. No. 5.3e-125;
Matches 410; Conservative 19; Mismatches 31; Indels 9; Gaps 3;
Qy 8 LLLVAAPRWLSQVQLQESGPGVLVRSQTLSTCTVSGTFTT-NYGMWVRQPPGRGLEW 67
Db 8 LFLVATATGVHSGVQLQESGPGVLVRSQTLSTCTVSGTFTT-NYGMWVRQPPGRGLEW 66
Qy 68 IGSFYSSGNTYNNPSLKSQVITSTDTSKNQFSLKLNMTAADTAVYYCVRDLFSVVG 127
Db 67 IGTISHDGSSTYFRDSVKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARQG--TIAGI 124
Qy 128 VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSW 187
Db 125 RH-----WGQGSLLTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSW 178
Qy 188 NSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKAEPK 247
Db 179 NSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKAEPK 238
Qy 248 SCDKTHTCPPCAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWY 307
Db 239 SCDKTHTCPPCAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWY 298
Qy 308 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 367
Db 299 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 358
Qy 368 AKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 427
Db 359 AKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 418
Qy 428 DSDGSFFLYSKLTVDKSRWQGNVFCSVMHEALHNHYTQKSLSLSPGK 476
Db 419 DSDGSFFLYSKLTVDKSRWQGNVFCSVMHEALHNHYTQKSLSLSPGK 467
RESULT 13
AAR22757
ID AAR22757 standard; Protein; 470 AA.
XX
AC AAR22757;
XX
DT 20-OCT-1992 (first entry)
XX
DE Reshaped CAMPATH-1 antibody heavy chain.
XX
KW Antigen; CDR; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS Rattus rattus.
FH Key
FT Region
FT 50..54 Location/Qualifiers
FT /note= "Complementarity determining region 1"
FT 69..87
FT /note= "Complementarity determining region 2"

FT Region 101...110
FT Peptide /note= "Complementarity determining region 3"
FT 1..19
FT Peptide /note= "signal peptide"
FT 20..470
FT Peptide /note= "mature peptide"
XX
PN WO9205274-A.
XX
PD 02-APR-1992.
XX
XX 16-SEP-1991; 91WO-GB01578.
PF
PR 17-SEP-1990; 90GB-0020282.
XX
XX (GORM/) GORMAN S D.
XX
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H;
XX
XX WPI; 1992-132139/16.
DR N-PSDB; AAQ23570.
XX
XX Humanisation of antibodies binding to human CD4 antigen - by
PT mutation of framework-encoding regions of DNA encoding variable
PT domain of rat or mouse antibody chain
XX
XX Disclosure; Fig 5; 74pp; English.
XX
XX The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.
CC Reshaped CD4 antibody can be used to induce tolerance against an
CC antigen. It can also be used to alleviate autoimmune diseases such
CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also AAR22754-R22763.
XX
XX Sequence 470 AA;

Query Match 84.3%; Score 2148; DB 13; Length 470;
Best Local Similarity 87.3%; Pred. No. 2.7e-124;
Matches 411; Conservative 16; Mismatches 34; Indels 10; Gaps 3;
Qy 8 LLLVAAPRWLSQVQLQESGFLGPKSETLSLTCVAVSGSISGCGYGMWIRPDPGKLEW 67
Db 8 LFLVATATGVHSGVQLQESGFLGPKSETLSLTCVAVSGSISGCGYGMWIRPDPGKLEW 66
Qy 68 IGSFYSSSG--NYYNPSLKSQVTTISTDTSKNQFSLKLSMTAADTAVYCYVRDLFSVV 125
Db 67 IGFTIRDKAKGYTTEYNPSVSKGRVTMLVDTSKNQFSLRLSSVTAAADTAVYCYVRDLFSVV 126
Qy 126 GMVYNNMFDVWGPGVLTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTV 185
Db 127 -----FDVWGQSLVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTV 179
Qy 186 SWNSGALTSGVHTFPVAVLQSSGLYSLSVVTVPSLSLGTQYICNVNHPKSNKVDKKA 245
Db 180 SWNSGALTSGVHTFPVAVLQSSGLYSLSVVTVPSLSLGTQYICNVNHPKSNKVDK 239
Qy 246 PKSCDKTHTCPCPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPVRKN 305
Db 240 PKSCDKTHTCPCPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPVRKN 299
Qy 306 WYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTI 365
Db 300 WYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTI 359
Qy 366 SKAQGPREFQVYTLTPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 425
Db 360 SKAQGPREFQVYTLTPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 419
Qy 426 VLDSGDSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPCK 476
Db 420 VLDSGDSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPCK 470

RESULT 14
ID AAW14927 standard; Protein; 467 AA.
XX AAW14927;
AC AAW14927;
XX 18-OCT-1997 (first entry)
DT Human gamma-4PE heavy chain.
XX
DE CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukaemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma 4PE.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 248
FT /note= "site of S229P mutation"
FT Misc-difference 255
FT /note= "site of L236E mutation"
XX
PN WO9709351-A1.
XX
XX 13-MAR-1997.
PD
XX
XX 05-SEP-1996; 96WO-US14324.
PF
XX
XX 06-SEP-1995; 95US-0523894.
PR
XX
XX (IDEC-) IDEC PHARM CORP.
PA
XX
XX Hanna N, Newman RA, Reff ME;
PI
XX
XX WPI; 1997-201913/18.
DR N-PSDB; AAT62870.
XX
XX Chimeric antibody comprising monkey variable domains and human
PT constant domains - affects CD4-mediated immune functions, esp.
PT useful for treatment of autoimmune disease, e.g. rheumatoid
PT arthritis
XX
XX Claim 6; Page 91-93; 155pp; English.
XX
XX 3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
CC regions of human gamma-4, gamma-4E carrying an L236E mutation in
CC the hinge region, and gamma-4PE carrying L236E and S229P mutations.
CC They can be incorporated into novel monoclonal and chimeric
CC antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
CC which the human IgG4 Fc binding domain framework is combined with
CC the antigen binding domains (see also AAW14922-23) of macaque anti-
CC human CD4 monoclonal antibody E9.1. These antibodies show high
CC affinity to human CD4, have little or no immunogenicity in humans
CC and show reduced or absence of effector function. The gamma-4E and
CC -4PE mutations confer activity enhanced stability and eliminate
CC depleting activity. The antibodies can be used to treat autoimmune
CC diseases such as rheumatoid arthritis.
XX
XX Sequence 467 AA;
Query Match 84.2%; Score 2145.5; DB 18; Length 467;
Best Local Similarity 85.9%; Pred. No. 3.8e-124;
Matches 409; Conservative 19; Mismatches 39; Indels 9; Gaps 2;
Qy 1 MKHLWFFLLVAAPRWLSQVQLQESGFLGPKSETLSLTCVAVSGSISGCGYGMWIRP 60
Db 1 MKHLWFFLLVAAPRWLSQVQLQESGFLGPKSETLSLTCVAVSGSISGCGYGMWIRP 60
Qy 61 PKGLEWIGSYSSSGNTYYNPSLKSQVTTISTDTSKNQFSLKLSMTAADTAVYCYVRDR 120
Db 61 PKGLEWIGSYSSSGNTYYNPSLKSQVTTISTDTSKNQFSLKLSMTAADTAVYCYVRDR 120

Db 61 PGKLEWIGVIYGGGGTNNPFLNNRVISIDTSLKSLKLSRVTAADTAVVYCASN 120
QY 121 LFSVWGMVNNWFDVNGPGLVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFP 180
Db 121 L-----KYLHWLLYWGQGVLTVSSASTKGPSVFFPLAPCSRSTSESTAALGCLVKDYFP 174
QY 181 EPTVSWNSGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKV 240
Db 175 EPTVSWNSGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKV 234
QY 241 DKAEKPKCDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
Db 235 DKRVESK---YGPFCPCPAPPEFEGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 291
QY 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 292 EVQFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 351
QY 361 IEKTIKAKQGPPEQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
Db 352 IEKTIKAKQGPPEQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 411
QY 421 KTTTPVLDSGDSFGLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 476
Db 412 KTTTPVLDSGDSFGLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 15
AAW14925
ID AAW14925 standard; Protein; 467 AA.
XX
AC
XX
AC
XX
DT 18-OCT-1997 (first entry)
XX
DE Human gamma-4 heavy chain.
DE
XX CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukaemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma 4.
XX Homo sapiens.
XX
XX WO9709351-A1.
XX
XX 13-MAR-1997.
XX
XX 05-SEP-1996; 96WO-US14324.
XX
XX 06-SEP-1995; 95US-0523894.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Reiff ME;
XX
XX WPI; 1997-201913/18.
XX
XX N-PSDB; AAT62868.
XX
XX Chimeric antibody comprising monkey variable domains and human
PT constant domains - affects CD4-mediated immune functions, esp.
PT useful for treatment of autoimmune disease, e.g. rheumatoid
PT arthritis
XX
XX Claim 6; Page 82-84; 155pp; English.
XX
XX 3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
CC regions of human gamma-4, gamma-4E carrying an L236E mutation in
CC the hinge region, and gamma-4PE carrying L236E and S229P mutations.
CC They can be incorporated into novel monoclonal and chimeric
CC antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
CC which the human IgG4 Fc binding domain framework is combined with
CC the antigen binding domains (see also AAW14922-23) of macaque anti-

CC human CD4 monoclonal antibody B9.1. These antibodies show high
CC affinity to human CD4, have little or no immunogenicity in humans
CC and show reduced or absence of effector function. They can be used
CC to treat autoimmune diseases such as rheumatoid arthritis.
XX
SQ Sequence 467 AA;
Query Match 84.1%; Score 2144.5; DB 18; Length 467;
Best Local Similarity 85.9%; Pred. No. 4.4e-124;
Matches 409; Conservative 19; Mismatches 39; Indels 9; Gaps 2;
QY 1 MKHLWFFLLVAAAPRWLSQVLOESGFLVKPSETLSLTCAYSGSGISGGYGHGWRQP 60
Db 1 MKHLWFFLLVAAAPRWLSQVLOESGFLVKPSETLSLTCAYSGSGISGGYGHGWRQP 60
QY 61 PGKLEWIGSYSSNGNTYNNPFLKSOVTITSTDSKNQFSLKLSNMTAADTAVVYCDR 120
Db 61 PGKLEWIGSYSSNGNTYNNPFLKSOVTITSTDSKNQFSLKLSNMTAADTAVVYCDR 120
QY 121 LFSVWGMVNNWFDVNGPGLVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFP 180
Db 121 L-----KYLHWLLYWGQGVLTVSSASTKGPSVFFPLAPCSRSTSESTAALGCLVKDYFP 174
QY 181 EPTVSWNSGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKV 240
Db 175 EPTVSWNSGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKV 234
QY 241 DKAEKPKCDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
Db 235 DKRVESK---YGPFCPCPAPPEFEGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 291
QY 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 292 EVQFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 351
QY 361 IEKTIKAKQGPPEQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
Db 352 IEKTIKAKQGPPEQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 411
QY 421 KTTTPVLDSGDSFGLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 476
Db 412 KTTTPVLDSGDSFGLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

Search completed: March 29, 2003, 09:10:22
Job time : 49.9575 secs

GenCore version 5.1.4.p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 9.04722 Seconds
(without alignments)
1531.829 Million cell updates/sec

Title: us-09-758-173-10

Perfect score: 1232

Sequence: 1 MRVPQLGLLLMLPGARC.....CQVTHEGSTVKTVPATCS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues 237916

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/prodata/1/pubpaa/FCI_NEW_PUB_PEP.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB_PEP.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB_PEP.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB_PEP.*
- 6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB_PEP.*
- 7: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB_PEP.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB_PEP.*
- 9: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB_PEP.*
- 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB_PEP.*
- 11: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB_PEP.*
- 12: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB_PEP.*
- 13: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB_PEP.*
- 14: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1232	100.0	236	9	US-10-124-905-10
2	1232	100.0	236	9	US-09-948-4298-10
3	1006	81.7	235	10	US-09-747-669-6
4	999.5	81.1	221	9	US-10-001-857-202
5	973	79.0	234	9	US-10-124-905-2
6	973	79.0	234	9	US-09-948-4298-2
7	950.5	77.2	219	10	US-09-974-449-38
8	885	71.8	235	9	US-09-852-797-70
9	885	71.8	235	10	US-09-853-161-70
10	885	71.8	235	10	US-09-852-659A-70
11	882	71.6	235	9	US-09-852-797-88
12	882	71.6	235	10	US-09-853-161-88
13	882	71.6	235	10	US-09-852-659A-88
14	854.5	69.4	244	10	US-09-925-301-1424
15	826	67.0	239	9	US-09-828-995B-26
16	815	66.2	216	10	US-09-736-371B-19
17	762.5	61.9	246	9	US-09-909-567B-49
18	683.5	55.5	216	10	US-09-291-299A-8
19	673	54.6	217	10	US-09-291-299A-7

20	639.5	51.9	216	10	US-09-291-299A-9
21	635.5	51.6	216	10	US-09-291-299A-10
22	569.5	46.2	147	9	US-09-988-115A-57
23	567	46.0	109	9	US-09-925-664-51
24	562	45.6	139	9	US-09-796-692-901
25	549	44.6	143	9	US-09-796-692-742
26	548	44.5	105	10	US-09-811-384-6
27	548	44.5	123	9	US-09-796-692-931
28	547	44.4	125	9	US-09-796-692-843
29	546	44.3	123	9	US-09-796-692-683
30	546	44.3	123	9	US-09-796-692-838
31	546	44.3	123	9	US-09-796-692-859
32	546	44.3	123	9	US-09-796-692-896
33	546	44.3	123	9	US-09-796-692-993
34	546	44.3	123	9	US-09-796-692-1011
35	546	44.3	123	9	US-09-796-692-1021
36	546	44.3	123	9	US-09-796-692-1041
37	546	44.3	123	9	US-09-796-692-1138
38	546	44.3	123	9	US-09-796-692-1142
39	546	44.3	154	9	US-09-796-692-706
40	545	44.2	105	10	US-09-864-761-41920
41	545	44.2	123	9	US-09-796-692-1105
42	543	44.1	106	9	US-09-535-868-14
43	542	44.0	127	9	US-09-796-692-836
44	541	43.9	123	9	US-09-796-692-982
45	541	43.9	123	9	US-09-796-692-991

ALIGNMENTS

RESULT 1

US-10-124-905-10
; Sequence 10, Application US/10124905
; Patent No. US20020166136A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 236 amino acids

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-10

Query Match      100.0%; Score 1232; DB 9; Length 236;
Best Local Similarity 100.0%; Pred. No. 5.6e-52;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNSIGGYDLHWYQQL 60
DB 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNSIGGYDLHWYQQL 60
QY 61 PGTAPKLLIYDINKRPGISDRFSGSKSGTAASLAITGLQTEDEADYYCOSYDSSLNAQV 120
DB 61 PGTAPKLLIYDINKRPGISDRFSGSKSGTAASLAITGLQTEDEADYYCOSYDSSLNAQV 120
QY 121 FGGGTRTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 121 FGGGTRTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 181 AGVETTTPSKSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
DB 181 AGVETTTPSKSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236

RESULT 3
US-09-747-669-6
; Sequence 6, Application US/09747669
; Patent No. US20020122807A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-747-669-6

Query Match      81.7%; Score 1006; DB 10; Length 235;
Best Local Similarity 83.9%; Pred. No. 2.5e-41;
Matches 193; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNSIGGYDLHWYQQLPSTAPK 66
DB 6 LLTLLTHCAGSWAGSVLTQPPSVSGAPGQKVTISCTGSTNSIGSKTVNWIQQLPSTAPK 65
QY 67 LLTIYDINKRPGISDRFSGSKSGTAASLAITGLQTEDEADYYCOSYDSSLNAQVFGGTR 126
DB 66 FLIYSNNQRPSGVDPDRFSGSKSGTASLAISGLQSEDEADYYCAAWDDSLNGWVFGGTR 125
QY 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 186
DB 126 LTVLGQPKAAPSVTLFPPSSEELQANKPLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
QY 187 TPSKSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
DB 186 TPSKSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 235

RESULT 4
US-10-001-857-202
; Sequence 202, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE:
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS:
; SOFTWARE:
; SEQ ID NO:
; LENGTH:
; TYPE:
; ORGANISM:
; FEATURE:
; OTHER INFORMATION:
US-09-948-429B-10
; Sequence 10, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-10
```

COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-6620

TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-2

Query Match 79.0%; Score 973; DB 9; Length 234;
Best Local Similarity 80.1%; Pred. No. 8.9e-40;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;
QY 1 MRVPAQLGLLLWLPGARCESVLTTPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQL 60
DB 1 MRVPAQLGLLLWLPGARCAVELTTPPSVSPGQTARITCGDNR--NEYVHWYQK 58
QY 61 PGTAPKLLIYDINKRPSGISDRFSGSGKGTAAASLAITGLQTEDEADYQCQSDSSSLNAQV 120
DB 59 PARAPILVIYDDSDRSGIPERFSGSGKNTATLTINGVEAGDEADYQCQWDRASHPV 118
QY 121 FGGGTRVTLVGGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 119 FGGGTRVTLVGGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
QY 181 AGVETTTPSQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 179 AGVETTTPSQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 7

US-09-974-449-38
; Sequence 38, Application US/09974449
; Patent No. US20020141989A1
; GENERAL INFORMATION:
; APPLICANT: Kricek, Franz
; APPLICANT: Stadler, Bodo
; APPLICANT: Vogel, Monique
; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST
; TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO
; FILE REFERENCE: ITS HIGH AFFINITY RECEPTOR
; CURRENT APPLICATION NUMBER: US/09/974,449
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: PCT/EP00/03288
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-449-38

Query Match 77.2%; Score 950.5; DB 10; Length 219;
Best Local Similarity 83.1%; Pred. No. 9.7e-39;
Matches 182; Conservative 16; Mismatches 18; Indels 3; Gaps 2;
QY 21 ESVLTQPPSVSGAPGQKVTISCTGTSNIGGYD-LHWYQQLFCTAPKLLIYDINKRPSGI 79
DB 1 ELAVVTQPSVSGSPGOSITISCTGTSNIGGYDVGYNYSWYQHPGKAPKLMIVDVSNRPSGV 60
QY 80 SDRFSGSKGTAAASLAITGLQTEDEADYQCQSDSSSLNAQVGGGTRTLVG--QPKAAP 137
DB 61 SNRPSGSKGNTASLTISGLQAEDADYCYSSYTSSTLGVGGGTRTLVGGGTRTLVGQPKAAP 120
QY 138 SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSQSNKNKYA 197
DB 121 SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSQSNKNKYA 180
QY 198 ASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 181 ASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 219

RESULT 8

US-09-852-797-70
; Sequence 70, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-70

Query Match 71.8%; Score 885; DB 9; Length 235;
Best Local Similarity 77.1%; Pred. No. 1.2e-35;
Matches 178; Conservative 11; Mismatches 38; Indels 4; Gaps 1;

QY 10 LLLLWLPGARCESV---LTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAP 65
DB 5 LLLLTLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGGQCAAWLQHQHPP 64
QY 66 KLLIYDINKRPSGISDRFSGSGKGTAAASLAITGLQTEDEADYQCQSDSSSLNAQVFGGTT 125
DB 65 KLLSYNNRNPSPGISERLSASRSGATSSLTITGLQPEDEADYCAAYDSSSLAVMFGGTT 124
QY 126 RLTVLGGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
DB 125 KLTVLGGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 184
QY 186 TTPSQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 185 TTPSQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 9

US-09-853-161-70
; Sequence 70, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P3

; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-70

Query Match 71.8%; Score 885; DB 10; Length 235;
Best Local Similarity 77.1%; Pred. No. 1,2e-35;
Matches 178; Conservative 11; Mismatches 38; Indels 4; Gaps 1;

QY 10 LLLWLPGARCESV----LTQPPSVSGAPGQKVTISCTGTSNTGGYDLHWYQQLPGTAP 65
DB 5 LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDGAAWLQHQHGP 64
QY 66 KLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCOSYDSSINQVFGGCT 125
DB 65 KLLSYNNRNPISGISERLSASRGATSSLTITGLQPEDEADYYCAAYDSSLAVMFGGCT 124
QY 126 RLTVLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTVANKADSSPVKAGVET 185
DB 125 KLTVLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTVANKADSSPVKAGVET 184
QY 186 TTPSKQSNKYYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 236
DB 185 TTPSKQSNKYYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 10

US-09-852-659A-70
; Sequence 70, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-70

Query Match 71.8%; Score 885; DB 10; Length 235;
Best Local Similarity 77.1%; Pred. No. 1,2e-35;
Matches 178; Conservative 11; Mismatches 38; Indels 4; Gaps 1;

QY 10 LLLWLPGARCESV----LTQPPSVSGAPGQKVTISCTGTSNTGGYDLHWYQQLPGTAP 65
DB 5 LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDGAAWLQHQHGP 64
QY 66 KLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCOSYDSSINQVFGGCT 125
DB 65 KLLSYNNRNPISGISERLSASRGATSSLTITGLQPEDEADYYCAAYDSSLAVMFGGCT 124
QY 126 RLTVLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTVANKADSSPVKAGVET 185
DB 125 KLTVLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTVANKADSSPVKAGVET 184
QY 186 TTPSKQSNKYYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 236
DB 185 TTPSKQSNKYYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 11

US-09-852-797-88
; Sequence 88, Application US/09852797
; Patent No. US2002017299A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-03-30

; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-88

Query Match 71.6%; Score 882; DB 9; Length 235;
Best Local Similarity 76.6%; Pred. No. 1.7e-35;
Matches 177; Conservative 12; Mismatches 38; Indels 4; Gaps 1;

QY 10 LLLWLPGARCESV----LTQPPSVGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAP 65
DB 5 LLLLTLLTHSAVSVAAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQCAAWLQHQHPP 64
QY 66 KLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCOSYDSSLNQVFGGT 125
DB 65 KLLSYRNNRPSGISERLSASRGATSSLTITGLQPEDEADYYCAAYDSSLAVVMFGGT 124
QY 126 RLTVLGQPKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 185
DB 125 KLTVLGQPKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 184
QY 186 TTPSKQSNKYAASSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 185 TTPSKQSNKYAASSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 12
US-09-853-161-88
; Sequence 88, Application US/09853161
; Patent No. US2002076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-88

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-88

Query Match 71.6%; Score 882; DB 10; Length 235;
Best Local Similarity 76.6%; Pred. No. 1.7e-35;
Matches 177; Conservative 12; Mismatches 38; Indels 4; Gaps 1;

QY 10 LLLWLPGARCESV----LTQPPSVGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAP 65
DB 5 LLLLTLLTHSAVSVAAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQCAAWLQHQHPP 64
QY 66 KLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCOSYDSSLNQVFGGT 125
DB 65 KLLSYRNNRPSGISERLSASRGATSSLTITGLQPEDEADYYCAAYDSSLAVVMFGGT 124
QY 126 RLTVLGQPKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 185
DB 125 KLTVLGQPKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 184
QY 186 TTPSKQSNKYAASSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 185 TTPSKQSNKYAASSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 13
US-09-852-659A-88
; Sequence 88, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-88

Query Match 71.6%; Score 882; DB 10; Length 235;
Best Local Similarity 76.6%; Pred. No. 1.7e-35;
Matches 177; Conservative 12; Mismatches 38; Indels 4; Gaps 1;

QY 10 LLLWLPGARCESV----LTQPPSVGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAP 65

Db 5 LLLTLLTHSAVSVOAGLTQPPSVSKDLRTATLTCTGNNNVGDQGAWLQHQHPP 64
Qy 66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYVCSYDSSSLNAQVFGGTT 125
Db 65 KLLSYRNNRPSGISSELSASRSGATSSLTITGLQPEDEADYCAAYDSSLVWVFGGTT 124
Qy 126 RLTVGQPKAAPSVTLPFSSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGVET 185
Db 125 KLTIVGQPKAAPSVTLPFSSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGVET 184
Qy 186 TTPSKQNNKYAASSYLSLTPQWKSRSYSCQVTHGSGTVEKTVAPTECS 236
Db 185 TTPSKQNNKYAASSYLSLTPQWKSRSYSCQVTHGSGTVEKTVAPTECS 235

RESULT 14
US-09-925-301-1424
; Sequence 1424, Application US/09925301
; Patent No. US2002052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL06
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1424
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (62)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (221)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1424

Query Match 69.4%; Score 854.5; DB 10; Length 244;
Best Local Similarity 70.7%; Pred. No. 3.5e-34;
Matches 174; Conservative 15; Mismatches 44; Indels 13; Gaps 3;

Qy 2 RVPAQLLG-LLLWLPL-----GARCESVLTQPPSVGAPGOKVTISCTGTSNIG 50
Db 1 RVRROSSGNLTMAWTPLLLTFTCTVSEASYELTQPPSVSPGQTARITCSGDA--LP 58
Qy 51 GYDLHWYQOLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYV 110
Db 59 KXYIWTQKSGQAVLVIVETTRPSAIPERFASSSGTMTLTISGAQVEADYVY 118
Qy 111 SYDSSLNAQVFGGTRTLTVLQPKAAPSVTLPFSSSEELQANKATLVCLISDFYFGAVTV 170
Db 119 STDSSSYRVFGGGTKLTVLQPKAAPSVTLPFSSSEELQANKATLVCLISDFYFGAVTV 178
Qy 171 AWKADSSPVKAGVETTTTPSKQNNKYAASSYLSLTPQWKSRSYSCQVTHGSGTVEKTV 230
Db 179 AWKADSSPVKAGVETTTTPSKQNNKYAASSYLSLTPQWKSRSYSCQVTHGSGTVEKTV 238
Qy 231 APTECS 236
Db 239 APTECS 244

RESULT 15

US-09-828-995B-26
; Sequence 26, Application US/09828995B
; Patent No. US20020165135A1
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: The 'Xaa' at location 147 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (148)..(148)
; OTHER INFORMATION: The 'Xaa' at location 148 stands for Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (149)..(149)
; OTHER INFORMATION: The 'Xaa' at location 149 stands for Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (169)..(169)
; OTHER INFORMATION: The 'Xaa' at location 169 stands for Ser, or Asn.
US-09-828-995B-26

Query Match 67.0%; Score 826; DB 9; Length 239;
Best Local Similarity 70.0%; Pred. No. 7.6e-33;
Matches 161; Conservative 21; Mismatches 48; Indels 0; Gaps 0;

Qy 7 LIGLLLLMLPGARCESVLTQPPSVGAPGOKVTISCTGTSNIGYDLHWYQOLPGTAPK 66
Db 10 LLTLTLLHCTGSAQAVLNQPNASVSGALGQKVTISCSGTDNDIDIFGVNMYQQLPGKAPT 69
Qy 67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYVCSYDSSSLNAQVFGGTR 126
Db 70 VLVDSDGDRPSGVDPDFSGSSGNSGTLTITGLQAEDEADYVCSYDSSSLNAQVFGSGTQ 129
Qy 127 LTVLQPKAAPSVTLPFSSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGVETT 186
Db 130 LTVLQPKAAPSVTLPFXXEELGANKATLVCLISDFYFXGVTAVKADGSPVTQGVETT 189
Qy 187 TTPSKQNNKYAASSYLSLTPQWKSRSYSCQVTHGSGTVEKTVAPTECS 236
Db 190 KPSQNNKYAASSYLSLTPDKWKSRSYSCQVTHGSGTVEKTVAPTECS 239

Search completed: March 29, 2003, 09:38:43
Job time : 10.0472 secs

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 8.38523 Seconds
(without alignments)
828.100 Million cell updates/sec

Title: US-09-758-173-10

Perfect score: 1232

Sequence: 1 MRVPAQLGLLLWLPARGC.....CQVTHEGSTVEKTVAPTCS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1232	100.0	236	3	US-08-487-550-10
2	1052.5	85.4	236	4	US-09-049-672A-7
3	973	79.0	234	3	US-08-487-550-2
4	965	78.3	235	4	US-09-049-672A-10
5	965	78.3	235	4	US-09-049-672A-12
6	955	77.5	235	2	US-08-378-939-12
7	885	71.8	235	4	US-09-152-060-70
8	882	71.6	235	4	US-08-152-060-88
9	857.5	69.6	233	4	US-08-523-894-6
10	836	67.9	240	4	US-09-049-672A-11
11	804.5	65.3	238	4	US-08-793-450-6
12	634.5	51.5	229	4	US-08-751-359-22
13	634.5	51.5	229	4	US-08-907-146-22
14	567	46.0	109	2	US-08-761-277A-51
15	548	44.5	105	1	US-08-422-101-9
16	548	44.5	105	1	US-08-422-091-9
17	548	44.5	105	2	US-08-422-092-9
18	548	44.5	105	2	US-08-788-800-6
19	548	44.5	105	3	US-08-422-093-9
20	548	44.5	105	3	US-08-422-112-9
21	544.5	44.2	200	6	5189147-10
22	535	43.4	104	4	US-09-025-769B-170
23	522	42.4	241	2	US-07-916-098A-56
24	508.5	41.3	236	1	US-08-157-101A-5
25	508	41.2	235	1	US-08-276-852-153
26	508	41.2	235	1	US-08-899-575-153
27	508	41.2	235	1	US-08-899-575-153

28	508	41.2	235	5	PCT-US95-08743-153	Sequence 153, Appl
29	502.5	40.8	235	3	US-08-812-586-16	Sequence 16, Appl
30	496.5	40.3	131	1	US-08-305-683A-4	Sequence 4, Appl
31	492.5	40.0	234	4	US-09-049-672A-6	Sequence 6, Appl
32	492.5	40.0	234	5	PCT-US94-07659-4	Sequence 4, Appl
33	492.5	40.0	310	4	US-09-079-029-11	Sequence 11, Appl
34	482.5	39.2	234	2	US-07-690-192-2	Sequence 2, Appl
35	476	38.6	112	4	US-09-035-769B-18	Sequence 18, Appl
36	475	38.6	239	1	US-08-353-400-37	Sequence 37, Appl
37	472	38.3	239	3	US-08-487-550-6	Sequence 6, Appl
38	471.5	38.3	110	4	US-09-240-274-63	Sequence 63, Appl
39	466	37.8	105	2	US-08-646-981-3	Sequence 3, Appl
40	457	37.1	111	4	US-08-983-607-35	Sequence 35, Appl
41	456.5	37.1	213	2	US-08-737-129A-4	Sequence 4, Appl
42	455.5	37.0	240	4	US-09-301-593-36	Sequence 36, Appl
43	455	36.9	235	2	US-08-303-569B-5	Sequence 5, Appl
44	455	36.9	235	2	US-08-116-247-5	Sequence 5, Appl
45	454	36.9	111	2	US-08-665-202-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-10
; Sequence 10, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-10

Query Match 100.0%; Score 1232; DB 3; Length 236;

Best Local Similarity 100.0%; Pred. No. 1.4e-91;

Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLLLWLPARGCSVLTQPPSVSGAPQKVTISCTGSTNIGGYDLHWYQQL 60

DB 1 MRVPAQLGLLLWLPARGCSVLTQPPSVSGAPQKVTISCTGSTNIGGYDLHWYQQL 60

66	Qy		KLIIYDINKP	SGISDR	FGSGYS	GTAA	SLAT	IGTQ	TEDEAD	YTCQ	SDSS	LNQA	VEGGT	125
66	Db		KLIIYGRN	PSGVP	PRFG	SGSGT	SA	SLAT	IGQA	EDAD	YTCQ	SDSS	LNQA	VEGGT
126	Qy		RLTVL	GGPKA	PSVT	FLP	SS	BELO	QAN	KAT	LV	CLIS	DFPG	AVTVA
126	Db		KLTVL	GGPKA	PSVT	FLP	SS	BELO	QAN	KAT	LV	CLIS	DFPG	AVTVA
166	Qy		TPPSKQ	NNKYA	AA	SSYL	SL	TPQW	KSHR	SYSC	QVTH	EGST	VEKT	VA
166	Db		TPPSKQ	NNKYA	AA	SSYL	SL	TPQW	KSHR	SYSC	QVTH	EGST	VEKT	VA

```

RESULT 3
US-08-487-550-2
; Sequence 2, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"

```

```

1  RESULT 3
2  US-08-487-550-2
3  ; Sequence 2, Application US/08487550
4  ; Patent No. 6113898
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Anderson, Darrell R.
7  ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
8  ; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 FRAGMENTED FORMS THEREOF
9  ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE T
10 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
11 ; NUMBER OF SEQUENCES: 12
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
14 ; STREET: 699 Prince Street
15 ; CITY: Alexandria
16 ; STATE: VA
17 ; COUNTRY: USA
18 ; ZIP: 22314
19 ; COMPUTER READABLE FORM:
20 ; MEDIUM TYPE: Floppy disk
21 ; COMPUTER: IBM PC compatible
22 ; OPERATING SYSTEM: PC-DOS/MS-DOS
23 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
24 ; CURRENT APPLICATION DATA:
25 ; APPLICATION NUMBER: US/08/487,550
26 ; FILING DATE: 07-JUN-1995
27 ; CLASSIFICATION: 435
28 ; ATTORNEY/AGENT INFORMATION:
29 ; NAME: Teskin, Robin L.
30 ; REGISTRATION NUMBER: 35,030
31 ; REFERENCE/DOCKET NUMBER: 012712-131
32 ; TELECOMMUNICATION INFORMATION:
33 ; TELEPHONE: 703-836-6620
34 ; TELEFAX: 703-836-2021
35 ; INFORMATION FOR SEQ ID NO: 2:
36 ; SEQUENCE CHARACTERISTICS:
37 ; LENGTH: 234 amino acids
38 ; TYPE: amino acid
39 ; TOPOLOGY: linear
40 ; MOLECULE TYPE: protein
41 US-08-487-550-2

```

Query Match	79.0%;	Score 973;	DB 3;	Length 234;
Best Local Similarity	80.1%;	Pred. No. 7.9e-71;		
Matches 189;	Conservative 13;	Mismatches 32;	Indels 2;	Gaps
QY	1	MRVPAQLGLGLLLWLPGARCESVLTQPSVSGAPGQKVITSGTSGTNSIGGYDLHWYQQL	60	
DBb	1	MRVPAQLGLGLLLWLPGARCAVELTQPSVSVSGQQTARITCGGDSNR	58	
QY	61	PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYCYOSYDSSINAQV	120	
DBb	59	PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCYQWDRASDHVP	118	
QY	121	FGGTRTLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDPYAGNAVTVAMKADSSPVK	180	
DBb	119	FGGTRTVTLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVK	178	
QY	181	AGVETTTSPSKSNKNYAASSYLSTPEQWKSHRYSQVTHGSGTVEKTVAPTECS	236	

Db 179 AGVETTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
|||||

RESULT 4
US-09-049-672A-10
; Sequence 10, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYRN0T10
; CLONE: 2872705
US-09-049-672A-10

Query Match 78.3%; Score 965; DB 4; Length 235;
Best Local Similarity 80.3%; Pred. No. 3.5e-70;
Matches 187; Conservative 19; Mismatches 25; Indels 2; Gaps 2;

Qy 5 AQLGLLLWLPGARCESVLTQPPSVSGAPQKVTISCTGTSNIGGYD-LHWYQQLPQT 63
Db 4 ALLFTLLTQGTGSAQALTPASVSGSQSITISCTGTSNIGGYD-LHWYQQLPQT 63
Qy 64 APKLIYDINKRPGISDRFSGSKSGTAAASLAITGLQTEDEADYYCQSYDSSLSNAQVFGG 123
Db 64 APKLMIEVNRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCQSYGVN-NIVVFGG 122
Qy 124 GTRLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183
Db 123 GTKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 182

Qy 184 ETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 183 ETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 5
US-09-049-672A-12
; Sequence 12, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGUT13
; CLONE: 3116314
US-09-049-672A-12

Query Match 78.3%; Score 965; DB 4; Length 235;
Best Local Similarity 80.0%; Pred. No. 3.5e-70;
Matches 184; Conservative 20; Mismatches 26; Indels 0; Gaps 0;

Qy 7 LLGLLLWLPGARCESVLTQPPSVSGAPQKVTISCTGTSNIGGYD-LHWYQQLPQTAPK 66
Db 6 LLLALLTTCAGSWAQSVLTQPPSVSGTFCQRTVITSCGTTSNIAINSVHWYQLVPGAAPK 65
Qy 67 LLIYDINKRPGISDRFSGSKSGTAAASLAITGLQTEDEADYYCQSYDSSLSNAQVFGGTR 126
Db 66 LLIYANDQASGVDRFSGSKSGTASLAISGLRPEDETDYYCATWDDSVSCWMEGGGTRK 125
Qy 127 LTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 186
Db 126 LTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185

```
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003PI.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-152-060-70

Query Match      71.8%; Score 885; DB 4; Length 235;
Best Local Similarity 77.1%; Pred No. 9e-64;
Matches 178; Conservative 11; Mismatches 38; Indels 4; Gaps 1;

QY 10 LLLLLLPGARCESV----LTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAP 65
Db 5 LLLLLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAATLQHQHPP 64
QY 66 KLLIYDINKRPGISDRFSGSKGTAAALITGLQTEADYVYCQSYDSSLNAQVFGGT 125
Db 65 KLLSYRNNRPGISERLSASRGATSLTITGLQPEADYICAAIDSSLAVWHPGGT 124
QY 126 RLTVLGOPKAAPSVTLFPPSSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGVET 185
Db 125 KLTVLGOPKAAPSVTLFPPSSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGVET 184
QY 186 TTTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 185 TTTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 8
US-09-152-060-88
; Sequence 88, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003PI.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
```

```
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-939-12

Query Match      77.5%; Score 955; DB 2; Length 235;
Best Local Similarity 79.8%; Pred No. 2.2e-69;
Matches 186; Conservative 18; Mismatches 27; Indels 2; Gaps 2;

QY 5 AQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDL-HWYQQLPGT 63
Db 4 ALLLLTLTQDTGSAWQAALTPASVSGSPGSGITISCTGTNNVGSYLVSWYQQHFGK 63
QY 64 AKLLIYDINKRPGISDRFSGSKGTAAALITGLQTEADYVYCQSYDSSLNAQVFGG 123
Db 64 APKIMTYEYKRPVSGVSNRFGSKGNTASLTISGLQAEADYVCCSYAGSYTV-VFGG 122
QY 124 GTRLTVLGOPKAAPSVTLFPPSSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGV 183
Db 123 GTKLTVLGOPKAAPSVTLFPPSSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGV 182
QY 184 ETTTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 183 ETTTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 7
US-09-152-060-70
; Sequence 70, Application US/09152060
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-523-894-6

Query Match          69.6%; Score 857.5; DB 4; Length 233;
Best Local Similarity 74.8%; Pred. No. 1.4e-61;
Matches 172; Conservative 16; Mismatches 39; Indels 3; Gaps

Qy 7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVITISCTGSTSNIIGGYDLHLWYQQLPGTAPK 66
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 7 LLGLLAHFTDSA-ASYELSPRSVSPGQTAGFTCGG--DNVGRKSVQWYQKPPQAPV 63

Qy 67 LLIYDINKRSGISDRPSSGSKGTAAISLAITGLQTDEADYYCQSYDSSLSNAOVFGGTR 126
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 64 LVIYADSRGSGIPARFSGNSGNTATLTISGVEAGDEADYYCQVWDSTADHWVFGGTR 123
;

Qy 127 LTVLGQPKAAPSVTLPFPSSSEELQANKATLVCLISDFYPGA VTVAMKADSSPVKAGVET 186
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 124 LTVLGQPKAAPSVTLPFPSSSEELQANKATLVCLISDFYPGA VTVAMKADSSPVKAGVET 183

Qy 187 TPSQSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 236
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 184 TPSQSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 10
US-09-049-672A-11
; Sequence 11, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HERewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

```

```
;
; TELETYPE: 703-413-3000
; TELEPHONE: 703-413-3000
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LNOBNOT08
; CLONE: 3056213
US-09-049-672A-11

Query Match 67.9%; Score 836; DB 4; Length 240;
Best Local Similarity 70.2%; Pred. No. 7.8e-60;
Matches 172; Conservative 17; Mismatches 42; Indels 14; Gaps 4;

Qy 1 MRVPAQLGLLLML-----PGARCESVLTQPPSVSGAPGQKVTISC-----TGSTNSIGG 51
Db 1 MSVPTMAWMLLLGLLAYSGVDSTVVTQBPSPFSVPGGTVTLTCTGLSSGVSSTSNPS 60

Qy 52 YDLHWYQQLPGTAPKLLIYDINKRPSGIDRFSGSKSGTAASLAITGLQTEDEADYYCQS 111
Db 61 ----WYQTPQAPRTLIYGTSSRGSGVDRFSGIILGNKAGLTIITGAQADSDIYCVL 116

Qy 112 YDSSLNAQVFGGTRTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA 171
Db 117 YRRS-GSNVFGGTKLSVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA 175

Qy 172 WKADSSPVKAGVETTPSKQSNKYAASSVLSLTPEQWKSRSYSCQVTHGSTEKVTVA 231
Db 176 WKADSSPVKAGVETTPSKQSNKYAASSVLSLTPEQWKSRSYSCQVTHGSTEKVTVA 235

Qy 232 PTECS 236
Db 236 PTECS 240

RESULT 11
US-08-793-450-6
; Sequence 6, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIH, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-6

Query Match 65.3%; Score 804.5; DB 4; Length 238;
Best Local Similarity 70.9%; Pred. No. 2.6e-57;
Matches 163; Conservative 10; Mismatches 40; Indels 17; Gaps 3;

Qy 17 GARCESVLTQPPSVSGAPGQKVTISCSTNSTNIGGYDLHWYQQLPGTAPKLLIYDINKRP 76
Db 16 GVHSDIEUTQDPAVSVAGVGTVRITCG--DSLRTYASWYQKPGQAPVLVIYGNKRRP 73

Qy 77 SGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGTRTLVLGQPKAA 136
Db 74 SGIPDRFSGSSGNTASLTITGAQAEDEADYFCNS-----CGKVFGGTKLTVLGQPKAA 128

Qy 137 PSVTLFPPS-----SBELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
Db 129 PSVTLFPPSBELOANKATLVCLISDFYPGAVTVAWKADGRPVKAGVETN 188

Qy 187 TPKSQSNKYAASSVLSLTPEQWKSRSYSCQVTHGSTEKVTVAPECS 236
Db 189 KPSQSNKYAASSVLSLTPEQWKSRSYSCQVTHGSTEKVTVAPECS 238

RESULT 12
US-08-751-359-22
; Sequence 22, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-751-359-22
```

Query Match		51.5%;	Score 634.5;	DB 4;	Length 229;
Best Local Similarity		55.8%;	Pred. No. 1e-43;		
Matches 130;		Conservative	32;	Mismatches	62;
				Indels	9;
				Gaps	5;
QY	5	AQLGLLLMLPGARCESVLTQPPSVSGAPGQKVITISCTGTSNIGGYDLHWYQO-LPGT	63		
DB	4	APLLAVLAHTSGSLVQAALTOPSSVSANPGETVKITCSGDRSYG-----WYQKAPGS	58		
QY	64	APKLLIYDINKRPSGISDRFSGSGTAAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG	123		
DB	59	APVTVIYANTNRPSDIPSRFSGSGSTATLITITGVQADDEAVYYCGSADSSSTAGIFGA	118		
QY	124	GTRLTVLGQPKAAPSVTLFPPSSEEL-QANKATLVCLISDFYPGAVTVAAKADSSPVKAG	182		
DB	119	GTTLVLGQPKVAPTITLPPPSKEELNEATKATLVCLINDFYFSPVTVDWIDGS-TRSG	177		
QY	183	VEITPQSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTEKTVAPTEC	235		
DB	178	-ETAPQQRQNSQYMASSYLSLSASDWSSSHETVTCRVTHNGTSITKTLKRSEC	229		
RESULT 14					
US-08-761-277A-51					
; Sequence 51, Application US/08761277A					
; Patent No. 5972334					
; GENERAL INFORMATION:					
; APPLICANT: Denney Jr., Dan W.					
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And					
; TITLE OF INVENTION: Leukemia					
; NUMBER OF SEQUENCES: 80					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Medlen & Carroll, LLP					
; STREET: 220 Montgomery Street, Suite 2200					
; CITY: San Francisco					
; STATE: California					
; COUNTRY: United States Of America					
; ZIP: 94104					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/761,277A					
; FILING DATE: 06-DEC-1996					
; CLASSIFICATION: 424					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/644,664					
; FILING DATE: 01-MAY-1996					
; ATTORNEY/AGENT INFORMATION:					
; NAME: MacKnight, Kamrin T.					
; REGISTRATION NUMBER: 38,230					
; REFERENCE/DOCKET NUMBER: GENITOPE-02406					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (415) 705-8410					
; TELEFAX: (415) 397-8338					
; INFORMATION FOR SEQ ID NO: 51:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 109 amino acids					
; TYPE: amino acid					
; TOPOLOGY: linear					
; MOLECULE TYPE: protein					
US-08-761-277A-51					
Query Match					
Best Local Similarity					
Matches 109;					
Conservative					
0;					
Mismatches					
0;					
Indels					
0;					
Gaps					
0;					
QY	128	TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAAKADSSPVKAGVETTT	187		
DB	1	TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAAKADSSPVKAGVETTT	60		
QY	188	PSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTEKTVAPTECS	236		
DB	61	PSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTEKTVAPTECS	109		
RESULT 15					
US-08-422-101-9					

```
; Sequence 9, Application US/08422101
; Patent No. 5739277
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,101
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-422-101-9

Query Match 44.5%; Score 548; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e-37;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTSKQ 191
Db 1 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTSKQ 60

Qy 192 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
Db 61 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 105

Search completed: March 29, 2003, 09:17:44
Job time : 9.38523 secs
```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 18:12:24 ; Search time 392.719 Seconds
(without alignments)
8205.894 Million cell updates/sec

Title: US-09-758-173-11
Perfect score: 1431
Sequence: 1 ATGAACACCTGTGCTTCTT.....CCCTGTCTCGGTAATGA 1431

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	18	Primitised anti-hu
2	1431	100.0	1431	19	Macaque primatized
3	1431	100.0	1431	24	DNA sequence of a
4	1315.8	91.9	1431	18	Primitised anti-hu
5	1315.8	91.9	1431	19	Macaque primatized
6	1315.8	91.9	1431	24	DNA sequence of a
7	1216.4	89.2	1567	22	Human immune syste
8	1261.2	88.1	1431	17	Monoclonal antibod
9	1261	88.1	1634	21	Human immune syste

10	1224.8	85.6	1418	17	Anti-rhesus D reco
11	1181	82.5	1404	18	Human gamma-4 heav
12	1177.8	82.3	1404	18	Human gamma-4PE he
13	1176.2	82.2	1404	18	Human gamma-4E hea
14	1151	80.4	1428	22	Nucleotide sequenc
15	1136.4	79.4	1428	18	Human anti-RSV mon
16	1134	79.2	1430	24	CDNA of the heavy
17	1134	79.2	1644	22	Human cDNA encodin
18	1133.8	79.2	1507	21	Human immunoglobul
19	1133.4	79.2	1798	21	Human colon cancer
20	1123.6	78.5	1428	18	Human anti-RSV mon
21	1122.8	78.5	1599	24	Human benign prost
22	1122.8	78.5	1599	24	Colon adenocarcino
23	1122.8	78.5	1599	24	Lung cancer relate
24	1122.8	78.5	1599	24	Antibody D heavy c
25	1121.2	78.4	1617	14	Traget plasmid Man
26	1120.8	78.3	19035	19	Encodes heavy chai
27	1119.6	78.2	1549	13	Plasmid Glambda-1B
28	1119	78.2	1442	22	Monoclonal antibod
29	1118	78.1	1449	20	Plasmid Glambda-1A
30	1118	78.1	1449	20	Macaque primatized
31	1115.8	78.0	6281	22	DNA sequence of a
32	1112.4	77.7	1437	19	Plasmid Hui9HCpcd
33	1112.4	77.7	1437	24	Primatized anti-hu
34	1110.8	77.6	1427	19	Reshaped CD4 antib
35	1110.8	77.6	1427	19	Plasmid Hui9HCpcd
36	1110.8	77.6	1427	19	Plasmid Hui9HCpcd
37	1109.8	77.6	1437	18	Primatized anti-hu
38	1109.8	77.6	1458	13	Reshaped CD4 antib
39	1109.2	77.5	1427	19	Plasmid Hui9HCpcd
40	1107.8	77.4	1576	14	Human anti-HBs hea
41	1102.8	77.1	6284	19	Plasmid Hui9HCpcd
42	1102.2	77.0	6557	17	Anti-IgE VH expres
43	1101	76.9	1431	22	Chimeric 4H6 anti-
44	1101	76.9	1431	22	Chimeric 4H6 anti-
45	1100.8	76.9	2912	22	Human cDNA encodin

ALIGNMENTS

RESULT 1	
AAAT62513	
ID	AAAT62513 standard; DNA; 1431 BP.
XX	
AC	AAAT62513;
XX	
DT	25-MAY-1997 (first entry)
XX	
DE	Primatized anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
XX	
KW	Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW	primatized antibody; B7 antigen; CD28; immunosuppressive;
KW	autoimmune disease; idiopathic thrombocytopenia purpura;
KW	systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW	type 1 diabetes mellitus; graft versus host disease;
KW	hetero-hybridoma; transfectoma; ss.
OS	Chimeric Macaca cynomolgus;
OS	Chimeric Homo sapiens.
XX	
FN	WO9640878-A1.
XX	
PD	19-DEC-1996.
XX	
PF	06-JUN-1996; 96WO-US10053.
XX	
PR	07-JUN-1995; 95US-0487550.
XX	
PA	(IDEC-) IDEC PHARM CORP.
XX	
PI	Anderson DR, Brans P, Hanna N, Shestowsky WS;
XX	

Db 1081 ATCGAGAAACCAATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAACAGGTGTACACCCCTG 1140
 QY 1141 CCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGAGCTGACCTGCTGGTCAAGGC 1200
 Db 1141 CCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGAGCTGACCTGCTGGTCAAGGC 1200
 QY 1201 TTTATTCACAGCAGCATPCCGCTGGAGTGGAGAGCAATGGGCGAGCCGAGAACAACTAC 1260
 Db 1201 TTTATTCACAGCAGCATPCCGCTGGAGTGGAGAGCAATGGGCGAGCCGAGAACAACTAC 1260
 QY 1261 AAGACACGCTCCCGTGTGGACTCCGAGCGCTCTTCTTCTTCTACAGCAGCTCAC 1320
 Db 1261 AAGACACGCTCCCGTGTGGACTCCGAGCGCTCTTCTTCTTCTACAGCAGCTCAC 1320
 QY 1321 GTGACAAGAGCAGGTGGCAGAGGGGAAAGCTTCTTCTATGCTCCGTGATGATGAGGCT 1380
 Db 1321 GTGACAAGAGCAGGTGGCAGAGGGGAAAGCTTCTTCTATGCTCCGTGATGATGAGGCT 1380
 QY 1381 CTGCACAACTACAGCAGAGAGAGCCTTCCCTGTCTCCGGGTAAATGA 1431
 Db 1381 CTGCACAACTACAGCAGAGAGAGCCTTCCCTGTCTCCGGGTAAATGA 1431

RESULT 4
 AAT62510
 ID AAT62510 standard; DNA; 1431 BP.
 AC AAT62510;
 XX
 DT 25-MAY-1997 (first entry)
 DE
 DE Primatised anti-human B7.1 antigen antibody 7C10 heavy chain DNA.
 XX
 KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
 KW primatised antibody; B7 antigen; CD28; immunosuppressive;
 KW autoimmune disease; idiopathic thrombocytopenia purpura;
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes mellitus; graft versus host disease;
 KW hetero-hybridoma; transfectoma; ss.
 XX
 OS Chimeric Macaca cynomolgus;
 OS Chimeric Homo sapiens.
 XX
 PN W09640878-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US10053.
 XX
 PR 07-JUN-1995; 95US-0487550.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Brans P, Hanna N, Sheatsowsky WS;
 XX
 DR WPI; 1997-108638/10.
 DR P-PSDB; AAW01818.
 XX
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
 PT useful for treating autoimmune disease or graft-versus-host disease
 XX
 PS Claim 7; Fig 8B; 81pp; English.
 XX
 CC 2 DNA sequences (AAT62509 and AAT62510) respectively code for
 CC primatised forms (AAW01817 and AAW01818) of the light and heavy chains
 CC of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
 CC 7C10. Cloned 7C10 light and heavy variable genes are inserted into
 CC an expression vector (pref. NEOSPLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of primatised
 CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
 CC antibodies have also been produced (see also AAW01819-22). The
 CC primatised antibodies inhibit the B7:CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders

CC and graft-versus-host disease.
 XX
 SQ Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;
 Query Match 91.9%; Score 1315.8; DB 18; Length 1431;
 Best Local Similarity 95.0%; Pred. No. 4.8e-262;
 Matches 1359; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 QY 1 ATGAAACACCTGTGGTTCCTCTCTGTGGCAGCTCCAGATGGTCTCTGTCCAG 60
 Db 1 ATGAAACACCTGTGGTTCCTCTCTGTGGCAGCTCCAGATGGTCTCTGTCCAG 60
 QY 61 GTGACGTGACAGAGTGGGCGCAGAGCTGGTGAAGCTTCGGAGACCTGTCTCCAC 120
 Db 61 GTGAAGCTGCAGCAGTGGGCGAAGAGCTTCTGCAGCCTTCGGAGACCTGTCCG 120
 QY 121 TCGCTGTCTCTGTGGCTCCATCAGCGGTGTTATGGCTGGGCTGGATCCGCA 180
 Db 121 TCGCTGTCTCTGTGGCTCCATCAGCGGTGTTATGGCTGGGCTGGATCCGCA 180
 QY 181 CCAGGGAAGGGCTGGAGTGGGAGTTTCTATAGTAGTAGTGGGAAACACCTACT 240
 Db 181 CCAGGGAAGGGCTGGAGTGGGAGTTTCTATAGTAGTAGTGGGAAACACCTACT 240
 QY 241 AACCCCTCCCTCAAGAGTCAAGTCAACATTTCAACAGACAGTCCAAAGAAC 300
 Db 241 AATCCCTCCCTCAAGAGTCAAGTCAACATTTCAAAAGACAGTCCAAAGAAC 300
 QY 301 CTGAAGCTGAATCTATGACCGCGCGACACGCGCTGATGTTTCTGTGTGAG 360
 Db 301 CTGAAGCTGAATCTGTGACCGCGCGACACGCGCTGATGTTTCTGTGTGAG 360
 QY 361 CTTTTCCTCAGTTGTTGAATGGTTTACAAACATGGTTTCGATGTCTGGGCG 420
 Db 361 CCGCTGATTCACACACCATTTGTTATGGCGCTGGTGCATGTCTGGGCG 420
 QY 421 CTGTGTACCGTCTCTCTCAGTGTAGCACCAGGGCCCATCGGTCTTCCCTGG 480
 Db 421 CTGTGTACCGTCTCTCTCAGTGTAGCACCAGGGCCCATCGGTCTTCCCTGG 480
 QY 481 TCCAAGAGCAGCTCTGGGGGACACGCGCCCTGGCTGCTGGTCAAGGACTACT 540
 Db 481 TCCAAGAGCAGCTCTGGGGGACACGCGCCCTGGCTGCTGGTCAAGGACTACT 540
 QY 541 GAAACCGGTGACCGTGTCTGTGAACTCAGGCGCCCTGACAGCGCGTGCACAC 600
 Db 541 GAAACCGGTGACCGTGTCTGTGAACTCAGGCGCCCTGACAGCGCGTGCACAC 600
 QY 601 GCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA 660
 Db 601 GCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA 660
 QY 661 AGCTTGGGACCCAGACCTACATCTGCACAGTGAATCAAGCCCGAGCAACCA 720
 Db 661 AGCTTGGGACCCAGACCTACATCTGCACAGTGAATCAAGCCCGAGCAACCA 720
 QY 721 GACAAAGAACAGAGCCCAAAATCTTTGTGACAAAATCTACACATGCCAC 780
 Db 721 GACAAAGAACAGAGCCCAAAATCTTTGTGACAAAATCTACACATGCCAC 780
 QY 781 CCTGAACCTCTGGGGGACCGTCACTTCTTCTTCTTCTTCTTCTTCTTCT 840
 Db 781 CCTGAACCTCTGGGGGACCGTCACTTCTTCTTCTTCTTCTTCTTCTTCT 840
 QY 841 ATGATCTCCCGGACCCCTGAGGTACATGCTGGTGGTGGAGCTGAGCCAGAAC 900
 Db 841 ATGATCTCCCGGACCCCTGAGGTACATGCTGGTGGTGGAGCTGAGCCAGAAC 900
 QY 901 GAGGTCAAGTTCACTGTGTAGTGGAGCGCTGGAGTGCATAATGCCAAGCA 960
 Db 901 GAGGTCAAGTTCACTGTGTAGTGGAGCGCTGGAGTGCATAATGCCAAGCA 960
 QY 961 CGGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTTCAGCGTCTCTCAC 1020

[illegible]

CC The present sequence is useful in the diagnosis, treatment and
CC prevention of disorders associated with the immune system and
CC cell proliferation.

Sequence 1634 BP; 369 A; 541 C; 432 G; 292 T; 0 other;

Query Match	88.1%;	Score 1261;	DB 21;	Length 1634;
Best Local Similarity	94.2%;	Pred. No. 9.6e-251;		
Matches 1348;	Conservative	0;	Mismatches 65;	Indels 18;
				Gaps

QY	1	ATGAAACACCTGTGGTTCTTCTCTCTCTGTGTGGAGCTCCAGATGGGTCTGTCTCCAG	60
DB	78	ATGAAACATCTGTGGTTCTTCTCTCTGTGTGGAGCTCCAGATGGGTCTGTCTCCAG	137
QY	61	GTGCAGCTGCAGAGTGGGSCCAGGACTGGTGAAGCCCTTCGGAGACCCCTGTCCCTCACC	120
DB	138	GTGCAGCTGCAGAGTTCGGGCCAGGACTGGTGAAGCCCTTCGGAGACCCCTGTCCCTCACC	197
QY	121	TGGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCAGGCC	180
DB	198	TGCATGTCTCTGGTGGCTCCATCA--GGAGTTACTATGGAATCGATCCGGTGGCC	254
QY	181	CCAGGGAAGGGCTGGAGTGGATTGGAGTGTCTATAGTAGTAGTGGGAAACACTACTATAC	240
DB	255	CCAGGGAAGGGAATCGAGTGGATTGGGTATATCTA---TACTAGTGGGAGCACCACCTAC	311
QY	241	AACCCCTCCCTCAAGAGTCAAGTCACATTTTCAAAGACAGCTCCAAAGAACAGTTCTCC	300
DB	312	AACCCCTCCCTCAAGAGTCAAGTCAATGTGAGTAGACAGCTCCAAAGAACAGTTCTCC	371
QY	301	CTGAAGCTGAACCTTATGACCGCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT	360
DB	372	CTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT	431
QY	361	CTTTTTTTCAGTGTGGTAATGGTTTACAACAACATGGTTTCGATGTCTGGGGCCCGGGAGTC	420
DB	432	CCCAACCGCTACTACTACTACGGTATGGA-----CTTCTGGGGCCCAAGGGAGCC	479
QY	421	CTGCTACACCGTCTCTCAGCTAGCATAGCAACCAAGGGCCCATCGTCTTCCCTCCGCAACCTCC	480
DB	480	CTGCTACCGCTCTCTCAGCGCTCCACAAGGGCCCATCGGTCTTCCCTCCGCAACCTCC	539
QY	481	TCCAAGAGCACCTCTGGGGGACAGCGGGCCCTGGGTGCTGGTCAAGGAATCTTCCCC	540
DB	540	TCCAAGAGCACCTCTGGGGGACAGCGGGCCCTGGGTGCTGGTCAAGGAATCTTCCCC	599
QY	541	GAACCGGTGACGGTGTGTGTGAACTCAGGGGCCCTGACAGCGGGCGTGGACACTTCCCG	600
DB	600	GAACCGGTGACGGTGTGTGTGAACTCAGGGGCCCTGACAGCGGGCGTGGACACTTCCCG	659
QY	601	GCTGTCTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGGTGGTACCGTGCCTCCAGC	660
DB	660	GCTGTCTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGGTGGTACCGTGCCTCCAGC	719
QY	661	AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGAGTG	720
DB	720	AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGAGTG	779
QY	721	GACAAAGAGAGAGGCCAAATCTTGTGACAAACCTCACATATGCCCAACGTTGCCAGCA	780
DB	780	GACAAAGAGTTGAGGCCAAATCTTGTGACAAACCTCACATATGCCCAACGTTGCCAGCA	839
QY	781	CCTGAACTCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAACCCCAAGGACACCTC	840
DB	840	CCTGAACTCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAACCCCAAGGACACCTC	899
QY	841	ATGATCTCTCCGGACCCCTGAGGTCAATCGCTGGTGGTGGAGCTGAGCCAGGAACCCCT	900
DB	900	ATGATCTCTCCGGACCCCTGAGGTCAATCGCTGGTGGTGGAGCTGAGCCAGGAACCCCT	959
QY	901	GAGTCAAGTTCCTAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAACCGG	960
DB	960	GAGTCAAGTTCCTAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAACCGG	1019

Db 601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC 660

XX

KW CD4; monoclonal antibody; chimeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
XX Homo sapiens.
OS

XX WO9709351-A1.

XX 13-MAR-1997.

XX 05-SEP-1996; 96WO-US14324.

XX 06-SEP-1995; 95US-0523894.

XX (IDEC-) IDEC PHARM CORP.

XX Hanna N, Newman RA, Reff ME;

XX WPI; 1997-201913/19.

XX P-PSDB; AAW14927.

XX Chimeric antibody comprising monkey variable domains and human
XX constant domains - affects CD4-mediated immune functions, esp.
XX useful for treatment of autoimmune disease, e.g. rheumatoid
XX arthritis

XX Disclosure; Page 91-93; 155pp; English.

XX DNA sequences (AA126868-70) respectively code for the heavy chain
XX regions of human gamma-4 (AA14925), gamma-4E carrying the L236E
XX mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
XX mutations. They can be used to provide novel monoclonal and
XX chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
XX gamma-4PE, in which the human IgG4 Fc binding domain framework is
XX combined with the antigen binding domains (see also AAW14922-23) of
XX macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
XX show high affinity to human CD4, have little or no immunogenicity
XX in humans and -4PE mutations confer activity enhanced stability and
XX gamma-4E and -4PE mutations confer activity enhanced stability and
XX eliminate depleting activity. The antibodies can be used to treat
XX autoimmune diseases such as rheumatoid arthritis.

XX Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;

Query Match 82.3%; Score 1177.8; DB 18; Length 1404;
Best Local Similarity 90.3%; Pred. No. 1.3e-233;
Matches 1292; Conservative 0; Mismatches 112; Indels 27; Gaps 2;

QY 1 ATGAACACCTGTGGTCTTCTCTCTCTGTCGCGAGCTCCAGATGGTCTGTCCAG 60
DB 1 ATGAACACCTGTGGTCTTCTCTCTCTGTCGCGAGCTCCAGATGGTCTGTCCAG 60
QY 61 GTGAGCTGCAGGAGTCGGGCGCCAGGACTGGTGAAGCTTCGGAGACCTGTCCCTCAC 120
DB 61 GTGAGCTGCAGGAGTCGGGCGCCAGGACTGGTGAAGCTTCGGAGACCTGTCCCTCAC 120
QY 121 TGCCTGTCTCTGTGGTCTCATAGCGGTGGTTATAGCTGGGGGTGATCCGCGAGCCC 180
DB 121 TGCAGTGTCTCTGTGGTCTCATAGCGGTGGTTATATATTGTTCTGGATCCGCGAGTCC 180
QY 181 CCAGGAGAGGGCTGAGTGGATTCGGAGTTTCTATAGTGTAGTGGGAACACCTACTAC 240
DB 181 CCAGGAGAGGGCTGAGTGGATTCGGAGTTTCTATAGTGTAGTGGGAACACCTACTAC 240
QY 241 AACCCCTCTCCCTCAAGAGTCAAGTCAACATTTTCAACAGACAGTCCAGAACCTGTCTCC 300
DB 241 AATCCCTCTCCCTCAACATCGAGTCTCCATTTTCAATAGACAGTCCAGAACCTGTCTCC 300
QY 301 CTGAAGCTGAATCTTATAGCCCGCGGACACGCGCGTGTATTACTGTGTGAGAGATCGT 360
DB 301 CTGAAGCTGAGGTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGTGAGAGTAATA -- 359

QY 361 CTTTTCCTCAGTTGTGGAATGGTTTCAACAACTGGTTCGATGTCTGGGCGCCGGGAGTC 420
DB 359 -----TATTGAATACTTCACTGGTTATTATATCTGGGCGCAGGAGTC 402
QY 421 CTGTCACCGTCTCTCAGTGTAGCACCAAGGGCCCATCGGTCTTCCCTTGGCACCCCTCC 480
DB 403 CTGTCACCGTCTCTCAGTGTAGCACCAAGGGCCCATCGGTCTTCCCTTGGCGCCCTGC 462
QY 481 TCCAAGAGCACCTCTGGGGCACAGCGGCTCTGGGCTGCTGGTCAAGGACTACTTCCCC 540
DB 463 TCCAAGAGCACCTCCGAGAGCACAGCGGCTCTGGGCTGCTGGTCAAGGACTACTTCCCC 522
QY 541 GAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACACGCGCGTGCACACCTTCCCG 600
DB 523 GAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACACGCGCGTGCACACCTTCCCG 582
QY 601 GCTGTCTTACAGTCTCAGGACTCTACTCTCTCAGAGCGTGTGACCGTCCCTCCAGC 660
DB 583 GCTGTCTTACAGTCTCAGGACTCTACTCTCTCAGAGCGTGTGACCGTCCCTCCAGC 642
QY 661 AGCTTGGGCGCCAGACCTACATCTGCAAGCTGAATCACAAAGCCAGCAACACCAAGGTG 720
DB 643 AGCTTGGGCGCAAGAGACCTACACCTGCAAGCTAGATCAAAAGCCAGCAACACCAAGGTG 702
QY 721 GACAAAGAAAGCAGAGCCCAAAATCTTGTGACAAAACTCACACATGCCCAACCGTGCACGA 780
DB 703 GACAAAGAGAGTTGAGTCCAAATATGG-----TCCCCCATGCCACCATGCCAGCA 753
QY 781 CTTGAATCTCTGGGGGAGCCGTCACTCTTCTCTTCCCTCCCAAAACCAAGGACACCTC 840
DB 754 CTTGAATCTCGAGGGGGAGCCATCACTCTCTTCTTCTTCCCTCCCAAAACCAAGGACACTCTC 813
QY 841 ATGATCTCCCGGACCCCTGAGTGTACATGCTGTGTGTGGTGGACGTGAGCCAGAAAGCCCT 900
DB 814 ATGATCTCCCGGACCCCTGAGTGTACATGCTGTGTGTGGTGGACGTGAGCCAGAAAGCCCT 873
QY 901 GAGGTCAAGTTCAACTGTGTGTGACGCGGTGGAGTGTGATATATGCCAAGAAAGCCG 960
DB 874 GAGGTCCAGTTCAACTGTGTGTGACGCGGTGGAGTGTGATATATGCCAAGAAAGCCG 933
QY 961 CGGGAGGAGCAGTCAACAGACAGCTACCGTGTGTGTGACGCGTCTCACCCTGTGCACAG 1020
DB 934 CGGGAGGAGCAGTTCAACAGACAGCTACCGTGTGTGTGACGCGTCTCACCCTGTGCACAG 993
QY 1021 GACTGCTGAATGGCAAGGAGTCAAGTCAAGTGTCTCCAAAGAGCCCTCCCAAGCCCTC 1080
DB 994 GACTGCTGAACGGCAAGGAGTCAAGTCAAGTGTCTCCAAAGAGCCCTCCCGTCTCTCC 1053
QY 1081 ATCGAGAAACCATCTTCCAAAGCCAAAGGCGAGCGCCCGAGAACCAAGTGTGACCCCTG 1140
DB 1054 ATCGAGAAACCATCTTCCAAAGCCAAAGGCGAGCGCCCGAGAACCAAGTGTGACCCCTG 1113
QY 1141 CCCCCATCCGGGATGAGCTGACCAAGAACAGGTCAGCTGACCTGCTGGTCAAAAGC 1200
DB 1114 CCCCCATCCCGAGGAGATGACCAAGAACAGGTCAGCTGACCTGCTGGTCAAAAGC 1173
QY 1201 TTCTATCCCGAGCAATCGCCGTGGAGTGGGAGCAATGGGACGCGGAGAACCAACTAC 1260
DB 1174 TTCTATCCCGAGCAATCGCCGTGGAGTGGGAGCAATGGGACGCGGAGAACCAACTAC 1233
QY 1261 AAGACCAACGCTCTCCGTGTGAGTCCGAGCGCTCTTCTCTCTACAGCAAGCTCAC 1320
DB 1234 AAGACCAACGCTCTCCGTGTGAGTCCGAGCGCTCTTCTCTCTACAGCAAGCTCAC 1293
QY 1321 GTGCAAGAGCAGGTGGCAGCAGGAGGAGCTTCTCTCATGTCTCGTGTATGATGAGGCT 1380
DB 1294 GTGCAAGAGCAGGTGGCAGGAGGAGGAGTGTCTCTCATGTCTCGTGTATGATGAGGCT 1353
QY 1381 CTGCAACCACTTACACGAGAGAGGCTCTCTCTGTCTCTCGGGTAAATGA 1431
DB 1354 CTGCAACCACTTACACACAGAGAGGCTCTCTCTGTCTCTGGGTAAATGA 1404

RESULT 13

AA162869
ID AAT62869 standard; DNA; 1404 BP.

XX AC AAT62869;

XX DT 18-OCT-1997 (first entry)

XX DE Human gamma-4E heavy chain DNA.

XX KW CD4; monoclonal antibody; chimeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma-4E; ss.

XX OS Homo sapiens.

XX PN WO9709351-A1.

XX PD 13-MAR-1997.

XX PF 05-SEP-1996; 96WO-US14324.

XX PR 06-SEP-1995; 95US-0523894.

XX PA (IDEC-) IDEC PHARM CORP.

XX PI Hanna N, Newman RA, Reff ME;

XX DR WPI; 1997-201913/18.

XX DR P-PSDB; AAW14926.

XX PT Chimeric antibody comprising monkey variable domains and human
PT constant domains - affects CD4-mediated immune functions, esp.
PT useful for treatment of autoimmune disease, e.g. rheumatoid
PT arthritis

XX PS Disclosure; Page 86-88; 155pp; English.

XX CC DNA sequences (AAT62868-70) respectively code for the heavy chain
CC regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236S and S229P
CC mutations. They can be used to provide novel monoclonal and
CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC gamma-4PE, in which the human IgG4 FC binding domain framework is
CC combined with the antigen binding domains (see also AAW14922-23) of
CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC show high affinity to human CD4, have little or no immunogenicity
CC in humans and show reduced or absence of effector function. The
CC gamma-4E and -4PE mutations confer activity enhanced stability and
CC eliminate depleting activity. The antibodies can be used to treat
CC autoimmune diseases such as rheumatoid arthritis.

XX SQ Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;

Query Match 82.2%; Score 1176.2; DB 18; Length 1404;
Best Local Similarity 90.2%; Pred. No. 2.8e-233;
Matches 1291; Conservative 0; Mismatches 113; Indels 27; Gaps 2;

QY 1 ATGAACACCTGTGGTCTTCCTCCTCGTGGTGGAGCTCCAGATGGGTCTGTCTCCAG 60
DB |||||
QY 1 ATGAACACCTGTGGTCTTCCTCCTCGTGGTGGAGCTCCAGATGGGTCTGTCTCCAG 60
DB |||||
QY 61 GTGCAGCTGCAGAGTCCGGGCCAGGACTGGTGAAGCTTCGGAGACCTGTCCCTCACC 120
DB |||||
QY 61 GTGCAGCTGCAGAGTCCGGGCCAGGACTGGTGAAGCTTCGGAGACCTGTCCCTCACC 120
DB |||||
QY 121 TGCCTGTCTCTGTGGCTCCATCAGCGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC 180
DB |||||
QY 121 TGCAGTGTCTCTGTGGCTCCATCAGCGTGGTATATTATTTGGTTCTGGATCCGCCAGTCC 180
DB |||||
QY 181 CCAGGAGAGGGCTGGAGTGGAGTTCTTAGTAGTAGTGGGAACACTACTAC 240
DB |||||

DB 181 CCAGGAGAGGAGCTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGACCAATTAC 240
QY 241 AACCCCTCCCTCAAGAGTCAAGTCAACATTTCAACAGACAGCTCCAGAACCAAGTCTCTCC 300
DB |||||
DB 241 AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACAGCTCCAGAACCTCTTCTCC 300
QY 301 CTGAAGCTGAACCTTATAGCCCGCCGGACACGGCCGCTGTATTACTGTGTGAGAGATCGT 360
DB |||||
DB 301 CTGAACCTGAGGTCTGTGACCGCCGGACACGGCCGCTTATTACTGTGTGCGAGTAATA-- 358
QY 361 CTTTTTTCAGTTGTGGATGGTTTACAACTGGTTTCGATGTCTGGGGCCCGGGAGTC 420
DB |||||
DB 359 -----TATTGAAATATCTTCACTGGTTATTATCTGGGGCCAGGGAGTC 402
QY 421 CTGCTCACCGTCTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTTCC 480
DB |||||
DB 403 CTGGTCAACCGTCTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGC 462
QY 481 TCCAAAGACACCTCTGTGGGGCACAGCGGCCCTGTGGCTGCCTGGTCAAGGACTACTTCCCC 540
DB |||||
DB 463 TCCAGGAGACCTCCGAGAGCACAGCGGCCCTGTGGCTGCCTGGTCAAGGACTACTTCCCC 522
QY 541 GAAACCGGTGACGGTGTCTGTGAACTCAGGGCCCTGACCCAGCGGGCTGCACACCTTCCCG 600
DB |||||
DB 523 GAAACCGGTGACGGTGTCTGTGAACTCAGGGCCCTCTGACCCAGCGGGCTGCACACCTTCCCG 582
QY 601 GCTGTCTTACAGTCTCTCTCAGGACTCTACTCTCTCAGCAGCGTGGTGACCGTCCCTCCAGC 660
DB |||||
DB 583 GCTGTCTTACAGTCTCTCTCAGGACTCTACTCTCTCAGCAGCGTGGTGACCGTCCCTCCAGC 642
QY 661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAAGCCCGACCAACCAAGGTG 720
DB |||||
DB 643 AGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAAGCCAGCAACCAAGGTG 702
QY 721 GACAAAGACAGAGCCCAATCTTTGTGACAAAACCTCACACATGCCACCGCTGCCAGCA 780
DB |||||
DB 703 GACAAAGAGTTGATCCAAATATGG-----TCCCCCATGCCCATCATGATGCCAGCA 753
QY 781 CCTGAATCTCTGGGGGACCGTCACTCTTCTCTTCCCCCAAAACCCAGAGCACCCCTC 840
DB |||||
DB 754 CTTGAGTTTCGAGGGGGGACCATCAGTCTTCTGTCTCCCCCAAAACCCAGAGCACCTCTC 813
QY 841 ATGATCTCTCCCGACCCCTGAGGTCAATGCGTGTGTGTGGACGTGAGCCACGAAGACCT 900
DB |||||
DB 814 ATGATCTCTCCCGACCCCTGAGGTCACTGCTGTGTGTGGACGTGAGCCAGGAAGACCC 873
QY 901 GAGTCAAGTTCAACTGGTACGTGACGGCGTGGAGTGCATATGCCAAGACAAAGCCG 960
DB |||||
DB 874 GAGGTCCAGTTCAACTGGTACGTGATGGGTGGAGTGCATATGCCAAGACAAAGCCG 933
QY 961 CGGAGGAGCAGTACAAACAGCACCGTACCGTGTGGTGCAGCGTCTCACCGTCTCTGCACAG 1020
DB |||||
DB 934 CGGAGGAGCAGTTCACAGCACCGTACCGTGTGGTGCAGCGTCTCACCGTCTCTGCACAG 993
QY 1021 GACTGGCTGAATGGCAAGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCC 1080
DB |||||
DB 994 GACTGGCTGAACGGCAAGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCCGTCTCC 1053
QY 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACACAGGTGTACACCTG 1140
DB |||||
DB 1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCTG 1113
QY 1141 CCCCATCCCGGGATGAGTGCACCAAGAACCCAGGTGCAGCTGACCTCGTGGTCAAAAGGC 1200
DB |||||
DB 1114 CCCCATCCCGAGGAGAGATGACCAAGAACCCAGGTGCAGCTGACCTGCTGGTCAAAAGGC 1173
QY 1201 TTCTATCCAGCGCATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAACCACTAC 1260
DB |||||
DB 1174 TTCTACCCCGCAGACATCGCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAACCACTAC 1233
QY 1261 AAGACCGCCTCCCGTGTGAGTCCGACCGGTCTCTTCTTCTCTTACAGCAAGCTCACC 1320
DB |||||
DB 1234 AAGACCGCCTCCCGTGTGAGTCCGACCGGTCTCTTCTTCTCTTACAGCAGGCTAACCC 1293

QY 1321 GTGACAAAGCAGGTTGGCAGCAGGGGAAAGCTTCTCTCATGTCTCCGTGATGATGAGGCT 1380
DB 1294 GTGACAAAGCAGGTTGGCAGCAGGGGAAAGTCTTCTCATGTCTCCGTGATGATGAGGCT 1353
QY 1381 CTGACAAACCACTACACAGCAGAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1431
DB 1354 CTGACAAACCACTACACAGCAGAGAGAGCTCTCCCTGTCTCTGGGTAATGA 1404

RESULT 14
AAH74680
ID AAH74680 standard; DNA; 1428 BP.
AC AAH74680;
XX
XX
DT 29-OCT-2001 (first entry)
XX
XX Nucleotide sequence of a single chain antibody.
XX
XX Complementarity determining region; CDR; single chain antibody; ScFv;
KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW envelope glycoprotein; ss.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH 1..1428
FT CDS
FT /tag= a
FT /product= "single chain antibody"

WO200158459-A1.
XX
XX 16-AUG-2001.
XX
XX 13-FEB-2001; 2001WO-JP00967.
XX
XX 14-FEB-2000; 2000JP-0034906.
XX
XX (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
XX Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
XX
XX WPI; 2001-496986/54.
XX
XX P-PSDB; AAG63640.
XX
XX Remedies for hepatitis C containing substances with antiviral effects
XX e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
XX compounds, by inhibiting binding of hepatitis C virus envelope
XX glycoprotein or CD81 -
XX
XX Claim 41; Page 105-108; 138pp; Japanese.

XX
XX The present sequence encodes a single chain antibody of the invention.
XX The specification describes a substance can inhibit the binding between
XX hepatitis C virus (HCV) and cells with potential HCV infection, cells
XX with expression of CD81, or CD81. This substance is especially an
XX antibody with affinity towards HCV E2/NS1 protein, containing amino
XX acid sequences based on the complementarity determining region (CDR) 1,
XX CDR2 and CDR3 of the H and L chain variable regions. The antibody
XX inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor.
XX The antibodies and drugs are used for treatment and/or prevention of
XX hepatitis C, or for diagnosis of hepatitis C.
XX
XX Sequence 1428 BP; 315 A; 462 C; 394 G; 257 T; 0 other;

XX
XX Query Match 80.4%; Score 1151; DB 22; Length 1428;
XX Best Local Similarity 88.3%; Pred. No. 4.5e-228;
XX Matches 1263; Conservative 0; Mismatches 165; Indels 3; Gaps 1;
XX
XX 1 ATGAACACCTGTGGTTCCTCTCCCTCTGGTGACAGCTCCAGATGGGTCTGTCCCGAG 60
XX
XX 1 ATGAACACCTGTGGTTCCTCTCCCTCTGGTGACAGCTCCAGATGGGTCTGTCCCGAG 60

QY 61 GTGAGCTGCAGGAGTCCGGCCCCAGGACTGGTGAAGCTTCGAGAGACCTGTCCCTCACC 120
DB 61 GTGAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCTGGGTCTCGTGAAGGTCTCC 120
QY 121 TGCCTGTCTCTGTGCTCCATCAGCGGTGGTATGCTGGGGCTGGATCCGCCAGCCC 180
DB 121 TGAAGGCTTCTGGAGGCACCTACATCGACCAACCTATC--GGCTGGGTGCGCAGGCC 177
QY 181 CCAGGAAGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTGGGAACACCTACTAC 240
DB 178 CTTGGACNAGGGCTTGGAGTGGAGGAGTATCCCTCTCTCTGTGGTCCGACACTAC 237
QY 241 AACCCCTCCCTCAAGAGTCAAGTCCATTTCAACAGACACGCTCAAGAACCAAGTTCCTCC 300
DB 238 GCACAGAAAGTTCCAGGGCAAGTCTCGATTACCGCGACGAGTCCACGACGACAGCTTAC 297
QY 301 CTGAAGCTGAATCTATGACCGCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
DB 238 CTGAAGCTGAATCTATGACCGCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 357
QY 361 CTTTTTTCAGTGTGGAAATGGTTTACAACTGGTTCGATGCTGGGGCCCGGGAGTC 420
DB 358 AGGGTTATTGTCTGTGGTTCTCTGTATGACTGGCTCGACCCCTGGGCGCAGGGCACC 417
QY 421 CTGGTCAACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCTGGCACCTCC 480
DB 418 CTGGTCAACCGTCTCTCAGCTAGTACCAAGGGCCCATCGGTCTTCCCTCTGGCACCTCC 477
QY 481 TCCAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGGACTACTTCCCC 540
DB 478 TCCAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGGACTACTTCCCC 537
QY 541 GAAACGGTGCAGGTGTCTGGAACTCAGGCGCCCTGACAGCGCGGTGCACACCTTCCCG 600
DB 538 GAAACGGTGCAGGTGTCTGGAACTCAGGCGCCCTGACAGCGCGGTGCACACCTTCCCG 597
QY 601 GCTGTCTTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGTGACCGTCCCTCCAGC 660
DB 598 GCTGTCTTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGTGACCGTCCCTCCAGC 657
QY 661 AGCTTGGCACCCAGACCTACATCTGCAAGCTGAACTCACAAGCCCGACACCAAGGTG 720
DB 658 AGCTTGGCACCCAGACCTACATCTGCAAGCTGAACTCACAAGCCCGACACCAAGGTG 717
QY 721 GACAGAAAGCAGAGCCCAAACTTTGTGACAAAACCTCACACATGCCCGTCCCGACCA 780
DB 718 GACAGAAAGTGTGAGCCCAAACTTTGTGACAAAACCTCACACATGCCCGTCCCGACCA 777
QY 781 CCTGAACCTCTCTGGGGGACCGTCAAGTCTTCTTCCCTCCCAAAACCCAAAGGACACCTC 840
DB 778 CCTGAACCTCTCTGGGGGACCGTCAAGTCTTCTTCCCTCCCAAAACCCAAAGGACACCTC 837
QY 841 ATGATCTCCCGACCCCTGAGGTACATGCGTGTGTGTGACGTGAGCCAGGAGACCT 900
DB 838 ATGATCTCCCGACCCCTGAGGTACATGCGTGTGTGTGACGTGAGCCAGGAGACCT 897
QY 901 GAGGTCAAGTTCAACTGTGTGAGCGGTGAGGTGCAATATGCAAGACAAAGCCG 960
DB 898 GAGGTCAAGTTCAACTGTGTGAGCGGTGAGGTGCAATATGCAAGACAAAGCCG 957
QY 961 CGGGAGGAGCAGTCAACAGCACGTACCGTGTGTGTGACCGTCTCAGCGTCTCCAGCAG 1020
DB 958 CGGGAGGAGCAGTCAACAGCACGTACCGGTTGTGTGACCGTCTCAGCGTCTCCAGCAG 1017
QY 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTTCCAAAGAGCCCTCCAGCCCC 1080
DB 1018 GACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTTCCAAAGAGCCCTCCAGCCCC 1077
QY 1081 ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCCACAGGTGTACACCTG 1140
DB 1078 ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCCACAGGTGTACACCTG 1137

Qy	974	ACAA	CAGCAGCTACCGGTGTGGTCAGCGTCTCTACCGTCTCTGCACGAGACTGGCTGAATG	1033
Db	971	ACAA	CAGCAGCTACCGGTGTGGTCAGCGTCTCTACCGTCTCTGCACGAGACTGGCTGAATG	1030
Qy	1034	GCAAGG	AGTAGTCAAGTCTCAACAAAGGCCCTCCACGCCCCATCGAGAAACCA	1093
Db	1031	GCAAGG	AGTAGTCAAGTCTCAACAAAGGCCCTCCACGCCCCATCGAGAAACCA	1090
Qy	1094	TCTCAA	AGCCAAAGGCGACGCCGAGAACCAACAGGTGTACACCTGCGCCCATCCCGGG	1153
Db	1091	TCTCAA	AGCCAAAGGCGACGCCGAGAACCAACAGGTGTACACCTGCGCCCATCCCGGG	1150
Qy	1154	ATGAGCT	GACACAGAACCAAGCTCAGCCTGACCTGCTGGTCAAGGCTTCTATCCACGC	1213
Db	1151	ATGAGCT	GACACAGAACCAAGCTCAGCCTGACCTGCTGGTCAAGGCTTCTATCCACGC	1210
Qy	1214	ACATCG	CCGTGTGGAGTGGGAGAGCAATGGCGACGCCGAGAACCACTACAAGACCAACGCCTC	1273
Db	1211	ACATCG	CCGTGTGGAGTGGGAGAGCAATGGCGACGCCGAGAACCACTACAAGACCAACGCCTC	1270
Qy	1274	CCGTGT	GTGGACTCCGAGGGTCTCTTCTCTCTACGCAAGCTCAACCGTGGACAAGAGCA	1333
Db	1271	CCGTGT	GTGGACTCCGAGGGTCTCTTCTCTCTACGCAAGCTCAACCGTGGACAAGAGCA	1330
Qy	1334	GGTGGC	AGCAGGGGAACTCTTCTCATGCTCCGTGCATGTCAGTGGCTCTGCACACCACT	1393
Db	1331	GGTGGC	AGCAGGGGAACTCTTCTCATGCTCCGTGCATGTCAGTGGCTCTGCACACCACT	1390
Qy	1394	ACACGC	AGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1391	ACACGC	AGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1428

Search completed: April 5, 2003, 20:19:44
Job time : 395.719 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:54 ; Search time 2723.68 Seconds
(without alignments)
8508.978 Million cell updates/sec

Title: US-09-758-173-11

Perfect score: 1431

Sequence: 1 ATGAACACCTGTGCTT.....CCCTGTCTCCGGTAATGA 1431

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hct:*
9: gb_est1:*
10: gb_est2:*
11: gb_hct:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	902	63.0	1020	14	BQ062878
2	864	60.4	947	14	BQ0709771
3	850.4	59.4	958	14	BQ0706140
4	842.4	58.9	926	12	BG755166
5	832	58.1	988	14	BQ708857
6	831.2	58.1	901	13	BM007892

7	824.4	57.6	1029	14	BQ063185
8	822.8	57.5	887	14	BQ711255
9	822.2	57.5	918	14	BQ708022
10	818.6	57.2	995	14	BM914540
11	808.8	56.5	881	14	BQ711291
12	800.2	55.9	1031	14	BQ064886
13	797.4	55.7	936	14	BQ711727
14	796	55.6	940	14	BQ705928
15	787.4	55.0	977	14	BQ710532
16	786.4	55.0	980	14	BM914504
17	785.2	54.9	843	13	BM007897
18	778.8	54.4	991	14	BQ708936
19	777.2	54.3	973	14	BQ706204
20	776	54.2	930	13	BM007597
21	770.6	53.9	981	14	BM914528
22	764.6	53.4	926	14	BQ710304
23	764.2	53.4	917	14	BQ708169
24	759.4	53.1	961	14	BQ710233
25	756.6	52.9	945	14	BQ712403
26	752.4	52.6	1012	14	BM914556
27	750.6	52.5	895	14	BQ708303
28	750.4	52.4	783	13	BM007838
29	748	52.3	1026	14	BM914288
30	741.4	51.8	914	14	BQ712363
31	737.4	51.5	913	14	BQ707472
32	734.2	51.3	906	14	BQ711709
33	733.8	51.3	944	14	BQ712397
34	733.6	51.3	919	14	BQ709339
35	732.8	51.2	936	14	BQ707530
36	732.4	51.2	855	13	BM007689
37	731.8	51.1	1014	14	BM914505
38	730.4	51.0	973	14	BQ708902
39	729.6	51.0	888	12	BG757604
40	728.8	50.9	941	14	BQ712021
41	728.6	50.9	925	14	BQ709853
42	728.4	50.9	991	14	BQ707621
43	726.8	50.8	870	12	BG757815
44	726.2	50.7	925	14	BQ709152
45	725.8	50.7	923	14	BQ881523

ALIGNMENTS

RESULT 1
BQ062878
LOCUS
DEFINITION BQ062878 1020 bp mRNA linear EST 02-APR-2002
5', mRNA sequence.
AGENCY BQ062878 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420

ACCESSION BQ062878
VERSION BQ062878.1
KEYWORDS EST. GI:19890085

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1020)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone Sequencing by: Agencourt Bioscience Corporation

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LCM2094 row: h column: 21

High quality sequence start: 21

High quality sequence stop: 681.

Location/Qualifiers

FEATURES

```
source 1. 1020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5924420"
/clone_lib="NIH MGC 99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph. Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 239 a 344 c 269 g 166 t 2 others
ORIGIN
Query Match 63.08; Score 902; DB 14; Length 1020;
Best Local Similarity 99.04; Pred. No. 4.2e-219; Indels 2; Gaps 1;
Matches 923; Conservative 0; Mismatches 17;
QY 489 CACCTCTGGGGGCACAGGGCCCTGGCTGCTCAAGAGACTTCTCCCGAACCGGT 548
DB 36 CACCTCTGGGGGCACAGGGCCCTGGCTGCTCAAGAGACTTCTCCCGAACCGGT 95
QY 549 GACGGTGTCTGGAACCTCAGCGGCCCTGACAGCGGGGTGACACCTTCCGGGTGTCCT 608
DB 96 GACGGTGTCTGGAACCTCAGCGGCCCTGACAGCGGGGTGACACCTTCCGGGTGTCCT 155
QY 609 ACAGTCTTCAGGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGG 668
DB 156 ACAGTCTTCAGGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGG 215
QY 669 CACCAGACCTACATCTCAACGCTGAATCAACGCCAGCAGCAACCAAGGTGGACAAGAA 728
DB 216 CACCAGACCTACATCTCAACGCTGAATCAACGCCAGCAGCAACCAAGGTGGACAAGAA 275
QY 729 AGCAGAGCCCAATCTTGTCACAAACTCACAATGCCACCGTCCCGAGCAGCTGAAT 788
DB 276 AGTTCAGCCCAATCTTGTCACAAACTCACAATGCCACCGTCCCGAGCAGCTGAAT 335
QY 789 CTTGGGGGAGCGTCAGTCTTCTCTCCCGCCCAAGCCAGCAGCAGCTCATGATCTC 848
DB 336 CTTGGGGGAGCGTCAGTCTTCTCTCCCGCCCAAGCCAGCAGCAGCTCATGATCTC 395
QY 849 CCGGACCCCTGAGGTCACATGCGTGGTGGAGCGTGAACCGAAGACCCCTGAGGTCAA 908
DB 396 CCGGACCCCTGAGGTCACATGCGTGGTGGAGCGTGAACCGAAGACCCCTGAGGTCAA 455
QY 909 GTTCAACTGTTAGTGGAGCGGCTGAGGTGCATTAATGCCAAGCAAGCCCGCGGAGGA 968
DB 456 GTTCAACTGTTAGTGGAGCGGCTGAGGTGCATTAATGCCAAGCAAGCCCGCGGAGGA 515
QY 969 GCAGTACACACGACGTCAGTCTGCTCAGCGTCTCTACCGTCTCTGACACGAGCTGGCT 1028
DB 516 GCAGTACACACGACGTCAGTCTGCTCAGCGTCTCTACCGTCTCTGACACGAGCTGGCT 575
QY 1029 GAATGGCAAGAGTACAAGTCAAGGTCTTCCAAAGAGCCCTCCAGCCCGCATCGAGAA 1088
DB 576 GAATGGCAAGAGTACAAGTCAAGGTCTTCCAAAGAGCCCTCCAGCCCGCATCGAGAA 635
QY 1089 ACCATCTTCAAGCCCAAGGCGCCCGGAGAACACAGGTGTACCCCTGCCCGCCCATC 1148
DB 636 AACCATCTTCAAGCCCAAGGCGCCCGGAGAACACAGGTGTACCCCTGCCCGCCCATC 695
QY 1149 CCGGGATGAGCTGACCAAGAACAGCTCAGCTGACCTGCTGGTCAAGAGGCTTCTATCC 1208
DB 696 CCGGGATGAGCTGACCAAGAACAGCTCAGCTGACCTGCTGGTCAAGAGGCTTCTATCC 755
QY 1209 CAGCGACATCGCGGTGGAGTGGAGAGCAATGGGAGCGGGA--GAACAACTACAGACC 1266
|||||
source 1. 1020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5924420"
/clone_lib="NIH MGC 99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph. Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 239 a 344 c 269 g 166 t 2 others
ORIGIN
Query Match 63.08; Score 902; DB 14; Length 1020;
Best Local Similarity 99.04; Pred. No. 4.2e-219; Indels 2; Gaps 1;
Matches 923; Conservative 0; Mismatches 17;
QY 489 CACCTCTGGGGGCACAGGGCCCTGGCTGCTCAAGAGACTTCTCCCGAACCGGT 548
DB 36 CACCTCTGGGGGCACAGGGCCCTGGCTGCTCAAGAGACTTCTCCCGAACCGGT 95
QY 549 GACGGTGTCTGGAACCTCAGCGGCCCTGACAGCGGGGTGACACCTTCCGGGTGTCCT 608
DB 96 GACGGTGTCTGGAACCTCAGCGGCCCTGACAGCGGGGTGACACCTTCCGGGTGTCCT 155
QY 609 ACAGTCTTCAGGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGG 668
DB 156 ACAGTCTTCAGGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGG 215
QY 669 CACCAGACCTACATCTCAACGCTGAATCAACGCCAGCAGCAACCAAGGTGGACAAGAA 728
DB 216 CACCAGACCTACATCTCAACGCTGAATCAACGCCAGCAGCAACCAAGGTGGACAAGAA 275
QY 729 AGCAGAGCCCAATCTTGTCACAAACTCACAATGCCACCGTCCCGAGCAGCTGAAT 788
DB 276 AGTTCAGCCCAATCTTGTCACAAACTCACAATGCCACCGTCCCGAGCAGCTGAAT 335
QY 789 CTTGGGGGAGCGTCAGTCTTCTCTCCCGCCCAAGCCAGCAGCAGCTCATGATCTC 848
DB 336 CTTGGGGGAGCGTCAGTCTTCTCTCCCGCCCAAGCCAGCAGCAGCTCATGATCTC 395
QY 849 CCGGACCCCTGAGGTCACATGCGTGGTGGAGCGTGAACCGAAGACCCCTGAGGTCAA 908
DB 396 CCGGACCCCTGAGGTCACATGCGTGGTGGAGCGTGAACCGAAGACCCCTGAGGTCAA 455
QY 909 GTTCAACTGTTAGTGGAGCGGCTGAGGTGCATTAATGCCAAGCAAGCCCGCGGAGGA 968
DB 456 GTTCAACTGTTAGTGGAGCGGCTGAGGTGCATTAATGCCAAGCAAGCCCGCGGAGGA 515
QY 969 GCAGTACACACGACGTCAGTCTGCTCAGCGTCTCTACCGTCTCTGACACGAGCTGGCT 1028
DB 516 GCAGTACACACGACGTCAGTCTGCTCAGCGTCTCTACCGTCTCTGACACGAGCTGGCT 575
QY 1029 GAATGGCAAGAGTACAAGTCAAGGTCTTCCAAAGAGCCCTCCAGCCCGCATCGAGAA 1088
DB 576 GAATGGCAAGAGTACAAGTCAAGGTCTTCCAAAGAGCCCTCCAGCCCGCATCGAGAA 635
QY 1089 ACCATCTTCAAGCCCAAGGCGCCCGGAGAACACAGGTGTACCCCTGCCCGCCCATC 1148
DB 636 AACCATCTTCAAGCCCAAGGCGCCCGGAGAACACAGGTGTACCCCTGCCCGCCCATC 695
QY 1149 CCGGGATGAGCTGACCAAGAACAGCTCAGCTGACCTGCTGGTCAAGAGGCTTCTATCC 1208
DB 696 CCGGGATGAGCTGACCAAGAACAGCTCAGCTGACCTGCTGGTCAAGAGGCTTCTATCC 755
QY 1209 CAGCGACATCGCGGTGGAGTGGAGAGCAATGGGAGCGGGA--GAACAACTACAGACC 1266
|||||
Db 756 CAGCGACATCCCGTGGAGTGGGAGAGCAATGGGAGCCCGGNAGAAACTACTACTAGACC 815
QY 1267 ACGCTCCCGTGGTGGACTCCGACGGGTCTCTTCTCTTACAGCAAGCTCACCGTGGAC 1326
Db 816 ACGCTCCCGTGGTGGACTCCGACGGGTCTCTTCTCTTACAGCAAGCTCACCGTGGGA 875
QY 1327 AAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGTCATGATGAGCTCTGCAC 1386
Db 876 CAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGTCATGATGAGCTCTGCAC 935
QY 1387 AACCACTACAGCAGAGAGAGCTTCTCTCTCGGTCTCGGGTAAA 1428
Db 936 AACCACTACAGCAGAGAGAGCTTCTCTCTCGGTCTCGGGTAAA 977
RESULT 2
BQ709771 BQ709771 947 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_8953965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
DEFINITION 5', mRNA sequence.
ACCESSION BQ709771
VERSION BQ709771.1 GI:21848670
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 947)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2466 row: m column: 16
High quality sequence start: 3
High quality sequence stop: 675.
Location/Qualifiers
1. 947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6278583"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 225 a 320 c 252 g 150 t
ORIGIN
Query Match 60.4%; Score 864; DB 14; Length 947;
Best Local Similarity 99.4%; Pred. No. 2e-209;
Matches 867; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 560 GGAACCTCAGCGCCCTGACAGCGGTGCACACCTTCCCGGTCTCTACAGTCTCTAG 619
Db 9 GGAACCTCAGCGCCCTGACAGCGGTGCACACCTTCCCGGTCTCTCTACAGTCTCTAG 68
QY 620 GACTCTACTCTCTCAGCAGCGTGGTACCGTGCCTTCCAGCAGCTTGGGACCCAGACCT 679
Db 69 GACTCTACTCTCTCAGCAGCGTGGTACCGTGCCTTCCAGCAGCTTGGGACCCAGACCT 128
|||||
```

```
QY 680 ASATCTGCAACGTGAATCAACAGCCAGCCAGCAACCAAGGTGACAAAGAGCAGAGCCCA 739
Db 129 ACATCTGCAACGTGAATCAAGCCAGCCAGCAACCAAGGTGACAAAGAGTGTAGGCCCA 188
QY 740 AATCTTGTCACAAACTCACATGCCACCTGCCAGCAGCCTGAATCTCTGGGGGAC 799
Db 189 AATCTTGTCACAAACTCACATGCCACCTGCCAGCAGCCTGAATCTCTGGGGGAC 248
QY 800 CGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGTATCTCCCGGACCCCTG 859
Db 249 CGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGTATCTCCCGGACCCCTG 308
QY 860 AGGTTCATCGCTGGTGGTGGAGGTGAGCAGCAGACACCTAGGTCAAGTTCAACTGGT 919
Db 309 AGGTTCATCGCTGGTGGTGGAGGTGAGCAGCAGACACCTAGGTCAAGTTCAACTGGT 368
QY 920 AGCTGACCGCGCTGGAGGTGTCATATGCCAAGACCAAGCCGGGAGAGCAGATACACA 979
Db 369 AGCTGACCGCGCTGGAGGTGTCATATGCCAAGACCAAGCCGGGAGAGCAGATACACA 428
QY 980 GCACGTACCGTGTGTCAGCTCTCACCGTCTTGACACAGGACTGGCTGAATGGCAAGG 1039
Db 429 GCACGTACCGTGTGTCAGCTCTCACCGTCTTGACACAGGACTGGCTGAATGGCAAGG 488
QY 1040 AGTACAAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAAACCATCTCCA 1099
Db 489 AGTACAAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAAACCATCTCCA 548
QY 1100 AAGCCAAAGGGGAGCCCGGAGAACACAGGTGTACACCTGCCGCCCATCCCGGGATGAGC 1159
Db 549 AAGCCAAAGGGGAGCCCGGAGAACACAGGTGTACACCTGCCGCCCATCCCGGGATGAGC 608
QY 1160 TGACCAAGAACCAAGTCAAGCTGACCTGCTGCTGCTCAAGAGTCTTATCCAGCGACATCG 1219
Db 609 TGACCAAGAACCAAGTCAAGCTGACCTGCTGCTGCTCAAGAGTCTTATCCAGCGACATCG 668
QY 1220 CCGTGGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAGACACGCTCCCGTGC 1279
Db 669 CCGTGGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAGACACGCTCCCGTGC 728
QY 1280 TGGACTCCGACGGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGACAAAGAGCAGGTGGC 1339
Db 729 TGGACTCCGACGGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGACAAAGAGCAGGTGGC 788
QY 1340 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACAGC 1399
Db 789 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACCACTACAGC 848
QY 1400 AGAAGAGCTCTCCCTGCTCCGGGTAAATGA 1431
Db 849 AGAAGAGCTCTCCCTGCTCCGGGTAAATGA 880

RESULT 3
LOCUS BO706140
DEFINITION AGNCOURT_8352177 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277512
5', mRNA sequence.
ACCESSION BO706140
VERSION BO706140.1 GI:21845039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 958)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2464 row: a column: 01
High quality sequence stop: 705.

FEATURES
source

1..958
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277512"
/lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

BASE COUNT 229 a 319 c 256 g 150 t 4 others
ORIGIN

Query Match 59.4%; Score 850.4; DB 14; Length 958;
Best Local Similarity 99.2%; Pred. No. 6e-206; 6; Indels 1; Gaps 1;
Matches 865; Conservative 0; Mismatches 0

QY 558 GTGGAATCAGGCGCCTGACAGCGCGTGACACCTTCCCGGCTGTCTACAGTCTCTC 617
Db 11 GTGGAATCAGGCGCCTGACAGCGCGTGACACCTTCCCGGCTGTCTACAGTCTCTC 70
QY 618 AGGACTCTACTCCCTCAGCAGCGTGTGACCGCTCCAGCAGCTTGGGACCCAGAC 677
Db 71 AGGACTCTACTCCCTCAGCAGCGTGTGACCGCTCCAGCAGCTTGGGACCCAGAC 130
QY 678 CTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGTGAAGC 737
Db 131 CTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGTGAAGC 190
QY 738 CAAATCTTGTGACAAACTCACAATGCGCCACCGTCCAGCAGCCTGAACTCTCTGGGGG 797
Db 191 CAAATCTTGTGACAAACTCACAATGCGCCACCGTCCAGCAGCCTGAACTCTCTGGGGG 250
QY 798 ACCGTCACTTCTCTCTTCCCAAAACCAAGGACACCTCTCATGATCTCCGAGACCC 857
Db 251 ACCGTCACTTCTCTCTTCCCAAAACCAAGGACACCTCTCATGATCTCCGAGACCC 310
QY 858 TGAGGTACATGCGTGTGTGAGCGTGAAGCCAGAGACCTCTGAGTCAAGTTCAACTG 917
Db 311 TGAGGTACATGCGTGTGTGAGCGTGAAGCCAGAGACCTCTGAGTCAAGTTCAACTG 370
QY 918 GTACGTGGAAGCGGTGAGGTGATTAATGCCAAGACAAAGCCGCGGAGGAGAGTACAA 977
Db 371 GTACGTGGAAGCGGTGAGGTGATTAATGCCAAGACAAAGCCGCGGAGGAGAGTACAA 430
QY 978 CAGCAGTACCGTGTGTGAGCGTCTCAACCTCTGACACAGGACTGGCTGAATGGCAA 1037
Db 431 CAGCAGTACCGTGTGTGAGCGTCTCAACCTCTGACACAGGACTGGCTGAATGGCAA 490
QY 1038 GGAGTACAAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAACCATCTC 1097
Db 491 GGAGTACAAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAACCATCTC 550
QY 1098 CAAAGCCAAAGGGAGCGCCCGAGAACCAAGGTGTACACCTTGGCCCCCATCCGGGATGA 1157
Db 551 CAAAGCCAAAGGGAGCGCCCGAGAACCAAGGTGTACACCTTGGCCCCCATCCGGGATGA 610
QY 1158 GCTGACCAAGAACCAAGGTGTGAGCGTCTGACCTGCTGCAAGGCTTCTATCCAGCGACAT 1217
Db 611 GCTGACCAAGAACCAAGGTGTGAGCGTCTGACCTGCTGCAAGGCTTCTATCCAGCGACAT 670

Qy	1218	CGCCGTGGAGTGGAGAGCAATAGGCGAGCCGGAGAAACAATCAAGAACCAAGCCTCCCGT	1277
Db	671	CGCCGTGGAGTGGAGAGCAATAGGCGAGCCGGAGAAACAATCAAGAACCAAGCCTCCCGT	730
Qy	1278	GCTGGACTCCGACGGCTCCTTCCTCTACAGCAGAGCTCACCGTGGACAGAGCAGGTG	1337
Db	731	GCTGGACTCCGACGGCTCCTTCCTCTACAGCAGAGCTCACCGTGGACAGAGCAGGTG	790
Qy	1338	GCAGCAGGGGAACGCTCTCTCATGCTCCGTGATGCATGAGGCTTCGCACCAACCTACAC	1397
Db	791	GCAGCAGGGGAACGCTCTCTCATGCTCCGTGATGCATGAGGCTTCGCACCAACCTACAC	850
Qy	1398	GCAG-AAAGAGCCTTCCTGTCTCCGGGTAAA	1428
Db	851	ACAGAAAGAGCCTTCCTGTCTCCGGGTAAA	882
RESULT 4			
BG755166 926 bp mRNA linear EST 15-MAY-2001			
LOCUS 602711488F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852076 5',			
DEFINITION mRNA sequence.			
ACCESSION BG755166			
VERSION BG755166.1 GI:14065819			
KEYWORDS EST.			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 926)			
NIH-MGC http://mgc.nci.nih.gov/ .			
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)			
UNPUBLISHED (1999)			
CONTACT: Robert Strausberg, Ph.D.			
Email: cgapbs-remail.nih.gov			
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.			
cDNA Library Preparation: Ling Hong/Rubin Laboratory			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: LLCM1695 row: o column: 21			
High quality sequence stop: 888.			
FEATURES			
source			
1. 926			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/clone="IMAGE:4852076"			
/clone_lib="NIH_MGC_48"			
/tissue_type="primary B-cells from tonsils (cell line)"			
/lab_host="DH10B (phage-resistant)"			
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;			
Site 2: EcoRI; cDNA made by oligo-dr priming.			
Directionally cloned into EcoRI/XhoI sites using the			
following 5' adaptor: GCACGAG(G). Size-selected >500bp			
for average insert size 1.8kb. Library constructed by Ling			
Hong in the laboratory of Gerald M. Rubin (University of			
California, Berkeley) using ZAP-cDNA synthesis kit			
(Stratagene) and Superscript II RT (Life Technologies).			
Note: this is a NIH_MGC Library."			
BASE COUNT	225 a	309 c	244 g 148 t
ORIGIN			
Query Match 58.9%; Score 842.4; DB 12; Length 926;			
Best Local Similarity 98.2%; Pred. No. 6.5e-204;			
Matches 852; Conservative 0; Mismatches 16; Indels 0; Gaps 0;			
Qy	564	CTCAGGCGCCCTGACAGCGGGGTGCACACCTTCCTCCGGCTGCTCCTCAGTCCCTCAGGACT	623
Db	2	CTCAGGCGCCCTGACAGCGGGGTGCACACCTTCCTCCGGCTGCTCCTCAGTCCCTCAGGACT	61
Qy	624	CTACTCCTCTCAGCAGCGGTGGTACCGTGCCCTTCACGACAGCTTGGGACACCGACACTACAT	683

FEATURES										
source	Location/Qualifiers	High quality sequence stop: 716.	Plate: LLCM2464	row: c	column: 02	found through the I.M.A.G.E. Consortium/LLNL at:	Clone distribution: MGC clone distribution information can be	DNA Sequencing by: Agencourt Bioscience Corporation	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	Tissue Procurement: Dr. Mark Watson
1..988	Location/Qualifiers									
	/organism="Homo sapiens"									
	/db xref="taxon:9606"									
	/clone="IMAGE:6277561"									
	/clone.lib="NIH_MGC_113"									
	/lab host="DH10B (phage-resistant)"									
	/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."									
BASE COUNT	230 a	338 c	258 g	162 t						
ORIGIN										
Query Match	58.1%;	Score 832;	DB 14;	Length 988;						
Best Local Similarity	94.7%;	Pred. No. 3e-201;								
Matches 905;	Conservative 0;	Mismatches 45;	Indels 6;	Gaps 4;						
QY	393	CTGGTTCGATGTC	TGGGGCCCGGAGTCCTGGT	CACCGTCTCTCTCAGT	TAGCACCACCAAGGG	452				
DB	5	CTACTTTGACTACT	TGGGGCCAGGGAACGCT	TGCTCACCGTCTCTCTGGGCT	CCACCAAGGG	64				
QY	453	CCCATCGGTC	TTTCCCCTGGCACCCCTCTCTCAAGAGCACCTCT	TGGGGGCACAGCGGCCCT	512					
DB	65	CCCATCGGTC	TTTCCCCTGGCACCCCTCTCTCAAGAGCACCTCT	TGGGGGCACAGCGGCCCT	124					
QY	513	GGGCTGCTGGT	CAAGACTACTTTCCCGAACCGGTGACGGTGTCTGGGA	ACTCAGGGC	572					
DB	125	GGGCTGCTGGT	CAAGACTACTTTCCCGAACCGGTGACGGTGTCTGGGA	ACTCAGGGC	184					
QY	573	CCTGACCAAGCGG	CTGCACACCTTTCCCGGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCT	632						
DB	185	CCTGACCAAGCGG	CTGCACACCTTTCCCGGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCT	244						
QY	633	CAGCAGCGTGGT	GACCGTCCCTCAGCAGCTTGGGCA	CCGACCTACATCTTGCACAGT	692					
DB	245	CAGCAGCGTGGT	GACCGTCCCTCAGCAGCTTGGGCA	CCGACCTACATCTTGCACAGT	304					
QY	693	GAATCAAGCCG	CAGCAACACCAAGTGGACAAGAACAGAGCAGAGCCAAATCTTGTGACAA	752						
DB	305	GAATCAAGCCG	CAGCAACACCAAGTGGACAAGAACAGAGTTCAGGCCAAATCTTGTGACAA	364						
QY	753	AACTCACATATG	CCCAACCGTCCAGCACCTTGAATCTCTCGGGGACCGTCAGTCTTCTCT	812						
DB	365	AACTCACATATG	CCCAACCGTCCAGCACCTTGAATCTCTCGGGGACCGTCAGTCTTCTCT	424						
QY	813	CTTCCCCCAAA	CCCCCAAGGACACCCCTCATGATCTCCCGGACCCCTCAGGTCACATCGGT	872						
DB	425	CTTCCCCCAAA	CCCCCAAGGACACCCCTCATGATCTCCCGGACCCCTCAGGTCACATCGGT	484						
QY	873	GGTGGTGA	CGTAGCCACGAAAGACCTTGAGGTCAAGTTCAACTGTGTA	CGTGGACGGCGT	932					
DB	485	GGTGGTGA	CGTAGCCACGAAAGACCTTGAGGTCAAGTTCAACTGTGTA	CGTGGACGGCGT	544					
QY	933	GGAGGTGAT	TAATGCCAAGACAAAGCCGCGGAGGACGAGTACAAACGACGTCACCGTGT	992						
DB	545	GGAGGTGAT	TAATGCCAAGACAAAGCCGCGGAGGACGAGTACAAACGACGTCACCGTGT	604						
QY	993	GGTCAGCGGT	CTCTACCGTCTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAAGTGC	1052						

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2469 row: 1 column: 20
High quality sequence stop: 667.
Location/Qualifiers
1. 918
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6279643"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 208 a 316 c 245 g 147 t 2 others
ORIGIN
Query Match 57.5%; Score 822.2; DB 14; Length 918;
Best Local Similarity 95.4%; Pred. No. 9.2e-199;
Matches 867; Conservative 0; Mismatches 40; Indels 2; Gaps 2;
Qy 398 TCGATGTCGGGGCCGGGAGTCTGTGTACCGTCTCTCAGTAGCACCAGGGCCCAT 457
Db 1 TTGACCGCTGGGGCCAGGGAACGCTGTGTACCGTCTCTCAGCTCCACCAAGGGCCCAT 60
Qy 458 CGGTCTTCCCTCGCACCTCTCTCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCT 517
Db 61 CGGTCTTCCCTCGCACCTCTCTCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCT 120
Qy 518 GCCTGGTCAAGGACTACTTCCCGAACCCGGTGACGGTGTCTGTGAACTCAGCGGCCCTGA 577
Db 121 GCCTGGTCAAGGACTACTTCCCGAACCCGGTGACGGTGTCTGTGAACTCAGCGGCCCTGA 180
Qy 578 CCACGGGGTGACACCTTCCGGCTGTCTTACAGTCTCTCAGACTCTACTCCTCAGCA 637
Db 181 CCACGGGGTGACACCTTCCGGCTGTCTTACAGTCTCTCAGACTCTACTCCTCAGCA 240
Qy 638 CGGTGGTGACCGTCCCTCCAGAGCTTGGGACCCAGACCTCATCTGCAAGTGAATC 697
Db 241 CGGTGGTGACCGTCCCTCCAGAGCTTGGGACCCAGACCTCATCTGCAAGTGAATC 300
Qy 698 ACAAGCCCGACCAACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAATC 757
Db 301 ACAAGCCCGACCAACCAAGGTGGACAAGAAAGTGTAGGCCAAATCTTGTGACAAAATC 360
Qy 758 ACATATGCCACCGTGGCAGACCTGAACTCTCTGGGGGACCGTCACTTCTCTTCC 817
Db 361 ACATATGCCACCGTGGCAGACCTGAACTCTCTGGGGGACCGTCACTTCTCTTCC 420
Qy 818 CCCCCAAACCAAGCACCTCATGATCTCCGGGACCCCTGAGGTACATGCTGTGGTGG 877
Db 421 CCCCCAAACCAAGCACCTCATGATCTCCGGGACCCCTGAGGTACATGCTGTGGTGG 480
Qy 878 TGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGTTACGTGGAGCGGTGGAGG 937

Db 481 TGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGTTAGTGGACGGCGTGGAGG 540
Qy 938 TGCATAATGCCAAGAAAGCCGGGAGGAGCAGTCAACAGCACCTACCGTGTGTCA 997
Db 541 TGCATAATGCCAAGAAAGCCGGGAGGAGCAGTCAACAGCACCTACCGTGTGTCA 600
Qy 998 GCGTCTCTCACCGTCTCTGACACGAGGACTGGCTGAATGGCAAGGAGTCAAGTGCAAGGTCT 1057
Db 601 GCGTCTCTCACCGTCTCTGACACGAGGACTGGCTGAATGGCAAGGAGTCAAGTGCAAGGTCT 660
Qy 1058 CCAACAAAGCCCTCCAGCCGCCCATTCGAGAAAAACATCTCCAAAGCCAAAGGGCAGCCCC 1117
Db 661 CCAACAAAGCCCTCCAGCCGCCCATTCGAGAAAAACATCTCCAAAGCCAAAGGGCAGCCCC 720
Qy 1118 GAGAACCCACAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAGAACCAAGGTCA 1177
Db 721 GAGAACCCACAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAGAACCAAGGTCA 780
Qy 1178 GCCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCCCGT-GGAGTGGGAGAGC 1236
Db 781 GCCTGACCTGCTGGTCAAAGGCTTCTATCCAGGACATCCCGGAGTGGGAGAGC 840
Qy 1237 AATGGGAG-CGGAGAAACAACTACAAGACCAACCGCTCCCTGCTGTGACTCCGACGGCTC 1295
Db 841 ATGGGGACGCGCGAGAACTACAAGACCAACCGCTCCCGGCTGGGACTCCCGACGG 900
Qy 1296 CTTCTTCTCT 1304
Db 901 GTCTTTCT 909
RESULT 10
LOCUS BM914540 995 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT 6615506 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480223
5', mRNA sequence.
ACCESSION BM914540
VERSION BM914540.1 GI:19364919
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 995)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2002 row: 1 column: 16
High quality sequence stop: 718.
Location/Qualifiers
1. 995
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480223"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a

5', mRNA sequence.
 BQ711291
 BQ711291.1 GI:21850190
 EST
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 881)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2468 row: c column: 01
 High quality sequence stop: 721.

FEATURES
 source
 1..881
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6279096"
 /clone_lib="NIH MGC 113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOT87; Site: 1: XhoI; Site: 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC Library."

BASE COUNT 220 a -285 c 237 g 139 t
 ORIGIN

Query Match 56.5%; Score 808.8; DB 14; Length 881;
 Best Local Similarity 99.8%; Pred. No. 2.4e-195;
 Matches 810; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 612 GTCTCTCAGAGCTTACTCCCTCAGCAGCGTGGTGCACCGTGCCTCCAGCAGCTTGGGCAC 671
 Db 1 GTCTCTCAGAGCTTACTCCCTCAGCAGCGTGGTGCACCGTGCCTCCAGCAGCTTGGGCAC 60

QY 672 CCAGACCTACATCTGCAACGCTGAATCAACAGCCAGCAACACCAAGGTGGACAAGAAGC 731
 Db 61 CCAGACCTACATCTGCAACGCTGAATCAACAGCCAGCAACACCAAGGTGGACAAGAAGT 120

QY 732 AGAGCCCAAACTTTGTGCAAACTCACAATGCCACCGTGCCTCCAGCAGCTTGAATCTCT 791
 Db 121 TGAGCCCAAACTTTGTGCAAACTCACAATGCCACCGTGCCTCCAGCAGCTTGAATCTCT 180

QY 792 GGGGGGACCGTTCAGTCTTCTCTTCTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCG 851
 Db 181 GGGGGGACCGTTCAGTCTTCTCTTCTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCG 240

QY 852 GACCCCTGAGGTACATCGGTGGTGGAGCTGAGCCAGAGACCCCTGAGGTCAAGTT 911
 Db 241 GACCCCTGAGGTACATCGGTGGTGGAGCTGAGCCAGAGACCCCTGAGGTCAAGTT 300

QY 912 CAATGTGTACGTGGACGGCGTGGAGGTGCATTAATGCCAAGCAAAAGCCGGGAGGAGCA 971
 Db 301 CAATGTGTACGTGGACGGCGTGGAGGTGCATTAATGCCAAGCAAAAGCCGGGAGGAGCA 360

QY 972 GTACAACAGCAGTACCGTGTGGTGCAGCGTCTCTCAGCGTCTCTGCACCAGGACTGGGTGAA 1031
 Db 361 GTACAACAGCAGTACCGTGTGGTGCAGCGTCTCTCAGCGTCTCTGCACCAGGACTGGGTGAA 420

QY	1032	TGCAAGGAGTACAAGTGCAGGTCTCCAA	CAAAGCCCTCCAGCCCCCATCGAGAAAC	1091
Db	421	TGCAAGGAGTACAAGTGCAGGTCTCCA	CAAAGCCCTCCAGCCCCCATCGAGAAAC	480
QY	1092	CATCTCCAAAGCCAAAGGCGAGCCCG	AGAGAACACACAGGTGTACACCTGCCCCCATCCCG	1151
Db	481	CATCTCCAAAGCCAAAGGCGAGCCCG	AGAGAACACACAGGTGTACACCTGCCCCCATCCCG	540
QY	1152	GGATGAGCTGACCAAGAACACAGGT	CAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAG	1211
Db	541	GGATGAGCTGACCAAGAACACAGGT	CAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAG	600
QY	1212	CGACATCGCCGTGAGTGGGAGAGCAAT	TGGCGAGCCGGAGAACAACTACAAGACCAAGC	1271
Db	601	CGACATCGCCGTGAGTGGGAGAGCAAT	TGGCGAGCCGGAGAACAACTACAAGACCAAGC	660
QY	1272	TCCCGTGTGACTCCGACGGCTCCTTCT	TCTTCTTACAGCAAGCTACCGTGGACAAGAG	1331
Db	661	TCCCGTGTGACTCCGACGGCTCCTTCT	TCTTCTTACAGCAAGCTACCGTGGACAAGAG	720
QY	1332	CAGTGTGCAGCAGGGGAAACGCTTCT	CATGCTCCGTGATGATGATGAGGCTCTGCACAACCA	1391
Db	721	CAGTGTGCAGCAGGGGAAACGCTTCT	CATGCTCCGTGATGATGATGAGGCTCTGCACAACCA	780
QY	1392	CTACACGACAGAGAGCCTCTCCCTGT	CTCCGG 1423	
Db	781	CTACACGACAGAGAGCCTCTCCCTGT	CTCCGG 812	
<p>RESULT 12</p> <p>BQ064886</p> <p>LOCUS</p> <p>DEFINITION BQ064886 1031 bp mRNA linear EST 02-APR-2002</p> <p>AGENCY AGENT 6887080 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929343</p> <p>5', mRNA sequence.</p> <p>ACCESSION BQ064886</p> <p>VERSION BQ064886.1 GI:19893932</p> <p>KEYWORDS EST.</p> <p>SOURCE human.</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>NIH-MGC http://mgc.nci.nih.gov/.</p> <p>National Institutes of Health, Mammalian Gene Collection (MGC)</p> <p>Unpublished (1999)</p> <p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: cgapbs-remail.nih.gov</p> <p>Tissue Procurement: Lou Staudt</p> <p>cDNA Library Preparation: Rubin Laboratory</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</p> <p>DNA Sequencing by: Agencourt Bioscience Corporation</p> <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</p> <p>Plate: LLCM2107 row: e column: 24</p> <p>High quality sequence stop: 573.</p> <p>Location/Qualifiers</p> <p>1..1031</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:5929343"</p> <p>/clone.lib="NIH_MGC_99"</p> <p>/tissue_type="lymphoma, cell line"</p> <p>/lab_host="DH10B (phage-resistant)"</p> <p>/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."</p>				
<p>FEATURES</p> <p>source</p>				

```

ACCESSION   BQ7111727.1  GI:21850626
VERSION     EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 936)
AUTHORS     NIH-MGC http://mgc.ncl.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2518 row: k column: 18
            High quality sequence stop: 547.
            Location/Qualifiers
                1..936
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:6301961"
                /lab_host="NIH MGC 113"
                /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."
BASE COUNT   231 a 306 c 245 g 152 t 2 others
ORIGIN
Query Match 55.7%; Score 797.4; DB 14; Length 936;
Best Local Similarity 98.3%; Pred. No. 2e-192;
Matches 826; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 593 CTTTCCCGCTCTTACAGTCTCTCAGACTCTACTCCCTCAGCAGCGTGTGACCGTGC 652
Db 10 CTTTCCCGCTCTTACAGTCTCTCAGACTCTACTCCCTCAGCAGCGTGTGACCGTGC 69

QY 653 CCTCAGCAGCTTGGCCAGCCAGACTTACATCTGCAAGCTGAATCAGCCAGCAACA 712
Db 70 CCTCAGCAGCTTGGCCAGCCAGACTTACATCTGCAAGCTGAATCAGCCAGCAACA 129

QY 713 CCAAGTGGACAAAGAGCAGAGCCCAATCTTGTGACAAACTCACATGCCACCGT 772
Db 130 CCAAGTGGACAAAGAGTGTGACCAATCTTGTGACAAACTCACATGCCACCGT 189

QY 773 GCCAGCACCTGAATCTCTGGGGGACCGTCACTTCTTCTTCCCCCAAAACCCCAAGG 832
Db 190 GCCAGCACCTGAATCTCTGGGGGACCGTCACTTCTTCTTCCCCCAAAACCCCAAGG 249

QY 833 ACACCTCATGATCTCCGGACCCCTGAGGTACATGTGTCAGTGTGGTGGAGCGTGCACG 892
Db 250 ACACCTCATGATCTCCGGACCCCTGAGGTACATGTGTCAGTGTGGTGGAGCGTGCACG 309

QY 893 AAGACCTGAGTCAAGTTCAACTGGTGGAGCGGTGAGGTGATATATCCCAAGA 952
Db 310 AAGACCTGAGTCAAGTTCAACTGGTGGAGCGGTGAGGTGATATATCCCAAGA 369

QY 953 CAAGCCCGGGAGAGCAGTACACAGCAGTACCGTGTGGTCAAGCTCTCACCGTCC 1012
Db 370 CAAGCCCGGGAGAGCAGTACACAGCAGTACCGTGTGGTCAAGCTCTCACCGTCC 429

1013 TGCACGAGTGGCTGATGGCAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCC 1072

RESULT 14
LOCUS       BQ705928
DEFINITION BQ705928 940 bp mRNA linear EST 16-JUL-2002
           AGENCOURT 7976186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214795
           5', mRNA sequence.
ACCESSION   BQ705928
VERSION     BQ705928.1  GI:21844827
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 940)
AUTHORS     NIH-MGC http://mgc.ncl.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2382 row: k column: 20
            High quality sequence stop: 619.
            Location/Qualifiers
                1..940
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:6214795"
                /lab_host="NIH MGC 113"
                /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."
BASE COUNT   235 a 318 c 240 g 147 t
ORIGIN

```

```
Query Match      55.6%; Score 796; DB 14; Length 940;
Best Local Similarity 99.3%; Pred. No. 4.5e-192;
Matches 810; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 617 CAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGA 676
DB 1 CAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGA 60

QY 677 CCTACATCTGCAAGTGAATCAACAAGCCCAAGCAACCAAGGTGGACAGAGAGAGC 736
DB 61 CCTACATCTGCAAGTGAATCAACAAGCCCAAGCAACCAAGGTGGACAGAGAGAGC 120

QY 737 CCAATCTTGTGACAAACTCACACATGCCACCGTGCACGACCTGAATCTCTGGGG 796
DB 121 CCAATCTTGTGACAAACTCACACATGCCACCGTGCACGACCTGAATCTCTGGGG 180

QY 797 GACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCC 856
DB 181 GACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCC 240

QY 857 CTGAGGTCACATGCGTGTGTGACGTGACCTGACGACGACCTGAGTCAAGTTCAACT 916
DB 241 CTGAGGTCACATGCGTGTGTGACGTGACCTGACGACGACCTGAGTCAAGTTCAACT 300

QY 917 GGTACGTGGACGGCGTGGAGTGCATATGCAAGCAAAAGCCGCGGAGAGAGAGTACA 976
DB 301 GGTACGTGGACGGCGTGGAGTGCATATGCAAGCAAAAGCCGCGGAGAGAGAGTACA 360

QY 977 ACAGCAGCTACCGTGTGTGACGCTCTCTACCGTCTGACACGAGGAGTGGCTGAATGGCA 1036
DB 361 ACAGCAGCTACCGTGTGTGACGCTCTCTACCGTCTGACACGAGGAGTGGCTGAATGGCA 420

QY 1037 AGGAGTACAGTGCAGGTCTTCAAAAGCCCTCCAGCGCCCATCGAGAAACCATCT 1096
DB 421 AGGAGTACAGTGCAGGTCTTCAAAAGCCCTCCAGCGCCCATCGAGAAACCATCT 480

QY 1097 CCAAGCCAAAGGCGAGCCGAGAACACAGGTGTACACCTCGCCGCCATCCCGGATG 1156
DB 481 CCAAGCCAAAGGCGAGCCGAGAACACAGGTGTACACCTCGCCGCCATCCCGGATG 540

QY 1157 AGCTGACCAAGAACCAAGTCAAGCTGACCTGCTGTGTTCAAGGGTCTTATCCAGGACCA 1216
DB 541 AGCTGACCAAGAACCAAGTCAAGCTGACCTGCTGTGTTCAAGGGTCTTATCCAGGACCA 600

QY 1217 TCGCGTGGAGTGGAGAGCAATGGGACCGGAGAACCACTTACAGACCAAGCTCCCG 1276
DB 601 TCGCGTGGAGTGGAGAGCAATGGGACCGGAGAACCACTTACAGACCAAGCTCCCG 660

QY 1277 TGCTGGACTCCGACGGCTCTTCTTCTTCTACAGCAAGCTCACCGTGGACAGAGCAGGT 1336
DB 661 TGCTGGACTCCGACGGCTCTTCTTCTTCTACAGCAAGCTCACCGTGGACAGAGCAGGT 720

QY 1337 GGCACAGGGGAACTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAACCACTACA 1396
DB 721 GGCACAGGGGAACTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAACCACTACA 780

QY 1397 CGC-AGAGAGCTCTCCCTGTCTCCGGTAAATGA 1431
DB 781 CGCAAAAAGAGCTCTCCCTGTCTCCGGTAAATGA 816

RESULT 15
LOCUS BQ710532
DEFINITION AGENCOURT_8352211 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277538
5', mRNA sequence.
ACCESSION BQ710532
VERSION BQ710532.1 GI:21849431
KEYWORDS .EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
```

```
REFERENCE 1 (bases 1 to 977)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: egapbs-x@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: b column: 03
High quality sequence stop: 749.
FEATURES
Location/Qualifiers
source
1..977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277538"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 227 a 331 c 264 g 154 t 1 others
ORIGIN
Query Match 55.0%; Score 787.4; DB 14; Length 977;
Best Local Similarity 92.5%; Pred. No. 7.1e-190;
Matches 886; Conservative 0; Mismatches 57; Indels 15; Gaps 5;
QY 475 CCCTCTCCAGAGACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGACTAC 534
DB 11 CCCTGTCTCCAGAGCACCTCCGAGAGACAGCGGCCCTGGGCTGCTGCTCAAGACTAC 70
QY 535 TTCCCGAACCCGTCACCGTGTGCGGAACCTCAGCGCCCTGACCAGCGGCTGCACACC 594
DB 71 TTCCCGAACCCGTCACCGTGTGCGGAACCTCAGCGGCTCTGACCAGCGGCTGCACACC 130
QY 595 TTCCCGGCTGTCTTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCC 654
DB 131 TTCCCGGCTGTCTTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCC 190
QY 655 TCCAGCAGCTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAAGCCCAAGCAACC 714
DB 191 TCCAGCAACTTCCGACCCAGACCTTACACCTGCAACGTAGATCAAGCCCAAGCAACC 250
QY 715 AAGGTGGACAAGAAAGAGAGCCCAAACTCTGTGACAAAACCTCACACATGCCCCCGTGC 774
DB 251 AAGGTGGACAAGAGCAGTTGAGCGCAAAATGTTGTGCGA-----GTGCCACCGTGC 301
QY 775 CAGACACCTGAACCTCTCGGGGGACCGTCAGTCTTCTCTTCTTCCCCCAAAACCCCAAGGAC 834
DB 302 CAGACACC--ACCTGTGGCAGGACCGTCAGTCTTCTTCTTCCCCCAAAACCCCAAGGAC 358
QY 835 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAA 894
DB 359 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAA 418
QY 895 GACCTTGAGTCAAGTTCAACTGGTACGTGGACGGGCTGAGGTGCATTAATGCCAAGACA 954
DB 419 GACCCCGAGTCCAGTTCAACTGGTACGTGGACGGGCTGAGGTGCATTAATGCCAAGACA 478
QY 955 AAGCCGCGGGAGGAGAGTACAACAGCAGTACCGTGTGGTCAAGCGTCTTCAAGCGTCTG 1014
DB 479 AAGCCGCGGGAGGAGAGTACAACAGCAGTTCACAGCAGTTCAGCGTGTGGTCAAGCGTCTG 538
```


GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 10.5919 Seconds
(without alignments)
2141.995 Million cell updates/sec

Title: US-09-758-173-10

Perfect score: 1232

Sequence: 1 MRVPAQLGLLLWLPGAR.....CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1027	83.4	235	2 S05270	Ig lambda chain pr
2	1014	82.3	233	2 S25752	Ig lambda chain -
3	1010.5	82.0	236	2 S25746	Ig lambda chain -
4	1006	81.7	216	2 S29258	Ig lambda chain V
5	1006	81.7	234	2 S25757	Ig lambda chain -
6	1003.5	81.5	217	2 JE0246	Ig lambda chain NI
7	1001	81.2	235	2 S25750	Ig lambda chain -
8	995	80.8	232	2 S25742	Ig lambda chain -
9	989.5	80.3	213	2 S21066	Ig lambda chain V
10	987	80.1	233	2 S25744	Ig lambda chain -
11	986	80.0	216	2 A42193	Ig lambda chain (B
12	967.5	78.5	235	2 S25754	Ig lambda chain -
13	946	76.8	216	2 S03401	Ig lambda chain (K
14	944	76.6	235	2 S14675	Ig lambda chain -
15	942	76.5	208	2 B49444	Ig lambda chain (N
16	934	75.8	235	2 S25759	Ig lambda chain -
17	923	74.9	235	2 S25758	Ig lambda chain -
18	894	72.6	232	2 S25756	Ig lambda chain -
19	884	71.8	216	2 JE0245	Ig lambda chain NI
20	879	71.3	233	2 S25748	Ig lambda chain -
21	877	71.2	231	2 S25738	Ig lambda chain -
22	875	71.0	233	2 S25741	Ig lambda chain -
23	872.5	70.8	233	2 S25747	Ig lambda chain -
24	866	70.3	231	2 S25751	Ig lambda chain -
25	861	69.9	216	2 S69130	Ig lambda chain (D
26	850	69.0	231	2 S25753	Ig lambda chain -
27	846.5	68.7	235	2 S25749	Ig lambda chain -
28	839	68.1	213	2 JE0247	Ig lambda chain NI
29	839	68.1	226	2 S25745	Ig lambda chain -

30 815 66.2 190 2 S25740 Ig lambda chain -
31 811 65.8 243 2 S25755 Ig lambda chain -
32 737.5 59.9 212 2 S70431 Ig lambda chain -
33 649.5 52.7 181 2 PT0220 Ig lambda chain V-
34 644.5 52.3 232 2 S17399 Ig lambda chain pr
35 643 52.2 230 2 S49449 Ig lambda chain -
36 630.5 51.2 213 2 A21177 Ig light chain pre
37 625.5 50.8 214 2 PC4156 Ig lambda chain V
38 606 49.2 118 2 S12441 Ig lambda chain (K
39 603 48.9 118 2 S12442 Ig lambda chain (K
40 581 47.2 118 2 S12443 Ig lambda chain (K
41 576 46.8 118 2 S12440 Ig lambda chain (M
42 573 46.5 118 2 A39949 Ig lambda chain J-
43 550 44.6 234 2 A39956 Ig lambda chain pr
44 548 44.5 105 1 L2HU Ig lambda chain C
45 547.5 44.4 149 2 S23626 Ig lambda chain V

ALIGNMENTS

RESULT 1

S05270

Ig lambda chain precursor - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C;Accession: S05270; S04601

R;Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A;Reference number: S05270

A;Accession: S05270

A;Molecule type: mRNA

A;Residues: 1-235 <KIS1>

A;Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395

R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A;Reference number: S04601; MUID:89296497; PMID:2500644

A;Accession: S04601

A;Molecule type: mRNA

A;Residues: 1-130 <KIS2>

A;Cross-references: EMBL:X14583

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-235/Product: Ig lambda chain #status predicted <MAT>

F;150-218/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 1027; DB 2; Length 235;

Best Local Similarity 87.0%; Pred. No. 8.5e-60;

Matches 200; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 7 LLGILLLWLPGARCESVLTQPPSVSGAPGQKVITSCGTSTNIGGYDLHWYQQLPGTAPK 66

Db 6 LLLLLTHCTGSAQSVLTQPPSVSAAPGQKVITSCGSSNIGNNYVYQQLPGTAPK 65

Qy 67 LLIYDINKRSGISDRPSGSGKGTAAALITGLQTEADYCYOSYDSSINAQVFGGTR 126

Db 66 LLIYDNNKRPSGIPDRPSGSGKGTSAITGLITGLQTEADYCYGTWDSLSAGVFGGTR 125

Qy 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAMKADSSPVKAGVETT 186

Db 126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAMKADSSPVKAGVETT 185

Qy 187 TPQSQNNKYAASYSLLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

Db 186 TPQSQNNKYAASYSLLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 2

S25752

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25752
R;Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25752
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57817; NID:G33733; PIDN:CAA40954.1; PID:G33734
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 1014; DB 2; Length 233;
Best Local Similarity 84.8%; Pred. No. 5.8e-59;
Matches 195; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQQLPGTAPK 66
Db 4 LLLTLTHCAGSQAQSVLTQPPSASGTPGQRTVISCSSNIGSNVNTVNYQQLPGTAPK 63

QY 67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYVCSYDSSNAQVFGGTR 126
Db 64 LLIYRNQRPSPGDPFRFSGSKSGTSASLAISGLQSEDEADYCAAWDDSLNGVVFGGTK 123

QY 127 LTVLGQPKAAPSVTLPFPSSSELOANKATLVCLISDFYPGAVTVAWKADSPVKAGVET 186
Db 124 LTVLGQPKAAPSVTLPFPSSSELOANKATLVCLISDFYPGAVTVAWKADSPVKAGVET 183

QY 187 TPKSQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 184 TPKSQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 3
S25746
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25746
R;Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25746
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-236 <COM>
A;Cross-references: EMBL:X57811; NID:G33721; PIDN:CAA40948.1; PID:G33722
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;151-219/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 1010.5; DB 2; Length 236;
Best Local Similarity 84.4%; Pred. No. 1e-58;
Matches 195; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNIG-GYDLHWYQQLPGTAP 65
Db 6 LLLTLTHCAGSQAQSVLTQPPSVSGAPGQKVTISCTGSTNIGAGHHVHWYQVPGTAP 65

QY 66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYVCSYDSSNAQVFGGTT 125
Db 66 KLLIYADNNRPSGVDPDRISGSKSGTSASLAITGLRAEADYVCSYDSSLSGHWFGAT 125

QY 126 RLTVLGQPKAAPSVTLPFPSSSELOANKATLVCLISDFYPGAVTVAWKADSPVKAGVET 185
Db 126 RLTVLGQPKAAPSVTLPFPSSSELOANKATLVCLISDFYPGAVTVAWKADSPVKAGVET 185

QY 186 TPKSQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 186 TPKSQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

Db 186 TTPSKSQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 4
S29258
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jan-2000
C;Accession: S29258
R;Chouchane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
Eur. J. Biochem. 207, 1115-1121, 1992
A;Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment er
A;Reference number: S29257; MUID:92362614; PMID:1495555
A;Accession: S29258
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-216 <CHO>
A;Note: only part of the coding sequence is given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: pyroglutamic acid
F;131-199/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

Query Match 81.7%; Score 1006; DB 2; Length 216;
Best Local Similarity 89.9%; Pred. No. 1.8e-56;
Matches 195; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

QY 21 ESVLTQPPSVSGAPGQKVTISCTGSTNIGG-YDLHWYQQLPGTAPKLLIYDINKRPSGI 79
Db 1 QSVLTQPPSVSGAPGQRTVISCSSNIGARYDYNWYQQLPGTAPKLLIYNTIRPSGV 60

QY 80 SDRFSGSKSGTAASLAITGLQTEDEADYVCSYDSSNAQVFGGTRTLTVLGQPKAAPS 139
Db 61 PDRFSGSKSGTSASLAITGLQAEDEGDYVCTYDIDSLTV-VFGGKTTLTVLGQPKAAPS 119

QY 140 TLFPSSSELOANKATLVCLISDFYPGAVTVAWKADSPVKAGVETTTPKSQSNKNKYAAS 199
Db 120 TLFPSSSELOANKATLVCLISDFYPGAVTVAWKADSPVKAGVETTTPKSQSNKNKYAAS 179

QY 200 SVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 180 SVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 216

RESULT 5
S25757
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25757
R;Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-234 <COM>
A;Cross-references: EMBL:X57822; NID:G33743; PIDN:CAA40959.1; PID:G33744
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;149-217/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 1006; DB 2; Length 234;
Best Local Similarity 83.0%; Pred. No. 1.9e-58;
Matches 191; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQQLPGTAPK 66
Db 5 LLLTLTHCAGSQAQSVLTQPPSASGTPGQRTVISCSSNIGSNVNTVNYQQLPGTAPK 64

QY 67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYVCSYDSSNAQVFGGTR 126
Db 67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYVCSYDSSNAQVFGGTR 126

```
Db 65 VLIYNNRPSGVDPDRFSGSKGTSASLAISGLQSDDEADYYCAWDDSLNGRLLOGGTK 124
QY 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
Db 125 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
QY 187 TPSKQSNKYAASYSLSLTPEQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 236
Db 185 TPSKQSNKYAASYSLSLTPEQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 234

RESULT 6
S25746
IG lambda chain NIG204 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0246
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Takaashi, I.; Shinoda,
submitted to JIPID, November 1998
A:Description: Structural relationship of lambda type light chains with AL amyloidosis.
A:Reference number: JE0245
A:Accession: JE0246
A:Molecule type: protein
A:Residues: 1-217 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:132-200/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 1003.5; DB 2; Length 217;
Best Local Similarity 89.4%; Pred. No. 2.6e-58;
Matches 194; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 21 ESVLTQPPSVSGAPGQKVTISCTGTSNIG-GYDLHWYQQLPGTAPKLLIYDINKRPSGI 79
Db 1 ZSVLTQPPSVSGAPGQGVTLSCGSSNIGAGYVPHWYQQLFCAAPKLLISDNYNRP 60

QY 80 SDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSNAQVFGGTRLTVLGQPKAAPSV 139
Db 61 PARFSGSKGTSASLAISGLQAEDEADYYCQSYDSSSLTAWVFGGTRLTVLGQPKAAPSV 120

QY 140 TLPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNKYAAS 199
Db 121 TLPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNKYAAS 180

QY 200 SYLSLTPEQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 236
Db 181 SYLSLTPEQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 217

RESULT 7
S25750
IG lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25750
R:Combratio, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lan
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25750
A:Molecule type: mRNA
A:Status: preliminary; translation not shown
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57815; NID:g33729; PIDN:CAA40952.1; PID:g33730
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-216/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 1001; DB 2; Length 235;
Best Local Similarity 83.5%; Pred. No. 4.1e-58;
Matches 192; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 7 LGLGILLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAPK 66
Db 181 LGLGILLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAPK 66

RESULT 9
S21066
IG lambda chain V region - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C:Accession: S21066
R:Diouha, A.; Lecroisey, A.; Henschen, A.; Ruttyn, Y.; Rouger, P.; Keil, B.
Protein Seq. Data Anal. 4, 319-324, 1991
A:Title: Partial amino acid sequence of the light chain of human anti-Rh(D) monoclonal ar
A:Reference number: S21066; MUID:92253545; PMID:1912484
A:Accession: S21066
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-213 <DLO>
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 74-Thr
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:128-196/Domain: immunoglobulin homology <IMM>
```

```
Db 6 LLLTLLTHCAGSQAQSVLTQPPSASGTPGQRTVISCAGSSNIGTNDVYVYQQLTGTPAK 65
QY 67 LLIYDINKRPSGIDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSNAQVFGGTR 126
Db 66 LLIYNNRPSGVDPDRFSGSKGSSASLAISGLQSEDEADYYCAWDDSLSGPVFGGTK 125
QY 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
Db 126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185
QY 187 TPSKQSNKYAASYSLSLTPEQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 236
Db 186 TPSKQSNKYAASYSLSLTPEQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 235

RESULT 8
S25742
IG lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25742
R:Combratio, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25742
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-232 <COM>
A:Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:147-215/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 995; DB 2; Length 232;
Best Local Similarity 84.3%; Pred. No. 9.9e-58;
Matches 194; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 7 LGLGILLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAPK 66
Db 3 LLLTLLTHCAGSQAQSVLTQPPSVAAPGQKVTISCGSSNIGNNYVSYVYQQLPGRAPK 62

QY 67 LLIYDINKRPSGIDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSNAQVFGGTR 126
Db 63 LLIYNNRPSAIPDRFSGSKGTSATLGLIAGLQTEADYYCQTDWDSLTVDVFGGTK 122

QY 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
Db 123 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 182

QY 187 TPSKQSNKYAASYSLSLTPEQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 236
Db 183 TPSKQSNKYAASYSLSLTPEQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 232

RESULT 9
S21066
IG lambda chain V region - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C:Accession: S21066
R:Diouha, A.; Lecroisey, A.; Henschen, A.; Ruttyn, Y.; Rouger, P.; Keil, B.
Protein Seq. Data Anal. 4, 319-324, 1991
A:Title: Partial amino acid sequence of the light chain of human anti-Rh(D) monoclonal ar
A:Reference number: S21066; MUID:92253545; PMID:1912484
A:Accession: S21066
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-213 <DLO>
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 74-Thr
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:128-196/Domain: immunoglobulin homology <IMM>
```

```
Query Match      80.3%; Score 989.5; DB 2; Length 213;
Best Local Similarity 88.5%; Pred. No. 2.1e-57;
Matches 192; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY 21 ESVLTQPPSVSGAPGQKVITISCTGSTNIGG-VDLHWYQQLPGTAPKLLIYDINKRPSGI 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QSVLTQPPSVSGAPGQKVITISCTGSTNIGG-NIARYDVNNYQQLPGTAPKLLIYGNITRPSGV 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 80 SDRFSGSKGTAASLAITGLQTEDEADYYCOSYDSSLSNAQVFGGTRTLTVLGQPKAAPSV 139
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PDRFSGSKGTSASLAITGLQAEDEGYYCQTDW-YYYVFGGTKLTVLGQPKAAPSV 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 140 TLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPSKQSNKKYAAS 199
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 TLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPSKQSNKKYAAS 176
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 213
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
S25744
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25744
R:Combrinato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25744
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57809; NID:g33714; PIDN:CAA40946.1; PID:g33715
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match      80.1%; Score 987; DB 2; Length 233;
Best Local Similarity 83.0%; Pred. No. 3.3e-57;
Matches 191; Conservative 16; Mismatches 21; Indels 2; Gaps 1;

QY 7 LIGLLLLLWLPGARCESVLTQPPSVSGAPGQKVITISCTGSTNIGGYDLHWYQQLPGTAPK 66
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 LLLTLTLTHCAGSQAQSVLTQPPSASGTPGQRTVITSCGSRSNVGSNNVNYQQLPGTAPK 65
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 67 LIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCOSYDSSLSNAQVFGGTR 126
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 LLIYNNQRPSPGVPDRFSGSKGTSASLAISGLQSEDEADYYCATWDS--TVVFGGGTK 123
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 127 LTVLGQPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 186
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 LTVQPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 183
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 187 TPSKQSNKKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 TPSKQSNKKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
A42193
Ig lambda chain (BJP-DIA) - human
N:Alternate names: amyloid fibril protein AL-DIA; Bence Jones protein; Ig lambda chain
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jan-2000
C:Accession: A42193; S18297
R:Klafki, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karas, M.; Hilschmann, N.
Biochemistry 31, 3265-3272, 1992
A:Title: Complete amino acid sequence determinations demonstrate identity of the urinary
A:Reference number: A42193; MUID:92207944; PMID:1554711
```

```
A:Accession: A42193
A:Molecule type: protein
A:Residues: 1-216 <KLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:131-199/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      80.0%; Score 986; DB 2; Length 216;
Best Local Similarity 86.1%; Pred. No. 3.5e-57;
Matches 186; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 21 ESVLTQPPSVSGAPGQKVITISCTGSTNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QSVLTQPPSASGTPGQRTVITISCGSSNIGSNVNTWYQQLPGTAPKLLIYTNQRPSGVP 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 81 DRFSGSKGTAASLAITGLQTEDEADYYCOSYDSSLSNAQVFGGTRTLTVLGQPKAAPSVT 140
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GRFSGSKGTSASLAISGLQSEDEADYYCATWDSVNGVFGGTKLTVLGQPKAAPSVT 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 141 LFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPSKQSNKKYAAS 200
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPSKQSNKKYAAS 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 201 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 216
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
S25754
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25754
R:Combrinato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25754
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57819; NID:g33737; PIDN:CAA40956.1; PID:g33738
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match      78.5%; Score 967.5; DB 2; Length 235;
Best Local Similarity 81.0%; Pred. No. 6e-56;
Matches 187; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

QY 7 LIGLLLLLWLPGARCESVLTQPPSVSGAPGQKVITISCTGSTNIGGYDLHWYQQLPGTAPK 66
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 LLLTLTHCAGSQAQSVLTQPPSASGTPGQRTVITISCGSSNIGSNVNTWYQQLPGTAPK 64
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 67 LIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCOSYDSSLSNAQ-VFGGTT 125
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 LLIHSNNQRPSPGVPDRFSGSKGTSASLAISGLQSEDEADYYCAAWDDSLNGRYVFGTGT 124
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 126 RLVLGQPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 185
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 KTVTLGQPKANPTVTLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 184
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 186 TPSKQSNKKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 TPSKQSNKKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
S03401
Ig lambda chain (Kol) - human
C:Species: Homo sapiens (man)
```

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C:Accession: S03401
R:Aratzin, H.D.; Palm, W.; Stangel, M.; Schmidt, W.E.; Friedrich, J.; Hilschmann, N.
Biol. Chem. Hoppe-Seyler 370, 263-272, 1989
A:Title: The primary structure of the crystallizable monoclonal immunoglobulin IgG1 Kol.
A:Reference number: S03401; MUID:89228564; PMID:2713105
A:Accession: S03401
A:Molecule type: protein
A:Residues: 1-216 <KRA>
A:Note: article in German with English abstract
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:131-199/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 76.8%; Score 946; DB 2; Length 216;
Best Local Similarity 83.3%; Pred. No. 1.4e-54;
Matches 180; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 21 ESULTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
Db 1 QSVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 60
QY 81 DRFSGSKGTAASLAITGLQTEDEADYQCQSDSSINAQVFGGTRLTVLGPKAAPSVT 140
Db 61 DRFSGSKGTAASLAITGLQTEDEADYCAWDVSNAYVFGTKVTLGPKANPTVT 120
QY 141 LPPPSSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGVETTTPSKQSNKKYAAASS 200
Db 121 LPPPSSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGVETTTPSKQSNKKYAAASS 180
QY 201 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 181 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 216

RESULT 14
S14675
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C:Accession: S14675; S12445
R:Vasicek, T. J.
submitted to the EMBL Data Library, February 1990
A:Reference number: S14675
A:Accession: S14675
A:Molecule type: DNA
A:Residues: 1-235 <VAS1>
A:Cross-references: EMBL:X51754
R:Vasicek, T. J.; Leder, P.
J. Exp. Med. 172, 609-620, 1990
A:Title: Structure and expression of the human immunoglobulin lambda genes.
A:Reference number: S12440; MUID:90324881; PMID:2115572
A:Accession: S12445
A:Molecule type: DNA
A:Residues: 1-129 <VAS2>
A:Cross-references: EMBL:X51754
C:Genetics:
A:Introns: 16/1; 130/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 944; DB 2; Length 235;
Best Local Similarity 78.5%; Pred. No. 2e-54;
Matches 183; Conservative 20; Mismatches 28; Indels 2; Gaps 2;

QY 5 AQLGLILLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYD-LHWYQQLPGT 63
Db 4 ALLIILTLTQGGSWAQSAQTQPPSASLGQSVTFSCGTSIDIGNYVSWYRHPGK 63
QY 64 APKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYQCQSDSSINAQVFGG 123

Db 64 APKLLMIYEVTKRPSGVNPRFRSGSKGNSTASLTVSGLQAEDEADYCYSSYAGS-NSLIFFGG 122
QY 124 GTRTLVLGQPKAAPSVTLPFPSSSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGV 183
Db 123 GTRTLVLGQPKAAPSVTLPFPSSSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGV 182
QY 184 ETTTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 183 ETTTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 15
B49444
Ig lambda chain (New) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 21-Jan-2000
C:Accession: B49444
R:Saul, F.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res
A:Reference number: A49444; MUID:93066153; PMID:1438175
A:Accession: B49444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-208 <SAU>
A:Note: sequence modified after extraction from NCBI backbone
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:123-191/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 942; DB 2; Length 208;
Best Local Similarity 85.7%; Pred. No. 2.4e-54;
Matches 186; Conservative 12; Mismatches 9; Indels 10; Gaps 3;

QY 21 ESULTQPPSVSGAPGQKVTISCTGTSNIG-GYDLHWYQQLPGTAPKLLIYDINKRPSGI 79
Db 1 QSVLTQPPSVSGAPGQKVTISCTGTSNIGAGHNKWKYQQLPGTAPKLLIFHNA----- 55
QY 80 SDRFSGSKGTAASLAITGLQTEDEADYQCQSDSSINAQVFGGTRLTVLGPKAAPS 139
Db 56 --RFSVSKSGTSATLAITGLQAEDEADYQCQSDRSL--RVFGGTRLTVLGPKAAPS 111
QY 140 TLFPSSSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGVETTTPSKQSNKKYAAAS 199
Db 112 TLFPSSSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGVETTTPSKQSNKKYAAAS 171
QY 200 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 172 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 208

Search completed: March 29, 2003, 09:16:20
Job time : 11.5919 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 5.62693 Seconds
(without alignments)
1739.566 Million cell updates/sec

Title: US-09-758-173-10

Perfect score: 1232

Sequence: 1 MRVPAQLGLLLWLPGARC.....CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	44.5	105	1	LAC_HUMAN
2	527	42.8	213	1	ILLI_HUMAN
3	463	37.6	130	1	LV1G_HUMAN
4	454	36.9	111	1	LV1D_HUMAN
5	432	35.1	111	1	LV1C_HUMAN
6	426	34.6	109	1	LV1F_HUMAN
7	424.5	34.5	112	1	LV2K_HUMAN
8	415	33.7	105	1	LAC_PIG
9	413.5	33.6	112	1	LV1H_HUMAN
10	412	33.4	105	1	LAC1_MOUSE
11	407.5	33.1	112	1	LV1B_HUMAN
12	402	32.6	109	1	LV1I_HUMAN
13	399	32.4	105	1	LAC_RABIT
14	396	32.1	111	1	LV1A_HUMAN
15	396	32.1	111	1	LV2B_HUMAN
16	395	32.1	111	1	LV2H_HUMAN
17	393	31.9	103	1	LV1E_HUMAN
18	392	31.8	111	1	LV2F_HUMAN
19	391	31.7	111	1	LV2I_HUMAN
20	385.5	31.3	104	1	LAC1_RAT
21	381	30.9	111	1	LV2D_HUMAN
22	380.5	30.9	104	1	LAC2_RAT
23	377	30.6	105	1	LAC3_MOUSE
24	374.5	30.4	104	1	LAC5_MOUSE
25	372	30.2	111	1	LV2A_HUMAN
26	371	30.1	111	1	LV2C_HUMAN
27	370	30.0	109	1	LV2E_HUMAN
28	369.5	30.0	104	1	LAC2_MOUSE
29	368	29.9	111	1	LV2G_HUMAN
30	352.5	28.6	110	1	LV2J_HUMAN
31	347	28.0	105	1	LAC5_MOUSE
32	344.5	28.0	112	1	LV6A_HUMAN
33	342	27.8	111	1	LV6C_HUMAN

RESULT 1

ID	LAC_HUMAN	STANDARD;	PRT;	105 AA.
AC	P01842; P80423;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig lambda chain C regions.			
GN	IGLC1 AND IGLC2 AND IGLC3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]	SEQUENCE (BENCE-JONES PROTEIN SH).			
RN	MEDLINE=70166723; PubMed=4909564;			
RA	Titani K., Wikler M., Shinoda T., Putnam F.W.;			
RT	"The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide bridges."			
RL	J. Biol. Chem. 245:2171-2176(1970).			
[2]	SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.			
RN	MEDLINE=69088380; PubMed=4883841;			
RA	Milstein C., Clegg J.B., Jarvis J.M.;			
RT	"Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jones protein."			
RL	Biochem. J. 110:631-652(1968).			
[3]	SEQUENCE (BENCE-JONES PROTEIN NIG-64).			
RN	MEDLINE=83186114; PubMed=6404900;			
RA	Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T., Shimizu A.;			
RT	"Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a suba subgroup."			
RL	J. Biochem. 93:421-429(1983).			
[4]	SEQUENCE (BENCE-JONES PROTEIN KERN).			
RN	MEDLINE=71150336; PubMed=5549568;			
RA	Ponstingl H., Hess M., Hilschmann N.;			
RT	"Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-protein Kern). V. The complete amino acid sequence and its genetic interpretation."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).			
[5]	PARTIAL SEQUENCE (MYELOMA PROTEIN NEWN).			
RN	MEDLINE=74109253; PubMed=4814727;			
RA	Chen B.L., Poljak R.J.;			
RT	"Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobulin (IgG New)."			
RL	Biochemistry 13:1295-1302(1974).			
[6]	SEQUENCE (DOT).			
RN	MEDLINE=95255298; PubMed=7737190;			
RA	Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;			

34	341	27.7	111	1	LV6D_HUMAN	P06318	homo sapien
35	340.5	27.6	129	1	KV1W_HUMAN	P04431	homo sapien
36	339	27.5	108	1	LV3A_HUMAN	P01714	homo sapien
37	339	27.5	111	1	LV3B_HUMAN	P08748	homo sapien
38	334.5	27.2	131	1	LV6E_HUMAN	P06319	homo sapien
39	329.5	26.7	117	1	KV1J_HUMAN	P01602	homo sapien
40	326.5	26.5	103	1	LAC_CHICK	P20763	gallus gall
41	326	26.5	106	1	LV4E_HUMAN	P06889	homo sapien
42	322	26.1	108	1	LV5A_HUMAN	P01719	homo sapien
43	319	25.9	106	1	LV4B_HUMAN	P01716	homo sapien
44	318	25.8	106	1	LV4A_HUMAN	P01715	homo sapien
45	314	25.5	111	1	LV2L_HUMAN	P80422	homo sapien

ALIGNMENTS

RT "Characterization of the two unique human anti-flavin monochloral
 immunoglobulins.";
 Eur. J. Biochem. 228:886-893 (1995).
 [7]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
 RX MEDLINE=75046825; PubMed=4215080;
 RA Poljak R.J., Anzel L.N., Avey H.P., Chen B.L., Phizackerley R.P.,
 RA Saul F.;
 RT "The three-dimensional structure of the fab' fragment of a human
 myeloma immunoglobulin at 2.0-A resolution.";
 Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444 (1974).
 [8]
 RN PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
 RX MEDLINE=75013804; PubMed=4415202;
 RA Fett J.W., Deutsch H.F.;
 RT "Primary structure of the Mcg lambda chain.";
 Biochemistry 13:4102-4114 (1974).
 [9]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
 RA Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
 RA Panagiotopoulos N.;
 RT "Rotational allomerism and divergent evolution of domains in
 immunoglobulin light chains.";
 Biochemistry 14:3953-3961 (1975).
 [10]
 RN X-RAY CRYSTALLOGRAPHY OF MCG.
 RX MEDLINE=90133913; PubMed=2515285;
 RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
 RT "Three-dimensional structure of a light chain dimer crystallized in
 water. Conformational flexibility of a molecule in two crystal
 forms.";
 J. Mol. Biol. 210:601-615 (1989).
 [11]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=82080680; PubMed=6273747;
 RA Huster P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
 RT "Clustered arrangement of immunoglobulin lambda constant region genes
 in man.";
 Nature 294:536-540 (1981).
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN
 FOUND IN PROTEINS SH. X. AND NIG-64. THE KERN PROTEIN HAS THE
 KERN. MARKER, THE NEWM PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN
 HAS THE KERN+ MARKER, AND THE MCG+ MARKER.
 CC -1- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE
 3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE
 (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
 SEQUENCE (LAMBDA-3).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00253; AAA59107.1; -;
 DR EMBL; L38562; AAB36581.1; ALT_INIT.
 DR EMBL; X51754; CAB38569.1; ALT_INIT.
 DR EMBL; X51755; CAA36049.1; -;
 DR EMBL; X51755; CAA36051.1; -;
 DR PIR; A02125; L2HU.
 DR PDB; 2MCG; 15-JUL-92.
 DR PDB; 7FAB; 31-JAN-94.
 DR Genew; HGNC:5855; IGUC1.
 DR Genew; HGNC:5856; IGLC2.
 DR Genew; HGNC:5857; IGLC3.
 DR MIM; 147220; -;
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003597; Iq_C1.
 DR Pfam; PF00047; Iq; 1.
 DR SMART; SM00407; IGL1; 1.
 DR PROSITE; PS00290; Iq_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
 FT NON_TER 1
 FT DISULFID 27 86
 FT DISULFID 104 104
 FT VARIANT 5 5
 FT VARIANT 7 7
 FT VARIANT 45 45
 FT VARIANT 56 56
 FT VARIANT 82 82
 FT STRAND 4 4
 FT STRAND 7 11
 FT HELIX 15 19
 FT TURN 20 21
 FT STRAND 23 33
 FT STRAND 38 43
 FT TURN 44 45
 FT STRAND 46 48
 FT TURN 50 51
 FT STRAND 52 54
 FT STRAND 58 59
 FT TURN 61 62
 FT STRAND 65 73
 FT HELIX 75 79
 FT TURN 80 80
 FT STRAND 84 90
 FT TURN 91 92
 FT STRAND 93 99
 SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;
 Query Match 44.5%; Score 548; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 5.3e-37;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAMKADSSPVKAGVETTTPSKQ 191
 DB 1 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAMKADSSPVKAGVETTTPSKQ 60
 QY 192 SNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
 DB 61 SNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 105
 RESULT 2
 ID ILLI_HUMAN STANDARD; PRT; 213 AA.
 AC P15814;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
 related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
 DE (CD179b antigen).
 DE IGLL1 OR IGL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89315835; PubMed=2501791;
 RA Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
 RA McKearn J.P.;
 RT "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
 expressed in pre-B cells and may encode the human immunoglobulin
 omega light-chain protein.";
 Proc. Natl. Acad. Sci. U.S.A. 86:5552-5556 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.


```

DE Ig lambda chain V-I region BL2 precursor.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
   sequence";
RL Nucleic Acids Res. 12:8407-8414(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; X01147; CAA25598.1; -.
DR PIR; A01966; LIHUBL.
DR HSSP; P01703; 7FAB.
DR DR
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IGv; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL      1          19
FT CHAIN       20        130    IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN      20        115    V SEGMENT.
FT DOMAIN     116        130    J SEGMENT.
FT DISULFD     41        108    BY SIMILARITY.
FT NON_TER    130        130
FT SEQUENCE   130 AA;  FA44BB17D3A55EBF CRC64;
SQ
Query Match              37.6%; Score 463; DB 1; Length 130;
Best Local Similarity    72.8%; Pred. No. 3,7e-30;
Matches 91; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 7 LLGLLLLWLPARCSEVLTPPPSVSGAPQKVITISCTGSTNIGDYDLHWVQQLPGTAPK 66
Db ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
6 LLLTLIHCTGSWAQSVLTQPPSVSAAPQKVITISCGSSSNIGNDYYSWYQQVPGTAPK 65
QY 67 LLIIYNKRPGGIDRFSGSKGTAAASLAITGLQTDEADYYCQSYDSLSNAQVFGGTR 126
Db ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
66 LLIIYNKRPSPGIDRFSGSKGTATLITGLQTDEADYYCYGTWNNSLSGWVFGGTRK 125

QY 127 LTVLG 131
Db ||||
Db 126 LTVLG 130

RESULT 4
LVLD_HUMAN
ID LVLD_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain v-l region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81186114; PubMed=6404900;
RA Kametani F., Takayasu I., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
   immunoglobulins. IV. Assignment of a subsubclass".
```

```
RL J. Biochem. 93:421-429 (1983).
DR PIR; A01965; LIHUNG.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 36.9%; Score 454; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 1.6e-29;
Matches 87; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 21 ESVLTQPPSVGAPGKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
DB 1 QSVLTQPPSVGAPGKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 60

QY 81 DRFSGSKGTAASLAITGLQTEADYYCQSDSSSLNAQVFGGTRLTVLG 131
DB 61 DRFSGSKGTSATLITGLTGTDEADYYCQSDSSSLVGMFGGTRVTVLG 111

RESULT 5
LV1C_HUMAN STANDARD; PRT; 111 AA.
ID LV1C_HUMAN
AC P01701;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region NEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
MEDLINE=69060892; PubMed=4177823;
Langer B., Steinmetz-Kayne M., Hilschmann N.;
"The complete amino acid sequence of Bence Jones protein New (lambda-
type). Subgroups in the variable part of immunoglobulin L-chains of
the lambda-type.";
Hoppe-Seyley's Z. Physiol. Chem. 349:945-951 (1968).
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01964; LIHUNG.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11453 MW; AAEBCA3C49F2AD3 CRC64;

Query Match 35.1%; Score 432; DB 1; Length 111;
Best Local Similarity 73.9%; Pred. No. 8.6e-28;
Matches 82; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 21 ESVLTQPPSVGAPGKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
DB 1 QSVLTQPPSVGAPGKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 60

QY 81 DRFSGSKGTAASLAITGLQTEADYYCQSDSSSLNAQVFGGTRLTVLG 131
DB 61 DRISASKSGTSATLITGLTGTDEADYYCATWDSSSLNAVVGSGTKVTVLG 111

RESULT 6
```

```
LV1F_HUMAN STANDARD; PRT; 109 AA.
ID LV1F_HUMAN
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
MEDLINE=83221661; PubMed=6407018;
Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
"Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain.";
Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690 (1983).
DR PIR; A01967; LIHUNG.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97 V SEGMENT.
FT DOMAIN 98 109 J SEGMENT.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785FGA8DF9BAC CRC64;

Query Match 34.6%; Score 426; DB 1; Length 109;
Best Local Similarity 74.5%; Pred. No. 2.5e-27;
Matches 82; Conservative 13; Mismatches 13; Indels 2; Gaps 1;

QY 21 ESVLTQPPSVGAPGKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
DB 1 QSVLTQPPSVGAPGKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGV 60

QY 81 DRFSGSKGTAASLAITGLQTEADYYCQSDSSSLNAQVFGGTRLTVL 130
DB 61 DRFSGSKGTSASLAISGRSEADYYCAAWDDSL--WVFGGTTTLTVL 108

RESULT 7
LV2K_HUMAN STANDARD; PRT; 112 AA.
ID LV2K_HUMAN
AC P04209;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region NIG-84.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
MEDLINE=85204383; PubMed=3922791;
Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
"Amino acid sequence of an amyloidogenic Bence Jones protein in
myeloma-associated systemic amyloidosis.";
FEBS Lett. 185:139-141 (1985).
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
DR PIR; A01971; L2HUNG.
DR HSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT DISULFID 22 90 BY SIMILARITY.
```

```

FT NON_TER 112 112
SQ SEQUENCE 112 AA; 11581 MW; 988FEF363AE1B4F3 CRC64;

Query Match
Best Local Similarity 34.5%; Score 424.5; DB 1; Length 112;
Matches 79; Conservative 16; Mismatches 16; Indels 1; Gaps 1;

QY 21 ESVLTQPPSVSGAPGQKVTISCTGTSNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
DB 1 QSLATQPPASVSGSPGOSITISCTGTTSDVGYDFVSWYQQHPGKAPKLLIYDVNSRPSGI 60

QY 80 SDRFSGSKSTASLAITGLQTEDEADYQCSDVSSLNQVFGGTRLTVLG 131
DB 61 SNRPSGSKNTASLTISGLQAEADYQCSFTTTSRAVFGGTRKLSVLG 112

RESULT 8
LAC_PIG
ID LAC_PIG STANDARD; PRT; 105 AA.
AC P01846;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain C region.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=78000254; PubMed=409425;
RA Novotny J., Franek F., Margolies M.N., Haber E.;
RT "Amino acid sequence of normal (microheterogeneous) porcine
immunoglobulin lambda chains.";
RL Biochemistry 16:3765-3772(1977).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MIXTURE OF NORMAL
IMMUNOGLOBULINS.
CC PIR; A02129; LIPG.
DR HSP; P01842; 2MCG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_c1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 27 86
FT DISULFID 104 104
FT SEQUENCE 105 AA; 11003 MW; 3817AAEBD74C396 CRC64;

Query Match
Best Local Similarity 74.3%; Score 415; DB 1; Length 105;
Matches 78; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 132 QPKAAPVTLFPSPSEELQANKATLVCLISDPFGAVTVKADSSPKVAGVETTPSKQ 191
DB 1 QPKAAPVTLFPSPSEELQNKATLVCLISDPFGAVTVKAGGTVTQGVETTPSKQ 60

QY 192 SNKTYAAGSYLTLTPEQMKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 61 SNKTYAAGSYLALSADKSSSGFTQVTHEGTVIEKIVTPECA 105

RESULT 9
LV1H_HUMAN
ID LV1H_HUMAN STANDARD; PRT; 112 AA.
AC P06887;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85257662; PubMed=2410269;
RA Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
physicochemical and antigenic features.";
RL Eur. J. Biochem. 150:349-357(1985).
CC -!- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
WERE POSITIONED BY HOMOLOGY.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
MARKERS.
CC PIR; A25479; LIHUMM.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 112 112
FT SEQUENCE 112 AA; 11789 MW; 748124F079CFFBE4 CRC64;

Query Match
Best Local Similarity 33.6%; Score 413.5; DB 1; Length 112;
Matches 77; Conservative 19; Mismatches 14; Indels 1; Gaps 1;

QY 21 ESVLTQPPSVSGAPGQKVTISCTGTSNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
DB 1 QSVLTQPPASGTPGGRVTISCGSSSVGSNZPAYWYQQLPGTAPKLLIYVNRPSGV 60

QY 80 SDRFSGSKSTASLAITGLQTEDEADYQCSDVSSLNQVFGGTRLTVL 130
DB 61 PDRFSRSRSGTSASLTISGLQSEADYCAAWDDSLDGYVFGTGKTVTL 111

RESULT 10
LAC1_MOUSE
ID LAC1_MOUSE STANDARD; PRT; 105 AA.
AC P01843;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83014953; PubMed=6812053;
RA Seising E., Miller J., Wilson R., Storb U.;
RT "Evolution of mouse immunoglobulin lambda genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
CC [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE=8114806; PubMed=6259534;
RA Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA Gelfer M.L., Baltimore D.;
RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RL Nature 290:65-67(1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE=82220143; PubMed=6283385;
RA Bothwell A.L.M., Paskind M., Rath M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382(1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=71107854; PubMed=5276767;

```

```
RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RC Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
RL -I- MISCELLANEOUS: THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1
CC NORMAL LAMBDA-2 CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING
CC A LARGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
CC APPEARS COMPLETELY NORMAL.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00582; AAA51636.1; --
DR EMBL; J00587; AAB59672.1; --
DR PIR; A02126; LIMS.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGL; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 27 86
FT DISULFID 104 104
FT CONFLICT 19 20
FT CONFLICT 56 56
FT CONFLICT 56 56
FT CONFLICT 75 75
FT CONFLICT 81 82
FT CONFLICT 85 85
FT CONFLICT 96 96
FT CONFLICT 96 96
SQ SEQUENCE 105 AA; 11575 MW; A89F2B09BCFCA018 CRC64;

Query Match 33.4%; Score 412; DB 1; Length 105;
Best Local Similarity 71.4%; Pred. No. 3.1e-26;
Matches 75; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYGAVTVAWKADSSPYKAGVETTTPSKQ 191
DB 1 QPKSPSVTLFPPSSEELQANKATLVCLISDFYGAVTVAWKADSSPYKAGVETTTPSKQ 60

QY 192 SNKKYAAASYLSLTPEQMKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 61 SNKKYMASSYLTLTARAWERHSSYSCQVTHEGHTVEKLSRADCS 105

RESULT 11
LV1B HUMAN STANDARD; PRT; 112 AA.
AC P01700;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region HA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=71103824; PubMed=5532227;
RX Shinoda T., Titani K., Putnam F.W.;
RT "Amino acid sequence of human lambda chains. II. Chymotryptic
RL J. Biol. Chem. 245:4475-4487(1970).
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01963; LIHUHA.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
```

```
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT MOD_RES 22 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 21 90 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 11896 MW; 8D73378F3F5CD039 CRC64;

Query Match 33.1%; Score 407.5; DB 1; Length 112;
Best Local Similarity 71.2%; Pred. No. 7.6e-26;
Matches 79; Conservative 17; Mismatches 14; Indels 1; Gaps 1;

QY 21 ESVLTQPPSVSGAPGQKVITISCTGSTSN-IGGYDLHWYQQLPGTAPKLLIYDINKRPSGI 79
DB 1 QSVLTQPPSVSGTQQRVTISCSGSSNGTGNVYVYQQLPGTAPKLLIYRDDKRPSSGV 60

QY 80 SDRFSGSKSGTAASLAITGLQTEADYCYOSYSSLSNAQVFGGTRLTVL 130
DB 61 PDRFSGSKSGTSASLAISGLRSEDEAHYHCAAWDYRLSAVVFGGTLQTLVL 111

RESULT 12
LV1I HUMAN STANDARD; PRT; 109 AA.
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region EPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86000126; PubMed=3929803;
RX Toft K.G., Sletten K., Husby G.;
RT "The amino-acid sequence of the variable region of a carbohydrate-
RT containing amyloid fibril protein EPS (immunoglobulin light chain,
RT type lambda)".
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC -I- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
CC PEPTIDES WERE POSITIONED BY HOMOLOG.
DR PIR; A24656; LIHUEP.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Amyloid; Glycoprotein.
FT CARBOHYD 104 104 N-LINKED (GLCNAC. .).
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24DSAC73 CRC64;

Query Match 32.6%; Score 402; DB 1; Length 109;
Best Local Similarity 70.3%; Pred. No. 2e-25;
Matches 78; Conservative 16; Mismatches 15; Indels 2; Gaps 1;

QY 21 ESVLTQPPSVSGAPGQKVITISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
DB 1 QSVLTQPPSLAAPGQQRVTSISCSGSSNTGKNVYVYQQLPGTAPKLLIFNNKRPSGIP 60

QY 81 DRFSGSKSGTAASLAITGLQTEADYCYOSYSSLSNAQVFGGTRLTVLG 131
DB 61 DRFSGSKSGTSATLIGITGLQTGDEALYYCGTWDN--RRSVFGGNTVTVVG 109

RESULT 13
LAC_RABIT STANDARD; PRT; 105 AA.
ID LAC_RABIT
AC P01847;
```

```
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP
RX MEDLINE=82091105; PubMed=6797414;
RA Garcia I., Jaton J.-C.;
RT "The primary structure of the constant region of Basilea-rabbit
RT immunoglobulin lambda-chains."
RL Biochem. J. 197;177-183(1981).
CC -!- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC
CC SPECIFICITY.
DR PIR; A02130; L7RB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 27
FT DISULFID 86
FT DISULFID 104
FT DISULFID 104 104 INTERCHAIN (WITH HEAVY CHAIN).
SQ SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;

Query Match 32.4%; Score 399; DB 1; Length 105;
Best Local Similarity 72.4%; Pred. No. 3.3e-25;
Matches 76; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 132 QPKAAPSVTLFPPSSSELOANKATLCLISDFYPGAVTVAVKADSSPVKAGVETTPSKQ 191
Db 1 QPAVTSVTLFPPSSSELDKDKATLCLISDFYPRVKNVKNKADGNSVTQGVDTTPSKQ 60

QY 192 SNKYYAASSYLSITPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 61 SNKYYAASSFLHLTANQWKSYSQSVTCQVTHEGHTVEKSLAPAECS 105

RESULT 14
LV1A_HUMAN STANDARD; PRT; 111 AA.
AC P01699;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region VOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RX MEDLINE=76023790; PubMed=809332;
RA Engelhard M., Hilschmann N.;
RT "Pattern of antibody structure. The amino acid sequence of a
RT monoclonal immunoglobulin L-chain of lambe-type, subgroup I
RT (Bence-Jones-protein vor.). A contribution to the elucidation of the
RT origin of antibody specificity."
RL Hoppe-Seyster's Z. Physiol. Chem. 356;1413-1444 (1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01962; LHUV0.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
```

```
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11514 MW; 21D9F64250DFC8E0 CRC64;

Query Match 32.1%; Score 396; DB 1; Length 111;
Best Local Similarity 65.8%; Pred. No. 6.1e-25;
Matches 73; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

QY 21 ESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
Db 1 QSVLTQPPSASGTPGQRTVITSCSGNFEDIGRNSVNWYQVHFGTAPRLIIYSSDQRRSGVP 60

QY 81 DRFGSSKSGTAAASLAITGLQTEDEADYYCOSYDSSLSNAQVFGGTRLTVLG 131
Db 61 DRFGSSKSGTASLASISGLQSENEADYFCATWDQSLDQPVFGGTRKTVLG 111

RESULT 15
LV2B_HUMAN STANDARD; PRT; 111 AA.
AC P01705;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region NEI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RX MEDLINE=72333223; PubMed=5043326;
RA Garver F.A., Hilschmann N.;
RT "The primary structure of a monoclonal human lambda-type
RT immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
RL Eur. J. Biochem. 26;10-32(1972).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01970; L2HUNI.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein; Glycoprotein.
FT DISULFID 22 90 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .).
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;

Query Match 32.1%; Score 396; DB 1; Length 111;
Best Local Similarity 68.5%; Pred. No. 6.1e-25;
Matches 76; Conservative 17; Mismatches 16; Indels 2; Gaps 2;

QY 21 ESVLTQPPSVSGAPGQKVTISCTGSTNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
Db 1 QSALTQPASVSGSPGQSIITISCTGTTSDVGSYNFVSYQQNPQKAPKLMIEGKRPESGV 60

QY 80 SDRFGSSKSGTAAASLAITGLQTEDEADYYCOSYDSSLSNAQVFGGTRLTVL 130
Db 61 SNRFGSSKSGKTASLTISGLQVEDEADYYCCSYAGN-STRVFGGTRVTVL 110
```

Search completed: March 29, 2003, 09:11:15
Job time : 5.62693 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 21.4044 Seconds
(without alignments)
2271.829 Million cell updates/sec

Title: US-09-758-173-10
 Perfect score: 1232
 Sequence: 1 MRVPAQLLGLLLWLPQARC.....COVTHEGSTVEKTVAPTECS 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seg length: 0

```
Maximum DB seq length: 0
Maximum DB seq length: 200000000
```

00000000007 : IIII I I I I I I I I I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```

1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phase.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.invertebrate.*
14: sp.unclassified.*
15: sp.rvms.*
16: sp.bacteriap.*
17: sp.archaeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query #	Score	Query			Description
			Match	Length	DB	
1	1045	84.8	237	4	Q8WUK4	Q8WUK4 homo sapien
2	1045	84.8	237	4	Q8WTU6	Q8WTU6 homo sapien
3	991.5	80.5	236	4	Q8EEG1	Q8EEG1 homo sapien
4	888	72.1	233	4	Q8TBG9	Q8TBG9 homo sapien
5	805.5	65.4	233	4	Q8G1G9	Q8G1G9 homo sapien
6	767.5	62.3	240	4	Q8WUK3	Q8WUK3 homo sapien
7	722	58.6	235	11	Q9NM11	Q9NM11 mus musculus
8	551	44.7	106	4	Q8TCJ5	Q8TCJ5 homo sapien
9	488.5	33.7	234	11	Q8VCP0	Q8VCP0 mus musculus
10	472	38.3	130	11	Q8D8W4	Q8D8W4 mus musculus
11	472	38.3	239	4	Q8TCD0	Q8TCD0 homo sapien
12	466	37.8	235	11	Q91W12	Q91W12 mus musculus
13	464.5	37.7	234	11	Q8R062	Q8R062 mus musculus
14	461.5	37.5	238	11	Q8VCI6	Q8VCI6 mus musculus
15	453.5	36.8	238	11	Q9NM37	Q9NM37 mus musculus
16	450.5	36.6	233	11	Q91WS9	Q91WS9 mus musculus

Query Match 84.8%; Score 1045; DB 4; Length 237;
Best Local Similarity 88.4%; Pred. No. 6.1e-82;

QY		7	LLGLLMLPGARCBSVLTPPSVSGAPGKVITISCTGSTSNIG-CYDLHWQQLPGTAP	65
			: :	
Db		6	LILLTLLAHCTSQAQSIVLTPPSVSGAPGRVTISCTGSSNIGACYDVHWHQQLPGTAP	65
QY		66	KLLIYDINKRPSGISDRFSGSKSCTAASLAITGLQTEADYYCYSDSSLNA-OVFGGG	128

ALIGNMENTS

RESULT 1

Q8WUK4	PRELIMINARY;	PRT;	237 AA.
ID	Q8WUK4		
AC	Q8WUK4;		
DT	01-MAR-2002 (Tremblurel. 20, Created)		
DT	01-MAR-2002 (Tremblurel. 20, Last sequence update)		
DT	01-JUN-2002 (Tremblurel. 21, Last annotation update)		
DE	Hypothetical 24.9 kDa protein.		
DE	Homo sapiens (Human).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI TaxId:9606.		

RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

EMBL; BC020233; AAH20233.1; -.
 InterPro; IPR003599; IG.
 InterPro; IPR003597; IG_c1.
 InterPro; IPR003006; IG_MHC.
 InterPro; IPR003596; IG_v.
 Pfam; PF00047; IG; 2.
 SMART; SM00409; IG; 2.
 SMART; SM00407; IGc1; 1.
 SMART; SM00406; IGv; 1.
 PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 Hypothetical protein_KW

SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

```

Db      66 KLLIYGNRRPSGVDPDRFSGSKSGTASAIATGLQAEADYYCQSDSLSGFVVFGGG 125
Qy      125 TRLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTAAWKADSSPVKAGVE 184
Db      126 TKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTAAWKADSSPVKAGVE 185
Qy      185 TTTPSQSNKKYAASSVLSLTTPQWKSHRSYSQCVTHGSGTVEKTVAPTECS 236
Db      186 TTTPSQSNKKYAASSVLSLTTPQWKSHRSYSQCVTHGSGTVEKTVAPTECS 237

RESULT 2
Q8WTU6 PRELIMINARY; PRT; 237 AA.
ID AC Q8WTU6;
DC DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE OS Hypothetical 24.9 kDa protein.
DE OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX RN NCBI_TaxId=9606;
OX RN [1]
RP RP SEQUENCE FROM N.A.
RC RC TISSUE=TONSIL;
CA CA Strausberg R.;
RL RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
EMBL EMBL; BC022098; AAH22098.1; -.
DR DR InterPro; IPR003599; IG.
DR DR InterPro; IPR003597; IG cl.
DR DR InterPro; IPR003006; IG_MHC.
DR DR InterPro; IPR003596; IG_v.
DR DR Pfam; PF00047; IG; 2.
DR DR SMART; SM00409; IG; 2.
DR DR SMART; SM00407; IGcl; 1.
DR DR SMART; SM00406; IGV; 1.
DR DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW KW Hypothetical protein.
SQ SQ SEQUENCE 237 AA; 24884 MW; E6CF371E75396B58 CRC64;

Query Match 84.8%; Score 1045; DB 4; Length 237;
Best Local Similarity 88.4%; Pred. No. 6.1e-82;
Matches 205; Conservative 10; Mismatches 15; Indels 2; Gaps

Qy      7 LIGLLLLLPARGCESVLTQPPSVGAPGQKVTISCTGTSNIG-GYDLHWYQQLPGTAP 65
Db      6 LLLTLTLAHCTGSWAQSVLTQPPSVGAPGQRTVTSCTGSSNIGAGYDVHWYQQLPGTAP 65
Qy      66 KLLIYDINKRSGISDRFSGSKSGTASAIATGLQTEADYYCQSDSLNQ-VFGGG 124
Db      66 KLLIYGNRRPSGVDPDRFSGSKSGTASAIATGLQAEADYYCQSDYLSASGVFGGG 125

Qy      125 TRLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTAAWKADSSPVKAGVE 184
Db      126 TKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTAAWKADSSPVKAGVE 185
Qy      185 TTTPSQSNKKYAASSVLSLTTPQWKSHRSYSQCVTHGSGTVEKTVAPTECS 236
Db      186 TTTPSQSNKKYAASSVLSLTTPQWKSHRSYSQCVTHGSGTVEKTVAPTECS 237

RESULT 3
Q95E61 PRELIMINARY; PRT; 236 AA.
ID AC Q95E61
DC DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT DT 01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DE Unknown Yproteins for MGC:17259).
OS OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


Db 179 GVETTPSKQNNKYAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 5

Q96169 PRELIMINARY; PRT; 233 AA.

AC Q96169

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE Unknown (protein for MGC:12849)

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=B-CELL;

RA Strausberg R.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC007782; AA07782.1; -

DR InterPro; IPR003598; IG_c2

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR001412; tRNA-synt_1.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00408; IGC2; 1.

DR PROSITE; PS00178; AA TRNA LIGASE I; UNKNOWN_1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Immunoglobulin domain

SQ SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;

Query Match 65.4%; Score 805.5; DB 4; Length 233;
Best Local Similarity 70.0%; Pred. No. 2.2e-61;
Matches 161; Conservative 21; Mismatches 45; Indels 3; Gaps 2;

QY 7 LLGLLLWLPARCESVLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPX 66
DB 7 LLG-LLSHCTGSTSVLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPX 66

QY 67 LLYIDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSLSNAQVFGGTR 126
DB 67 LLYIDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSLSNAQVFGGTR 126

QY 64 LVVYENKEREPAGIPERLSALTSEETATLTISWAGDEADYFCQWDTTSQYVFGTGTQ 123
DB 64 LVVYENKEREPAGIPERLSALTSEETATLTISWAGDEADYFCQWDTTSQYVFGTGTQ 123

QY 127 LTVLGQPKAPSVTLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPX 186
DB 127 LTVLGQPKAPSVTLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPX 186

QY 124 VTVLGQPKAPSVTLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPX 183
DB 124 VTVLGQPKAPSVTLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPX 183

QY 187 TPKSQNNKYAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 236
DB 187 TPKSQNNKYAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 236

QY 184 KPSQNNKYAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 233
DB 184 KPSQNNKYAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 6

Q8WUK3 PRELIMINARY; PRT; 240 AA.

AC Q8WUK3

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DE Unknown (protein for MGC:12849)

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=TONSIL;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC020236; AA020236.1; -

DR InterPro; IPR003599; IG.

DR InterPro; IPR003597; IG_c1.

DR InterPro; IPR003006; IG_MHC.

SQ SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IGC1; 2.

DR SMART; SM00407; IGC1; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;

Query Match 62.3%; Score 767.5; DB 4; Length 240;
Best Local Similarity 69.2%; Pred. No. 4.2e-58;
Matches 153; Conservative 21; Mismatches 38; Indels 9; Gaps 4;

QY 23 VLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPKLLIY----DINKRPSG 78
DB 23 VLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPKLLIY----DINKRPSG 78

QY 79 ISDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSLSNAQ---VFGGTRTLTVLGQPKA 135
DB 79 ISDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSLSNAQ---VFGGTRTLTVLGQPKA 135

QY 81 IPDRFSGSGGADRYLTLSNLSQDDEAEYHC--GESHTIDGQVGVFGGTTKLTVLSPKA 139
DB 81 IPDRFSGSGGADRYLTLSNLSQDDEAEYHC--GESHTIDGQVGVFGGTTKLTVLSPKA 139

QY 136 APSVTLPSPSSSELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNK 195
DB 136 APSVTLPSPSSSELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNK 195

QY 140 APSVTLPSPSSSELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNK 199
DB 140 APSVTLPSPSSSELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNK 199

QY 196 YAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 236
DB 196 YAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 236

QY 200 YAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 240
DB 200 YAASSVLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 240

RESULT 7

Q99M11 PRELIMINARY; PRT; 235 AA.

AC Q99M11

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DE Hypothetical 25.4 kDa protein.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC002129; AA002129.1; -

DR HSP; P01703; 7FAB.

DR InterPro; IPR003599; IG.

DR InterPro; IPR003597; IG_c1.

DR InterPro; IPR003600; IG_like.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IGC1; 1.

DR SMART; SM00407; IGV; 1.

DR SMART; SM00410; IG_like; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 58.6%; Score 722; DB 11; Length 235;
Best Local Similarity 61.1%; Pred. No. 3.3e-54;
Matches 143; Conservative 29; Mismatches 58; Indels 4; Gaps 2;

QY 5 AQLIGLLLLWLPARCESVLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPX 64
DB 5 AQLIGLLLLWLPARCESVLTQPPSVGAPQKVTISCTGSTNIGYDLHWYQQLPGTAPX 64

QY 4 APLLVFLHLLTGTSCAQLVLTQPPSVSTSLGSTAKLPCKSTIGSYVNNVYQYMGSR 63
DB 4 APLLVFLHLLTGTSCAQLVLTQPPSVSTSLGSTAKLPCKSTIGSYVNNVYQYMGSR 63

QY 65 PKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSLSNAQVFG 122
DB 65 PKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSLSNAQVFG 122

QY 64 PTNNIYDGLRPSGVSDRFGSGSIDSSNSAFLTIQNVQADDEADYYCQSYSSGI--RVFG 121
DB 64 PTNNIYDGLRPSGVSDRFGSGSIDSSNSAFLTIQNVQADDEADYYCQSYSSGI--RVFG 121

QY 123 GGTGRLTVLGPAAAPSVTLFPSSSEELQANKATLVCLISDFYFGAVTVVANKADSSPVKAG 182
 Db 122 GGTGRLTVLGPAAAPSVTLFPSSSEELQANKATLVCLISDFYFGAVTVVANKADSSPVKAG 181
 QY 183 VETTPSKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 236
 Db 182 VETTPSKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 235

RESULT 8

Q8TCJ5 ID Q8TCJ5 PRELIMINARY; PRT; 106 AA.
 AC Q8TCJ5
 DT 01-JUN-2002 (TremBLrel. 21, Created)
 DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Hypothetical 11.3 kDa protein (Fragment).
 GN DKF26670810.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPH NODE;
 RA Duesterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL713800; CAD28551.1;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;

Query Match 44.7%; Score 551; DB 4; Length 106;
 Best Local Similarity 99.1%; Pred. No. 5.4e-40; Indels 0; Gaps 0;
 Matches 105; Conservative 1; Mismatches 0;

QY 131 GPKAAPSVTLFPSSSEELQANKATLVCLISDFYFGAVTVVANKADSSPVKAGVETTPSK 190
 Db 1 GPKAAPSVTLFPSSSEELQANKATLVCLISDFYFGAVTVVANKADSSPVKAGVETTPSK 60
 QY 191 QSNKYAASSYLSLTPQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 236
 Db 61 QSNKYAASSYLSLTPQWKSHRSYSCQVTHGEGSTVEKTVAPTECS 106

RESULT 9

Q8VCP0 ID Q8VCP0 PRELIMINARY; PRT; 234 AA.
 AC Q8VCP0
 DT 01-WAR-2002 (TremBLrel. 20, Created)
 DT 01-WAR-2002 (TremBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Hypothetical 25.7 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019474; AAH19474.1;
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00409; IG_2.
 DR SMART; SM00407; IGC1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS08290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
 Query Match 39.7%; Score 488.5; DB 11; Length 234;
 Best Local Similarity 44.8%; Pred. No. 3.6e-34;
 Matches 107; Conservative 42; Mismatches 81; Indels 9; Gaps 7;
 QY 1 MRYPAQLGLGLLLWLPGARCESVLQ-PPSVSGAPGQKVTICTGSTNIGGYDLHWYQQ 59
 Db 1 MSVPTQVLGLLLCLTGARCDIQLQSPASLSASGEVTVITCRAS-ENIYSY-LAWYQQ 58
 QY 60 LPTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYQSYDSSLSNAQ 119
 Db 59 KQKSPQLLVNAKTLADGVPSRFSRSGTQFSKLNSLQPEDFSGSYCQHHSGI--PF 116
 QY 120 VFGGGRLLTVLGPAAAPSVTLFPSSSEELQANKATLVCLISDFYFGAVTVVANKADSSPV 179
 Db 117 TFGSGTKLEI-KRADAAPTVSIFPPSSSEQLTSGGASVVCFLNNFYPKDIINVKKIDGSR 175
 QY 180 KAGV-ETTPSKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGEGST--VEKTVAPTEC 235
 Db 176 QNGVLNSWTDQDSKDYSGMSSTLTLTCKDEYRHNSYTCEATHKTSTSPIVKSFNRNEC 234

RESULT 10

Q9DSW4 ID Q9DSW4 PRELIMINARY; PRT; 130 AA.
 AC Q9DSW4
 DT 01-JUN-2001 (TremBLrel. 17, Created)
 DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
 DE 1810027001Rik protein.
 GN 1810027001Rik
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; PubMed=11217851;
 RX MEDLINE=21085560; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK007622; BAB25142.1;
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:1916426; 1810027001Rik.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 130 AA; 14253 MW; 438197975E766E54 CRC64;
 Query Match 38.3%; Score 472; DB 11; Length 130;
 Best Local Similarity 69.6%; Pred. No. 4.3e-33;

```
Matches 87; Conservative 15; Mismatches 23; Indels 0; Gaps 0;
QY 112 YDSSLNAQVGGGTRLTVLGQPKAAPSVTLPFPSSSELOANKATLVCLISDFYPGAVTVA 171
DB 6 HESISQCVWFGGKTLVLGQPKSPSVTLFPSPSELETKNATLVCTITDFYFGWTVTD 65
QY 172 WKADSSPVKAGVETTPSKOSNNKYAASSVLSLTPEQWKSRSYSCQVTHGSGTVEKTVA 231
DB 66 WKVDGTPVQGMETTPQSKOSNNKYASSVLSLTARAWERHSSYSCQVTHGHTVEKSL 125
QY 232 PTECS 236
DB 126 RADCS 130

RESULT 11
ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023362; AAH23362.1; -.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 38.3%; Score 472; DB 4; Length 239;
Best Local Similarity 42.0%; Pred. No. 9.7e-33;
Matches 102; Conservative 52; Mismatches 77; Indels 12; Gaps 7;
QY 1 MRVPAQLGLLLWLPGARCESVLTQPP-SVSGAPGQKVTISCTGSGNI---GGYDLHW 56
DB 1 MRLPAQLGLLLWLPVGSSGDVMTQSPSLPVTLLGQPASISCRSTQSLVSDGNTYLNW 60
QY 57 YQQLPGTAPKLLIYDINKRPSGISDRFSGSGKGTAAASLTGLQTEDEADYVCSYDSSL 116
DB 61 PQQPGQSPRLIYKVNDRSDGVPDRFSGSGGTDTLKITRVEAEDYGVYFCM--QGTH 118
QY 117 NAQVFGGTRLTVLGQPKAAPSVTLPFPSSSELOANKATLVCLISDFYPGAVTVAWKADS 176
DB 119 WPSTFGGQTKLEI-KRTVAAPSFIFFPSDEQLKSGTASVCLNNFYPRAKQWQVDN 177
QY 177 SPVKAG--VETTPSKOSNNKYAASSVLSLTPEQWKSRSYSCQVTHG--STVEKTVAP 232
DB 178 A-LOGSNQBSVTEQDSKSTYSLSTLSKADYEKHKVACEVTHQGLSPVTKSFNR 236
QY 233 TEC 235
DB 237 GEC 239

RESULT 12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 37.8%; Score 466; DB 11; Length 235;
Best Local Similarity 44.1%; Pred. No. 3.1e-32;
Matches 98; Conservative 47; Mismatches 67; Indels 10; Gaps 6;
QY 18 ARCSESVLTQPPSV-SGAPGQKVTISCTGSGNIIGYDLHWYQQLPGTAPKLIYDINKRP 76
DB 20 SRGQIVLTQSPAIMSASFGSRVTMTCSASS---VSHMHYQKSGTSPKRWIYDTFKLT 76
QY 77 SGISDRFSGSGKGTAAASLTGLQTEDEADYVCSYDSSLNAQVGGGTRLTVLGQPKAA 136
DB 77 SGVDFRFGSGSGSYSLTISNMEADVATYICQW--SRNPPTFGVGTKLE-LKRADA 133
QY 137 PSVTLFPSSSELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGV-ETTPSKQSNK 195
DB 134 PTVSIFPSSSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQGVNLNSWTDQDSKST 193
QY 196 YAASSYLSLTPEQWKSRSYSCQVTHGSGT--VEKTVAPTEC 235
DB 194 YMSGSTLTLTKEYERHNSYTCATHKTSTSPIVKSFNRNEC 235
```

```
RESULT 13
ID Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;
```

```
Query Match 37.7%; Score 464.5; DB 11; Length 234;
Best Local Similarity 44.4%; Pred. No. 4.2e-32;
Matches 106; Conservative 40; Mismatches 84; Indels 9; Gaps 7;
QY 1 MRVPAQLGLLLWLPGARCESVLTQ-PFVSAGAPGQKVTISCTGSGNIIGYDLHWYQ 59
DB 1 MWSSAQFLGLLLCFQGTQCDIQMTQTTSLSASLGDRVTISCSAS-QGINSY-LNMYQ 58
QY 60 LPGTAPKLLIYDINKRPSGISDRFSGSGKGTAAASLTGLQTEDEADYVCSYDSSLNAQ 119
DB 59 KPDGTVKLLIYTSLSHSGVPSRFSGSGTHYSLTISNLEPEDIATYICQY--SQPFF 116
QY 120 VFGGTRLTVLGQPKAAPSVTLPFPSSSELOANKATLVCLISDFYPGAVTVAWKADSPV 179
DB 117 TFGSGTKLEI-KRADAPTIVSIFPSSSEQLTSGGASVVCFLNNFYPKDINVKWIDGSR 175
QY 180 KAGV-ETTPSKQSNKYYAASSVLSLTPEQWKSRSYSCQVTHGSGT--VEKTVAPTEC 235
DB 176 QNGVLNSWTDQDSKSTYSSNSTLTLTKEYERHNSYTCATHKTSTSPIVKSFNRNEC 234
```

```

DR HSP: P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 1.
DR SMART; SM00406; IgV; 1.
DR SMART; SM00410; Ig like; 1.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
KW Hypothetical protein_1.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 36.88; Score 453.5; DB 11; Length 238;
Best Local Similarity 40.5%; Pred. No. 3.8e-31;
Matches 98; Conservative 52; Mismatches 81; Indels 11; Gaps

QY 1 MRVPAQLGLLLMPCARGESVLTOPP-SVSGAPGQKVITICTGSTSNI--GGVDLHW 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MKLPVRLI-VLMFWIPASSDDVMVTPTSLPVSIGDQASISCRSSQSVHSNGNTYLEW 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 57 YQOLFPTAKLLIYDINKRPGSISDRFSGSKSGTAASIAITGLQTEADAYCYOSVDSSL 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 YLQKPGQPKLLIYKVNRPISGVDFRFGSGSGTDTLKI SRVEAEDLGVIYC--FGSH 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 117 NQVFGSGGTRTLVLGQPKAAPSVTLPSPSEELQANKATLVCLISDFVPGAVTVAMKADS 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 VPYTFGSGTKLEI-KRADAAPTWSIIPPSSEQLTSGGASVCFLNYPDKDINVKWKIDG 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 177 SPVKAGV-ETTPSQGNKKYAAASSYLSLTPTQCKSHRSYSCQVTHEGST--VEKTVAPT 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 SERQGVNLNSDQDSKDSYMSSTLTLTQDEYRHNSYTCATHTKTSPIVKSFNRN 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 234 EC 235
   || ||
Db 237 EC 238

Search completed: March 29, 2003, 09:14:40
Job time : 21.4044 secs

```

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 24.273 Seconds
(without alignments)
1295.559 Million cell updates/sec

Title: US-09-758-173-10

Perfect score: 1232

Sequence: 1 MRVPAQLLGLLLWLPQARC.....CQVTHEGSTVKTVAFTPCS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

```

1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1232	100.0	236	19	AAW63764
2	1232	100.0	236	23	AAU11645
3	1229	99.8	236	18	AAW01821
4	1052.5	85.4	236	22	AAW01821
5	1006	81.7	235	20	AAW88465
6	1001	81.2	236	22	AAW88465
7	979.5	79.5	217	14	AAW42163
8	973	79.0	234	18	AAW01817
9	973	79.0	234	19	AAW63760
10	973	79.0	234	23	AAU11538

11	971.5	78.9	217	19	AAW40533	Antibody HB4C5 lig
12	968.5	78.6	248	22	ABG26352	Novel human diago
13	965	78.3	235	22	AAW36212	Human immune syste
14	965	78.3	235	22	AAW36212	Human immune syste
15	958.5	77.8	236	22	ABG19293	Novel human diago
16	957	77.7	235	22	AAW64472	Human type anti hum
17	957	77.7	614	23	ABW06275	Plasimid scFv(CCO46
18	955	77.5	235	14	AAW31024	Antibody D light c
19	950.5	77.2	219	21	AAW30594	Variable and first
20	945	76.7	235	22	AAW64474	Human type anti hum
21	945	76.7	235	22	AAW64476	Human type anti hum
22	944	76.6	249	22	ABG12886	Novel human diago
23	941	76.4	244	22	ABG19296	Novel human diago
24	935	75.9	235	22	AAW64470	Human type anti hum
25	934.5	75.9	235	22	ABG19301	Human type anti hum
26	934	75.8	235	22	ABG19290	Novel human diago
27	927	75.2	251	22	ABG19291	Novel human diago
28	911.5	74.0	236	22	ABG22850	Novel human diago
29	898	72.9	235	22	AAW78781	Novel human diago
30	891.5	72.4	236	22	ABG19298	Human protein SEQ
31	890	72.2	235	21	AAW15347	Novel human diago
32	888	72.1	238	22	AAW08381	Human immune syste
33	885	71.8	235	19	AAW75214	Anti-OGGp antibod
34	884	71.8	233	9	AAW81260	Human secreted pro
35	882	71.6	235	19	AAW75231	VDJC regions of hu
36	877	71.2	238	22	ABG19299	Human secreted pro
37	876	71.1	233	23	AAU82012	Novel human diago
38	875	71.0	238	22	ABG19297	Novel human diago
39	871.5	70.7	232	22	AAU14412	Human secreted pro
40	867.5	70.4	232	22	AAW23527	Human novel protei
41	866	70.3	231	22	AAU14176	Human EST encoded
42	866	70.3	269	23	ABP41361	Human ovarian anti
43	863.5	70.1	247	22	ABG19295	Novel human diago
44	857.5	69.6	233	18	AAW14924	Ant-CD4 monkey-hum
45	854.5	69.4	244	21	AAW43979	Human cancer assoc

ALIGNMENTS

RESULT 1
AAW63764
ID AAW63764 standard; Protein; 236 AA.
XX AAW63764;
XX AC
XX DT 29-SEP-1998 (first entry)
XX DE Macaque primatized 16C10 light chain protein.
XX KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation.
XX OS Macaca fascicularis.
XX PN WO9819706-A1.
XX PD 14-MAY-1998.
XX PF 29-OCT-1997; 97WO-US19906.
XX PR 08-NOV-1996; 96US-0746361.
XX PA (IDEC-) IDEC PHARM CORP.
XX PI Anderson DR, Brans P, Hanna N;
XX WPI; 1998-286601/25.
XX DR N-PSDB; AAW35488.
XX

PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 PS Example 7; Fig 5a; 87pp; English.
 XX
 CC This sequence represents a primatised form of the antibody 16C10 light
 CC chain from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 SQ Sequence 236 AA;

Query Match 100.0%; Score 1232; DB 19; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.2e-66;
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRVPAQLLGLLLMLPGARCESVLTQPPSVSGAPQKVITICTGTSNIGGYDLHWYQQL 60
 Db 1 MRVPAQLLGLLLMLPGARCESVLTQPPSVSGAPQKVITICTGTSNIGGYDLHWYQQL 60
 QY 61 PGTAFLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYCYQSDSSLNAQV 120
 Db 61 PGTAFLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYCYQSDSSLNAQV 120
 QY 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
 Db 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
 QY 181 AGVETTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
 Db 181 AGVETTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236

RESULT 2
 AAU01645
 ID AAU01645 standard; Protein; 236 AA.
 XX
 AC AAU01645;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Protein sequence of primatised form of the light chain of 16C10 antibody.
 XX
 KW Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; mutein.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX
 PN WO200195567-A1.
 XX
 PD 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US16364.
 XX
 XX 22-MAY-2000; 2000US-0576424.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 XX
 XX Anderson DR, Hanna N, Brams P;
 XX
 XX WPI; 2002-089895/12.
 XX N-PSDB; AAS17246.
 DR
 DR Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease such as
 PT allergy -
 PT
 XX Example 8; Fig 5a; 89pp; English.
 XX
 CC The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present protein
 CC sequence represents the light chain of 16C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).
 XX

SQ Sequence 236 AA;

Query Match 100.0%; Score 1232; DB 23; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.2e-66;
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRVPAQLLGLLLMLPGARCESVLTQPPSVSGAPQKVITICTGTSNIGGYDLHWYQQL 60
 Db 1 MRVPAQLLGLLLMLPGARCESVLTQPPSVSGAPQKVITICTGTSNIGGYDLHWYQQL 60

QY 61 PGTAFLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYCYQSDSSLNAQV 120
 Db 61 PGTAFLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYCYQSDSSLNAQV 120
 QY 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
 Db 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
 QY 181 AGVETTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
 Db 181 AGVETTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236

RESULT 3

AAW01821
 ID AAW01821 standard; Protein; 236 AA.

XX
 AC AAW01821;
 XX
 DT 25-MAY-1997 (first entry)
 XX
 DE Primatised anti-human B7.1 antigen antibody 16C10 light chain.
 XX
 KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;

KW primatised antibody; B7 antigen; CD28; immunosuppressive;
 KW autoimmune disease; idiopathic thrombocytopenia purpura;
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes mellitus; graft versus host disease;
 KW hetero-hybridoma; transfectoma.
 XX
 OS Chimeric Macaca cynomolgus;
 OS Chimeric Homo sapiens.
 PN WO9640878-A1.
 XX
 XX 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US10053.
 XX
 PR 07-JUN-1995; 95US-0487550.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Brans P, Hanna N, Shestowsky WS;
 DR WPI; 1997-108638/10.
 DR N-PSDB; AAT62512.
 XX
 XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
 PT useful for treating autoimmune disease or graft-versus-host disease
 PT
 XX
 PS Claim 14; Fig 10A; 81pp; English.
 XX
 CC 2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
 CC heavy variable genes (see also AAT62512 and AAT62513) are inserted into
 CC an expression vector (see. NEOSPLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatised
 CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
 CC antibodies have also been produced (see also AAW01817-20). The
 CC primatised antibodies inhibit the B7:CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders
 CC and graft-versus-host disease.
 XX
 SQ Sequence 236 AA;

Query Match 99.8%; Score 1229; DB 19; Length 236;
 Best Local Similarity 99.6%; Pred. No. 1.8e-66;
 Matches 235; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRVPAQLGLLLWLPFGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQL 60
 Db |||||
 QY 61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAAASLAITGLQTEDEADYYCQSDSSLSNAQV 120
 Db |||||
 QY 121 FCGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
 Db |||||
 QY 181 AGVETTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
 Db |||||
 QY 181 AGVETTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236

RESULT 4
 AAB36209
 ID AAB36209 standard; protein; 236 AA.
 XX
 AC AAB36209;
 XX
 DT 15-FEB-2001 (first entry)
 XX

Human immune system associated protein HISAP-7.

XX Human; immune system associated protein; HISAP-7; immune disorder;
 KW infection; autoimmune disease; cancer.
 XX
 OS Homo sapiens.
 PN US6135941-A.
 XX
 XX 24-OCT-2000.
 XX
 XX 27-MAR-1998; 98US-0049672.
 XX
 PR 27-MAR-1998; 98US-0049672.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
 PI Hillman JL, Au-Young J;
 DR WPI; 2001-030926/04.
 DR N-PSDB; AAC66525.
 XX
 XX New human immune system associated proteins (HISAP) and polynucleotides
 PT encoding the HISAP, useful for diagnosing, treating or preventing
 PT immune or cell proliferative disorders or infections -
 XX
 PS Claim 1; Column 59-62; 54pp; English.
 XX
 CC The present invention provides the coding and protein sequences for a
 CC number of human immune system associated proteins (HISAPs). These can be
 CC used in the diagnosis and treatment of various autoimmune disorders,
 CC infections and cell proliferation diseases. The diseases include AIDS,
 CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
 CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
 CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
 CC erythematosus, arteriosclerosis, cirrhosis and cancer.
 XX
 SQ Sequence 236 AA;
 Query Match 85.4%; Score 1052.5; DB 22; Length 236;
 Best Local Similarity 88.3%; Pred. No. 6.6e-56;
 Matches 204; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
 QY 7 LGLLLWLPFGARCESVLTQPPSVSGAPGQKVTISCTGTSNIG-GYDLHWYQQLPCTAP 65
 Db |||||
 QY 66 KLLIYDINKRPSGISDRFSGSKSGTAAASLAITGLQTEDEADYYCQSDSSLSNAQVFGGT 125
 Db |||||
 QY 66 KLLIYGRNRPSGVPDRFSGSKSGTASLAITGLQTEDEADYYCQSDSSLSGWFVFGGT 125
 QY 126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
 Db |||||
 QY 126 KLTJVLGQPKAAPSVTLFPPSSEELQANRATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
 QY 186 TTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
 Db |||||
 QY 186 TTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
 RESULT 5
 AAW88465
 ID AAW88465 standard; Protein; 235 AA.
 XX
 AC AAW88465;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Monoclonal antibody 4B5 light chain variable region.
 XX
 KW Antigen binding fragment 4B5; monoclonal antibody; cancer;
 KW neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
 KW sarcoma; lung carcinoma; metastasis; anti-idiotypic antibody;


```

Db 7 LLLTLTHCAGWAOSVLTQPPSAGTGGQRTVITSCGASSNIGNDVYVYQQLTGTPAK 66
QY 67 LLIYDINKRPSGIDRFSGSKSGTAAASLAITGLQTEDEADYVCSYDSSLNQAVFGGQTR 126
Db 67 LLIYRNQRPSPVDRFSGSKSGSSASLAISGLQSEDEADYCAAWDDSLSGPVFGGQTK 126
QY 127 LTVLGOPKAAPSVTLPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
Db 127 LTVLGOPKAAPSVTLPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
QY 187 TPKSKNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
Db 187 TPKSKNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236

RESULT 7
AAR42163
ID AAR42163 standard; Protein; 217 AA.
AC AAR42163;
XX
DT 27-APR-1994 (first entry)
DE Anti-HIV-1 recombinant antibody 447-52D light chain.
XX
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW acquired immune deficiency syndrome; chimeric antibody;
KW surface glycoprotein gp120; V3 loop.
XX
OS Homo sapiens.
XX
PN WO9319785-A.
PD 14-OCT-1993.
XX
PF 23-MAR-1993; 93WO-US02629.
XX
PR 01-APR-1992; 92US-0861701.
XX
PA (MERI ) MERCK & CO INC.
PA (JOHN/) JOHNSON L S.
PA (PFAR/) PFARR D S.
XX
PI Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;
XX
DR WPI; 1993-336600/42.
DR N-PSDB; AAQ49835.
XX
PT New recombinant human antibody - with HIV neutralising activity
PT against at least two isolates, useful for preventing or treating
PT infection in diagnosis, etc.
XX
PS Example 9; Fig 2B; 154pp; English.
XX
CC EBV-transformed cell lines and mouse-human heterohybridomas
CC producing human MAbS specific for the gp120 V3 loop of HIV-1 MN
CC isolate were obtained. Mab 447-52D was found to recognise the
CC tetrapeptide motif GPGR, i.e. the Principal Neutralising
CC Determinant common to the V3 loop of different HIV isolates.
CC A recombinant Ab was produced in which the L chain V region was
CC derived from 447-52D and to which a signal sequence and a L chain
CC intronic sequence are appended, fused to a fragment contg. a short
CC intronic segment of the human lambda 2 C region and the human
CC lambda 2 constant encoding domain.
XX
SQ Sequence 217 AA;
Query Match 79.5%; Score 979.5; DB 14; Length 217;
Best Local Similarity 87.6%; Pred. No. 1.4e-51;
Matches 190; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

```

QY 21 ESVLTQPPSVGAPGQKVTISCTGSTNIGGYDLHWYQQLPTAPKLLIYDINKRPSGIS 80

```

Db 1 QSVLTQPPSVGAPGQKVTISCTGSTNIGGYDLHWYQQLPTAPKLLIYDINKRPSGIS 60
QY 81 DRESGSKGTAAASLAITGLQTEDEADYVCSYDSSLNQAVFGGQTR 139
Db 61 DRESGSKGTAAASLAITGLQTEDEADYVCSYDSSLNQAVFGGQTR 139
QY 140 TLPFPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQNNKYAAS 199
Db 121 TLPFPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQNNKYAAS 180
QY 200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
Db 181 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 217

RESULT 8
AAW01817
ID AAW01817 standard; Protein; 234 AA.
XX
AC AAW01817;
XX
DT 25-MAY-1997 (first entry)
DE Primatised anti-human B7.1 antigen antibody 7C10 light chain.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brans P, Hanna N, Shestowsky WS;
XX
DR WPI; 1997-108638/10.
DR N-PSDB; AAT62509.
XX
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
XX
PS Claim 6; Fig 8A; 81pp; English.
XX
CC 2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
CC variable genes (see also AAT62509 and AAT62510) are inserted into
CC an expression vector (pref. NEOSPLA) which contains human light and
CC heavy chain constant region genes to allow prodn. of the primatised
CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC antibodies have also been produced (see also AAW01819-22). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.
XX
SQ Sequence 234 AA;
Query Match 79.0%; Score 973; DB 18; Length 234;
Best Local Similarity 80.1%; Pred. No. 3.7e-51;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

```

17

XX The present invention relates to a new use of a monoclonal antibody CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen CC (CD86) for inducing the apoptosis of B7+ cells. The invention is CC

This sequence represents a primatized form of the antibody 7C10 light chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopenic purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab' can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotypic reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions

CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present protein
 CC sequence represents the light chain of 7C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).
 XX
 XX

SQ Sequence 234 AA;

Query Match 79.0%; Score 973; DB 23; Length 234;
 Best Local Similarity 80.1%; Pred. No. 3.7e-51;
 Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

QY 1 MRVPAQLGLLLWLPGARCESVLTQPSVSGAPGKVTISCTGTSNIGGYDLHWYQOL 60
 DB 1 MRVPAQLGLLLWLPGARCAVELTQPSVSPGQTARITCGSDNSR--NEYVHWYQOK 58
 QY 61 PGTAAPKLLIYDINKRPSGISDRFSGSKGTAAASLAITGLQTEDEADYQCQSDSLNAQV 120
 DB 59 PARAPILVIYDSDRPSGIPERFSGSKGNATLTINGVEAGDEADYQCQWDRASDHVP 118
 QY 121 FGGGTRTLVLPQKAPSVTLTPPPSEELQANKATLVCLISDFYFGAVTVAWKADSSPVK 180
 DB 119 FGGGTRVTVLPQKAPSVTLTPPPSEELQANKATLVCLISDFYFGAVTVAWKADSSPVK 178
 QY 181 AGVETTTQKSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
 DB 179 AGVETTTQKSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 11
 AAW40533
 ID AAW40533 standard; Protein; 217 AA.
 XX
 AC AAW40533;
 XX
 DT 27-AUG-1998 (first entry)
 XX
 DE Antibody HB4C5 light chain sequence.
 XX
 KW Antibody light chain; carboxypeptidase; bovine pancreas; cancer;
 KW porcine pancreas; radioimmunoinaging.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..112
 FT /note= "light chain fragment that is claimed for in
 FT Claim 11"
 FT Domain 23..35
 FT /note= "complementarity determining region (CDR)-1;
 FT sequence claimed in claim 17"
 FT Domain 51..57
 FT /note= "complementarity determining region (CDR)-2;
 FT sequence claimed in claim 17"
 FT Domain 90..101
 FT /note= "complementarity determining region (CDR)-3;
 FT sequence claimed in claim 17"

JP10075791-A.

24-MAR-1998.

XX

PF 30-AUG-1996; 96JP-0246825.
 XX
 PR 30-AUG-1996; 96JP-0246825.
 XX
 PA (MOMI) MORINAGA & CO LTD.
 XX
 DR WPI; 1998-244364/22.
 DR N-PSDB; AAV11293.
 XX
 PT New antibody light chain or its fragment - useful for preparation of
 PT therapeutic(s) or cancer radio-immuno-imaging agent(s)
 XX
 PS Claim 10; Fig 11; 20pp; Japanese.
 XX
 CC This represents a antibody HB4C5 light chain. This antibody light chain
 CC or its fragment is specific for carboxypeptidase from bovine or porcine
 CC pancreas and is reactive with human cancer tissue. The antibody light
 CC chain and its fragment can be used for preparation of a cancer
 CC radioimmunoinaging reagent and therapeutic compositions.
 XX
 SQ Sequence 217 AA;

Query Match 78.9%; Score 971.5; DB 19; Length 217;
 Best Local Similarity 86.6%; Pred. No. 4.3e-51;
 Matches 188; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

QY 21 ESVLTQPPSVSGAPGKVTISCTGTSNIGGYDLHWYQOLPGTAPKLLIYDINKRPSGIS 80
 DB 1 QSVLTQPPSVSAAAPGKVTISCGNSNIGNNVSVYQHLPGTAPKLLIYDINKRPSGIS 60
 QY 81 DRFSGSKGTAAASLAITGLQTEDEADYQCQSDSLNAQ-VFGGTRTLVLPQKAPSV 139
 DB 61 DRFSGSKGTAAASLAITGLQTEDEADYCATWTSILRVNWLFGGKTLVLPQKAPSV 120
 QY 140 TLPPPSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGVETTTQKSNKYAAS 199
 DB 121 TLPPPSSEELQANKATLVCLISDFYFGAVTVAWKADSSPVKAGVETTTQKSNKYAAS 180
 QY 200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
 DB 181 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 217

RESULT 12
 ABG26352
 ID ABG26352 standard; Protein; 248 AA.
 XX
 AC ABG26352;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #26343.
 XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSSE-) HYSSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS90539.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 56711; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 248 AA;
SQ
Query Match 78.6%; Score 968.5; DB 22; Length 248;
Best Local Similarity 79.2%; Pred. No. 7.4e-51;
Matches 190; Conservative 18; Mismatches 25; Indels 7; Gaps 2;
Qy 4 PAQLGLLLWL-----PGARCESVLTPPSVSGAPGQKVTISCTGTSNIGGYDLHWY 57
Db 9 PWPAGALLTLTHCAVPSWAQSVLTQAPASGTFPGQRTVISCSSNIGNPNVWY 68
Qy 58 QQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYICQSYDSSLN 117
Db 69 QQLPGTAPKLLIYRNQRPSPGVDRFSGSKSGTASLAISGLQSEDEAQYCAAWDDSLN 128
Qy 118 -AQVFGGTLTVLGQKAPSVTLFPSSSEELQANKATLVCLISDFYPCAVTVAWKADS 176
Db 129 GSYVFGTGKTVLGQPKANPTVTLFPSSSEELQANKATLVCLISDFYPCAVTVAWKADG 188
Qy 177 SPVKAGVETTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 189 SPVKAGVETNPKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 248
RESULT 13
ID AAB36212
XX AAB36212 standard; protein; 235 AA.
AC AAB36212;
XX
XX 15-FEB-2001 (first entry)
DT
XX Human immune system associated protein HISAP-10.
DE
XX Human; immune system associated protein; HISAP-10; immune disorder;
KW infection; autoimmune disease; cancer.
XX
XX Homo sapiens.
OS
XX US6135941-A.
PN
XX 24-OCT-2000.
PD
XX 27-MAR-1998; 98US-0049672.
PF

XX 27-MAR-1998; 98US-0049672.
PR (INCY-) INCYTE PHARM INC.
PA
XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
PI
XX MPI: 2001-030926/04.
DR N-PSDB; AAC66528.
DR
XX New human immune system associated proteins (HISAP) and polynucleotides
CC encoding the HISAP, useful for diagnosing, treating or preventing
PT immune or cell proliferative disorders or infections -
XX
XX Claim 1; Column 65-68; 54pp; English.
XX The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
XX Sequence 235 AA;
SQ
Query Match 78.3%; Score 965; DB 22; Length 235;
Best Local Similarity 80.3%; Pred. No. 1.1e-50;
Matches 187; Conservative 19; Mismatches 25; Indels 2; Gaps 2;
Qy 5 AQLGLLLWLPGARCESVLTPPSVSGAPGQKVTISCTGTSNIGGYD-LHWYQQLPGT 63
Db 4 ALLPFLTLTQTGSAWAQSVLTQAPASVSGSPQSTIISCTGTSNIGGYDGVNYSYQSPGT 63
Qy 64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYICQSYDSSLNAQVFGG 123
Db 64 APKLLIYEVSNRPSGVSNRFRSGSKSGNTASLTISGLQAEDEADYICSSYVGN-NIVVFGG 122
Qy 124 GTRLTVLGQKAPASVTLFPSSSEELQANKATLVCLISDFYPCAVTVAWKADSSPVKAGV 183
Db 123 GTKLTVLGQKAPASVTLFPSSSEELQANKATLVCLISDFYPCAVTVAWKADSSPVKAGV 182
Qy 184 ETTTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
Db 183 ETTTPSKQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235
RESULT 14
ID AAB36214
XX AAB36214 standard; protein; 235 AA.
AC AAB36214;
XX
XX 15-FEB-2001 (first entry)
DT
XX Human immune system associated protein HISAP-12.
DE
XX Human; immune system associated protein; HISAP-12; immune disorder;
KW infection; autoimmune disease; cancer.
XX
XX Homo sapiens.
OS
XX US6135941-A.
PN
XX 24-OCT-2000.
PD
XX 27-MAR-1998; 98US-0049672.
PF
XX 27-MAR-1998; 98US-0049672.
PR
XX (INCY-) INCYTE PHARM INC.
PA

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 32.3734 Seconds
(without alignments)
6735.375 Million cell updates/sec

Title: US-09-758-173-9
Perfect score: 711
Sequence: 1 ATGAGGTCCCGCTCAGCT.....CCCTACAGATGTTTCATGA 711

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCUTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	711	3	US-08-487-550-9
2	582.6	81.9	935	3	US-09-049-672A-20
3	540.2	76.0	705	3	US-08-487-550-1
4	530.2	74.6	895	3	US-09-049-672A-25
5	510.6	71.8	891	3	US-09-049-672A-23
6	502.6	70.7	902	2	US-08-378-939-11
7	484.2	68.1	885	4	US-09-152-060-47
8	482.6	67.9	879	4	US-09-152-060-29
9	468.4	65.9	702	3	US-08-523-894-5
10	416.4	58.6	919	3	US-09-049-672A-24
11	412	57.9	928	4	US-09-152-060-46
12	367.4	51.7	716	4	US-08-793-450-5
13	323.6	45.5	584	4	US-09-404-879A-268
14	306.2	43.1	771	4	US-08-991-789A-241
15	306.2	43.1	771	4	US-09-062-451-241
16	306.2	43.1	771	4	US-09-598-326-241
17	264.4	37.2	408	4	US-09-025-769B-169
18	255.4	35.9	393	1	US-08-305-683A-3
19	254.8	35.8	933	3	US-09-079-029-8
20	253.2	35.6	642	2	US-08-634-783A-4
21	253.2	35.6	642	3	US-09-070-817-4
22	246.8	34.7	346	2	US-08-761-277A-50
23	244.2	34.3	330	4	US-09-240-274-132
24	242.4	34.1	318	2	US-08-648-981-4
25	242.4	34.1	333	2	US-08-477-553A-43
26	242.2	34.1	774	2	US-08-665-202-4
27	242.2	34.1	908	4	US-09-273-839A-9

28 241.2 33.9 327 4 US-09-240-274-223 Sequence 223, App
29 237.6 33.4 333 1 US-08-264-093-5 Sequence 5, Appl
30 236.6 33.3 336 2 US-08-345-321-3 Sequence 3, Appl
31 234.8 33.0 327 4 US-09-240-274-128 Sequence 128, App
32 233.2 32.8 327 4 US-09-240-274-126 Sequence 126, App
33 231.6 32.6 327 4 US-09-240-274-129 Sequence 129, App
34 231.6 32.6 327 4 US-09-240-274-130 Sequence 130, App
35 226.6 31.9 330 1 US-08-199-911-1 Sequence 1, Appl
36 226.6 31.9 336 4 US-09-240-274-133 Sequence 133, App
37 226.4 31.8 318 1 US-08-436-463-9 Sequence 9, Appl
38 226.4 31.8 318 1 US-08-024-253-9 Sequence 134, App
39 223 31.4 330 4 US-09-240-274-123 Sequence 123, App
40 220.4 31.0 327 4 US-09-240-274-125 Sequence 125, App
41 220.4 31.0 327 4 US-09-240-274-125 Sequence 125, App
42 217.4 30.6 342 4 US-09-240-274-131 Sequence 131, App
43 216.2 30.4 327 4 US-09-240-274-124 Sequence 124, App
44 208.8 29.4 333 2 US-08-652-816A-27 Sequence 27, Appl
45 204.4 28.7 327 4 US-09-240-274-127 Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-487-550-9
; Sequence 9, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCES/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..711
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..711
; US-08-487-550-9

Query Match

100.0%; Score 711; DB 3; Length 711;

Best Local Similarity 100.0%; Pred. No. 2.4e-187;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGAGGTCCTCCGCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCAGGTGACAGATGT 60
DB 1 ATGAGGTCCTCCGCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCAGGTGACAGATGT 60
QY 61 GAGTGTCTGCTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAGGTACCAATC 120
DB 61 GAGTGTCTGCTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAGGTACCAATC 120
QY 121 TCGTGCACTGGGAGCACCTCCAACTTGGAGTTATGATCTACATTTGTTACAGAGCTC 180
DB 121 TCGTGCACTGGGAGCACCTCCAACTTGGAGTTATGATCTACATTTGTTACAGAGCTC 180
QY 181 CCAGAAAGGCCCCCAACTCTCTATCTATGACATTAACAGGACCCCTCAGGAATTTCT 240
DB 181 CCAGAAAGGCCCCCAACTCTCTATCTATGACATTTAAAGGACCCCTCAGGAATTTCT 240
QY 241 GACCAATTTCTGGCTCGAGTCTGGTACCGGGCTCTGGCCATCATCTGGGCTCCAG 300
DB 241 GACCAATTTCTGGCTCGAGTCTGGTACCGGGCTCTGGCCATCATCTGGGCTCCAG 300
QY 301 ACTGAGGATGAGCTGATTTACTTGCAGTCTCTATGACAGCAGCTGAATGTCTCAGGTA 360
DB 301 ACTGAGGATGAGCTGATTTACTTGCAGTCTCTATGACAGCAGCTGAATGTCTCAGGTA 360
QY 361 TTCGAGGAGGAGACCGGCTGACCGTCTAGGTGAGCCCAAGGCTGCCCCCTGGTCACT 420
DB 361 TTCGAGGAGGAGACCGGCTGACCGTCTAGGTGAGCCCAAGGCTGCCCCCTGGTCACT 420
QY 421 CTGTTCCCGCTCTCTGAGGAGCTTCAAGCAACAGGCACTGGTGTCTCATTA 480
DB 421 CTGTTCCCGCTCTCTGAGGAGCTTCAAGCAACAGGCACTGGTGTCTCATTA 480
QY 481 AGTGAATTTTACCCGGGAGCGGTGACAGTGGCTGGAGGAGATAGACGCCCCGTCAAG 540
DB 481 AGTGAATTTTACCCGGGAGCGGTGACAGTGGCTGGAGGAGATAGACGCCCCGTCAAG 540
QY 541 GCGGAGTGGAGACCAACACCTTCCAAACAAAGCAACAGTACGCGGCGCAGC 600
DB 541 GCGGAGTGGAGACCAACACCTTCCAAACAAAGCAACAGTACGCGGCGCAGC 600
QY 601 TACCTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAACTACAGCTCCAGGTCAG 660
DB 601 TACCTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAACTACAGCTCCAGGTCAG 660
QY 661 CATGAAGGAGCAGCGTGGAGAGACAGTGGCCCTACAGAACTGTTCTATGA 711
DB 661 CATGAAGGAGCAGCGTGGAGAGACAGTGGCCCTACAGAACTGTTCTATGA 711
```

RESULT 2

US-09-672A-20
Sequence 20, Application US/09049672A
Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: ADRETU05
CLONE: 2492122
US-09-049-672A-20

Query Match 81.9%; Score 582.6; DB 3; Length 935;

Best Local Similarity 89.8%; Pred. No. 7.8e-152;
Matches 637; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

```
QY 4 AGGGTCCCCGCTCAGCTCTGGGGCTCTGCTCTGCTCTGCTCCAGGTGACAGATGTGAG 63
DB 74 ATGGCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 133
QY 64 TCTCTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAGGTCAACATCTCG 123
DB 134 TCTGTGCTGACGACGCGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAGGTCAACATCTCT 193
QY 124 TGCCTGGGAGCACCTCCAACTTGG---AGGTTATGATCTACATTGGTACCAAGCAGCTC 180
DB 194 TGCCTGGGAGCACCTCCAACTTGGGGCAGGTTATGATGTACACTGGTACCAAGCAGCTT 253
QY 181 CCAGGAAGGCCCCCAACTCTCTCATCTATGACATTAACAGGACCCCTCAGGAATTTCT 240
DB 254 CCAGGAAGGCCCCCAACTCTCTCATCTATGTTAGTAAATCGGGCTCTCAGGGGTCTCT 313
QY 241 GACCGATTCTCTGGCTCCAACTCTGGTACCGCGGCTCTCTGGCCATCACTGGGCTCCAG 300
DB 314 GACCGATTCTCTGGCTCCAACTCTGGCACCCTCAGCTCTCTGGCCATCACTGGGCTCCAG 373
QY 301 ACTGAGGATGAGGCTGATTTACTGCGAGTCTCTATGACAGCAGCTGTAATGTCTCAGGTA 360
DB 374 GCTGAGGATGAGGCTGATTTACTGCGAGTCTCTATGACAGCAGCTGTAATGTCTGTTA 433
QY 361 TTCGGAGGAGGACCGGCTGACCGTCTAGGTACGCCAAGGCTGCCCCCTCGGTCACT 420
DB 434 TTCGGAGGAGGACCGGCTGACCGTCTCGGTACGCCAAGGCTGCCCCCTCGGTCACT 493
QY 421 CTGTTCCCGCTCTCTCTGAGGAGCTTCAAGCAACAGGCCCACTGTGTGTCTCATTA 480
DB 494 CTGTTCCCGCTCTCTCTGAGGAGCTTCAAGCAACAGGCCCACTGTGTGTCTCATTA 553
QY 481 AGTGACTTCTACCGGAGCGGTGACAGTGGCTGGAAGCAGATAGCAGCCCGCTCAAG 540
DB 554 AGTGACTTCTACCGGAGCGGTGACAGTGGCTGGAAGCAGATAGCAGCCCGCTCAAG 613
QY 541 GCGGAGTGGAGACCACTCCATCCCTCCAAACAAAGCAACAGTACGCGGCCAGCAGC 600
```


APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0497 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 895 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGUT13

CLONE: 3116314

US-09-049-672A-25

Query Match 74.6%; Score 530.2; DB 3; Length 895;
Best Local Similarity 87.5%; Pred. No. 2.3e-137;
Matches 580; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 47 CAGGTGACGATGTGAGTCTGCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGC 106
DB 80 CAGGTCTGGGCCAGTCTGTGCTGACTCAGCCCCCTCAGCGTCTGGACCCCGGC 139
QY 107 AGAGGTCAACATCTGTCGATCTGGGAGCACTTCAACATTTGGAGTTATGATTTACATT 166
DB 140 AGAGGTCAACATCTTCTTCTGGAACCACTTCAACATCTGGAATTTCTGTCATT 199
QY 167 GTTACAGCAGTCCAGGAAGCGGCCCAACTCTCATCTATGACATTAACAGCCAC 226
DB 200 GTTACCAATTAAGTTCCAGAGCGGCCCAACTCTCATCTATGATGATGATGAGCGTG 259
QY 227 CTTACAGGAATTTCTGACCGATTTCTTGGCTTCAAGTCTGTTACCGGGCTCCCTGGCCA 286
DB 260 CTTCCGGGGTCTTACCGATTTCTTGGCTTCAAGTCTGACCTCAGCTTCCCTGGCCA 319
QY 287 TCACTGGGTCCAGATGAGATGAGGTGATTTATCTGCGCAGTCTTATGACAGCAGCC 346
DB 320 TCAGTGGGTCCGGCCCGAGGATGAATTTATCTGTGCAACATGGGATGACAGTG 379
QY 347 TGAATCTCAGGTATTCGAGGAGGAGCCGCTGACCGTCTAGTCTAGGCGCAAGGCTG 406
DB 380 TCAGTGGTGGATTTCCGGGAGGAGGACCAAGCTGACCGTCTAGTCTAGGCGCAAGGCTG 439
QY 407 CCGCTCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAGGCGCAC 466
DB 440 CCGCTCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAGGCGCAC 499
QY 467 TGGTGTCTCATAAGTACTTCTACCGGGAGCGGTGACGTGGCGCTGGAAGGAGGAGATA 526
DB 500 TGGTGTCTCATAAGTACTTCTACCGGGAGCGGTGACGTGGCGCTGGAAGGAGGAGATA 559
QY 527 GCAGCCCCGTCAAGCGGGAGTGGAGCACCAACACCTTCCAAACAAAGCAACAAAGT 586
DB 560 GCAGCCCCGTCAAGCGGGAGTGGAGCACCAACACCTTCCAAACAAAGCAACAAAGT 619
QY 587 ACAGCGCCAGCAGTCACTGAGCCTGACGCTGAGCAGTGAAGTCCCAAGAGCTACA 646
DB 620 ACAGCGCCAGCAGTCACTGAGCCTGACGCTGAGCAGTGAAGTCCCAAGAGCTACA 679
QY 647 GCTGCCAGTCAAGATGAAGGAGCACCGTGGAGAGACAGTGGCCCCCTCAGATGTT 706
DB 680 GCTGCCAGTCAAGATGAAGGAGCACCGTGGAGAGACAGTGGCCCCCTCAGATGTT 739
QY 707 CAT 709
DB 740 CAT 742

RESULT 5

US-09-049-672A-23

Sequence 23, Application US/09049672A

Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Tang, Y. Tom

APPLICANT: Yue, Henry

APPLICANT: Au-Young, Janice

APPLICANT: Corley, Neil C.

APPLICANT: Guebler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,672A

FILING DATE: HEREWITH

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0497 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 891 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: THYNOT10

CLONE: 2872705

US-09-049-672A-23

Query Match 71.8%; Score 510.6; DB 3; Length 891;

Best Local Similarity 84.5%; Pred. No. 5.9e-132;

Matches 599; Conservative 0; Mismatches 104; Indels 6; Gaps 2;

QY 4 AGGTCCTCCCTCAGCTCCCTGGGCTCTGCTGCTCCAGGTGCACGATGTGAG 63
DB 34 ATGGCTGGGCTCTGCTATTCTCTACCTCTCCTCAGTGGGACAGGGTCTGGGGCCAG 93
QY 64 TCTGTCTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATCTCG 123
DB 94 TCTGCCCTGACTCAGCGCTGCTCCGTTGCTGGGTCTCTGGACAGTGCATCACCATCTCC 153
QY 124 TGCCTGGGAGCCTCCCAACATTGGAGTTAT---GATCTACATTGGTACAGCAGCTC 180
DB 154 TGCCTGGAAACCAAGCAGTGCCTGGTGGTTATTAACATGTTCTCTCTGGTACCAACAGTCC 213
QY 181 CCAGGAACGGCCCCCAAACTCATCTATGACATTAACAGGAGCCCTCAGGAATTTCT 240
DB 214 CCAGGACGGCCCCCAAACTCATGATTTATGAGGTGAGTANTCGGCCCTCAGGGGTTTCT 273

Qy	241	GACCGATTCTCTGGCTCCAAAGTCTGTGTACCGCGGCTCCCTGGCCCATCACTGGGCTCCAG	300
Db	274	AATCGGTTCTCTGGCTCCAAGTCTGGCAACACCGGCTCCCTGACCATCTCTGGGCTCCAG	333
Qy	301	ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCCTGAATGCTCAGGTA	360
Db	334	GCTGAGGACGAGGCTGATTATTACTGCAGCTCATATGTAGGCAAC--AACATTGTGGTA	390
Qy	361	TTCGGAGGAGGACCCGGCTGACCGTCTTAGTTCAGCCCAAGGCTGCCCCCTCGGTCACT	420
Db	391	TTCGGCGAGGAGCAAGCTGACCGTCTTAGTTCAGCCCAAGGCTGCCCCCTCGGTCACT	450
Qy	421	CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAGCCACACTGGTGTGTCTCAT	480
Db	451	CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAGCCACACTGGTGTGTCTCAT	510
Qy	481	AGTGACTTCTACCCGGAGCCGTGACAGTGCCTGGAGGACAGATAGCAGCCCGCTCAAG	540
Db	511	AGTGACTTCTACCCGGAGCCGTGACAGTGCCTGGAGGACAGATAGCAGCCCGCTCAAG	570
Qy	541	GCGGAGTGGAGACCAACCAACCCCTCCAAACAAGCAACAACAGTACGCGGCCAGCAGC	600
Db	571	GCGGAGTGGAGACCAACCAACCCCTCCAAACAAGCAACAACAGTACGCGGCCAGCAGC	630
Qy	601	TACTTGAGCCCTGACGCTGAGCAGTGAAGTCCCAACAGAGCTACAGCTGCCAGGTTCAG	660
Db	631	TATCTGAGCCCTGACGCTGAGCAGTGAAGTCCCAACAGAGCTACAGCTGCCAGGTTCAG	690
Qy	661	CATGAAGGGAGCACCGCTGGGAGAGACAGTGGCCCTACAGAATGTTTCAT	709
Db	691	CATGAAGGGAGCACCGCTGGGAGAGACAGTGGCCCTACAGAATGTTTCAT	739

RESULT 6

US-08-378-939-11
: Sequence 11 Application IIS/08378939

Patent No. 5876361
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.

```
?  
? COUNTRY: U.S.  
?  
? ZIP: 20004  
?  
? COMPUTER READABLE FORM:  
?  
? MEDIUM TYPE: Floppy disk  
?  
? COMPUTER: IBM PC compatible  
?  
? OPERATING SYSTEM: PC-DOS/MS-DOS  
?  
? SOFTWARE: Patent In Release #1.0, Version #1.25  
?  
? CURRENT APPLICATION DATA:  
?  
? APPLICATION NUMBER: US/08/378,939  
?
```

```

: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/952640
: FILING DATE: 01-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: ERNST, BARBARA G
: REGISTRATION NUMBER: 30,377
: REFERENCE/DOCKET NUMBER: 1808-118
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 783-6040
: TELEFAX: (202) 783-6031
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 902 base pairs
: TYPE: nucleic acid
:

```

RESULT 7

US-09-152-060-47
: Sequence 47 Application US/09152060

GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-47

Query Match 68.1%; Score 484.2; DB 4; Length 885;
Best Local Similarity 80.9%; Pred. No. 1.2e-124;
Matches 564; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
QY 13 GCTCAGCTCTCGGGCTCTGCTGCTCTGGCTCCACAGGTGCACGATGTGAGTCTGCTCG 72
DB 30 GTTCTGCTCTCTGACCTCTCTCACTCACTCTGAGTGTGAGTGCAGCGAGGGCTG 89
QY 73 ACACAGCCGCTCTAGTGTCTGGGGCCCCCAGGGCAGAAAGGTCAACATCTCGTGTCACTGGG 132
DB 90 ACTCAGCCCTCTGGTGTCCAAGGACTTGACACAGACCGCCACACTCACTGTGACCCGGG 149
QY 133 AGCAGCTCAACATTTGGAGTTATGATCTACATTTGGTACCAGCAGCTCCAGGACGGCC 192
DB 150 AACAAACAATGTTGGCCACCAAGAGCAGCTTGGCTGCAGCAGCACAGGGCCACCT 209
QY 193 CCCAACTCTCATCTATGACATTAACAGCGACCTCAGGAATTTCTGACCGATTCTCT 252
DB 210 CCCAACTCTCTCTACAGGATTAATACCGGCCCTCAGGGATCTCAGAGGATTAATCT 269
QY 253 GGTCTCAAATGTGTTACCGCGCTCTCTGGCCATCACTGGGCTCCAGACTGAGGATGAG 312
DB 270 GCATCCAGGTGAGGAGCCACATCTCTCTGACCATTAATCTGGACTCCAGCTGAGGACG 329
QY 313 GCTGATTATTAATGTCAGTCTTATGACAGCAGCTGATGCTCAGGATTTGGAGGAGGG 372
DB 330 GCTGACTATTAATGTCGACGATATGACAGCAGCTCGACGATTTGGATGTTGGCGGAGGG 389
QY 373 ACCCGCTGACCGTCTTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCCGCC 432
DB 390 ACCAAGCTGACCGTCTTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCCGCC 449
QY 433 TCCTCTGAGGAGTTCAAGCCAAAGGCCACAATGTTGTTCTCATAGTGAATTTCTAC 492
DB 450 TCCTCTGAGGAGTTCAAGCCAAAGGCCACAATGTTGTTCTCATAGTGAATTTCTAC 509
QY 493 CGGGAGCGCTGACAGTGGCTTGGAGGAGATAGCAGCCCGCTCAAGCGGAGTGAG 552
DB 510 CCGGGAGCGCTGACAGTGGCTTGGAGGAGATAGCAGCCCGCTCAAGCGGAGTGAG 569

QY 553 ACCACCAACCTCTCCAAACAAAGCAACAACTACGCGCCAGCAGTACCTGAGCCTG 612
DB 570 ACCACCAACCTCTCCAAACAAAGCAACAACTACGCGCCAGCAGTACCTGAGCCTG 629
QY 613 ACGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTCAACGATGAAGGAGC 672
DB 630 ACGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTCAACGATGAAGGAGC 689
QY 673 ACGTGGAGAGCAGTGGCCCTTACAGATGTTTCA 709
DB 690 ACCGTGGAGAGCAGTGGCCCTTACAGATGTTTCA 726

RESULT 8

US-09-152-060-29
; Sequence 29, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-29

Query Match 67.9%; Score 482.6; DB 4; Length 879;
Best Local Similarity 80.8%; Pred. No. 3.2e-124;
Matches 563; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 13 GCTCAGCTCTCGGGCTCTGCTGCTCTGGCTCCACAGGTGCACGATGTGAGTCTGCTCG 72
DB 22 GTTCTGCTCTCTGACCTCTCTCACTCACTCTGCACTGTGAGTGTGAGGAGGGCTG 81
QY 73 ACACAGCCGCTCTAGTGTCTGGGGCCCCCAGGGCAGAAAGGTCAACATCTCGTGCATGGG 132
DB 82 ACTCAGCCCTCTGGTGTCCAAGGACTTGAGACAGACCGCCACACTCACTGTGACCGGG 141
QY 133 AGCAGCTCCACATTTGAGGTTATGATCTACATTTGTTACAGCAGCTCCAGGACGGCC 192
DB 142 AACAAACAATGTTGGCCACCAAGGAGCAGCTTGGCTGCAGCAGCACAGGGCCACCT 201
QY 193 CCCAACTCTCATCTATGACATTAACAGCGACCTCAGGAATTTCTCAGCGATTTCTCT 252
DB 202 CCCAACTCTCTCTACAGGATTAATACCGGCCCTCAGGGATCTCAGAGGATTAATCT 261
QY 253 GGTCCAAGTCTGTTACCGCGCTCTCCCTGGCCATCACTGGGCTCCAGACTGAGGATGAG 312

```
Db 262 GCATCCAGGTCAGGAGCCATCTCCCTGACCATTAAGTCTGAGCTCCAGGCTGAGGACGAG 321
Qy 313 GCTGATTAATTACTGCCAGTCTTATGACAGAGCCTGAATGCTCAGGTATTCGAGGAGGG 372
Db 322 GCTGACTATTACTGCGCAGCATATGACAGAGCCTCGCATGTTGGATGTTTCGGCGGAGG 381
Qy 373 ACCGGCTGACCGTCTTAGGTGACGCCAAGGCTGCCCGCTCGGTCACTCTGTTCGGCCCC 432
Db 382 ACCAAGCTGACCGTCTTAGGTGACGCCAAGGCTGCCCGCTCGGTCACTCTGTTCGGCCCC 441
Qy 433 TCCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGCTGTGTCTCATAAGTGAATCTTAC 492
Db 442 TCCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGCTGTGTCTCATAAGTGAATCTTAC 501
Qy 493 CCGGAGCCGTGACAGTGGCTGGAAGGCAGATAGCAGCCCCCGTCAAGGCGGAGTGGAG 552
Db 502 CCGGAGCCGTGACAGTGGCTGGAAGGCAGATAGCAGCCCCCGTCAAGGCGGAGTGGAG 561
Qy 553 ACCACCAACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACCTGAGCCTG 612
Db 562 ACCACCAACCCCTCCAAACAGAGCAACAAAGTACGCGGCCAGCAGCTACCTGAGCCTG 621
Qy 613 ACGCTGAGCAGTGGAGTCCCAAGAGGTACAGCTGCCAGGTACGCAATGAAGGAGC 672
Db 622 ACGCTGAGCAGTGGAGTCCCAAGAGGTACAGCTGCCAGGTACGCAATGAAGGAGC 681
Qy 673 ACCGTGGAGAGACAGTGGCCCCCTACAGATGTTTCAT 709
Db 682 ACCGTGGAGAGACAGTGGCCCCCTACAGATGTTTCAT 718
```

RESULT 9

```
US-08-523-894-5
; Sequence 5, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Ref. Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; NUMBER OF INVENTION: 59
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

```
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: lambda variable and constant domains in
; CHROMOSOME/SEGMENT: CE9.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..702
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..702
; US-08-523-894-5
Query Match 65.9%; Score 468.4; DB 3; Length 702;
Best Local Similarity 79.9%; Pred. No. 2.5e-120;
Matches 566; Conservative 0; Mismatches 136; Indels 6; Gaps 1;
Qy 4 AGGGTCCCGCTCAGCTCCTGGGGCTCTGCTGCTCTGGCTCCAGGTGCAGATGTGAG 63
Db 1 ATGGGCTGGGCTCTGCTGCTCTGGGCTCTGCTCTTACAGACTCTGCGGCTCC 60
Qy 64 TCTGTCTGACACACGCGCCCTCAGTGTCTGGGGCCCGAGGCGAAGGTCAACATCTCG 123
Db 61 TATGAGTTGAGTCAGCCTCGCTCAGTGTCTGGTGTCCCGAGGACACGCG-----CCGG 114
Qy 124 TGCATGAGGAGCACCTCCAAACATTGGAGGTTATGATCTATGACATTACAGGACCTTCTGAC 183
Db 115 TTACACTGTGGGGGAGACAACTGTTGGAAGGAAAGTGTACAGTGGTACCGAGGAAGCCA 174
Qy 184 GGAAAGGCGCCCAAACTCTCATCTATGACATTACAGGCGACCTCAGGAATTTCTGAC 243
Db 175 CCGCAGGCGCCCTGTGCTGGTCTATCTATGACAGCGAACCGGCTCTCAGGGATCCCTGGG 234
Qy 244 CGATTCTCTGGCTCCAAAGTCTGGTACCGGGCTCTCGGCTCATCTGGGCTCCAGACT 303
Db 235 CGATTCTCTGGCTCCAACTCAGGAGAACCGGCCACCTGACCATCAGCGGGTCCGAGGCC 294
Qy 304 GAGGATGAGGCTGATTATTTATGTCAGTCTTATGACAGGAGCTGAAATGCTCAGGTATTTC 363
Db 295 GGGGATGAGGCTGACTATTACTGTGAGGTGGGACAGTACTGCTGATCATTTGGGTCTTC 354
Qy 364 GGAGGAGGACCGGCTGACCGCTCTGAGTCCAGCCCAAGGCTGCGGCTCGGTCACTCTG 423
Db 355 GCGGAGGAGACCGGCTGACCGCTCTGAGTCCAGCCCAAGGCTGCGGCTCGGTCACTCTG 414
Qy 424 TTCCCGCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCATTAAGT 483
Db 415 TTCCCGCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCATTAAGT 474
Qy 484 GACTTCTACCCGGAGCCGTGACAGTGGGCTTGAAGGCGAGATAGCAGCCCCCGTCAAGGGCG 543
Db 475 GACTTCTACCCGGAGCCGTGACAGTGGGCTTGAAGGCGAGATAGCAGCCCCCGTCAAGGGCG 534
Qy 544 GGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTAC 603
Db 535 GGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTAC 594
Qy 604 CTGAGCTGACCGCTGAGCAGTGGAAAGTCCCAAGAGCTTACAGCTGCCAGGTGACGAT 663
Db 595 CTGAGCTGACCGCTGAGCAGTGGAAAGTCCCAAGAGCTTACAGCTGCCAGGTGACGAT 654
Qy 664 GAAGGAGCAGCCTGGAGAGCAGTGGGCGCTTACAGATGTTTCATGA 711
Db 655 GAAGGAGCAGCCTGGAGAGCAGTGGGCGCTTACAGATGTTTCATGA 702
```

RESULT 10

```
US-09-049-672A-24
; Sequence 24, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
```

APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Carrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LMODNOT08
CLONE: 3056213
US-09-049-672A-24

Query Match 58.6%; Score 416.4; DB 3; Length 919;
Best Local Similarity 78.7%; Pred. No. 6.2e-106;
Matches 524; Conservative 0; Mismatches 136; Indels 6; Gaps 2;

QY 47 CAGGTGCACGATGTGAGTCTGTCTGACACAGCGCGCCCTCAGTGTCTGGGGCCCGAGGC 106
DB 106 CAGGAGTGATTTCTCAGATGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCTGGAG 165
QY 107 AGNAGTCAACATCTCGTCACTGGAGAC---CTCCAACTTGGAGGTATGATCATAC 163
DB 166 GGACAGTCACTCACTTGTGGCTTGTGAGTCTGTGGCTCAGTCTCTACTAGTAACCTCA 225
QY 164 ATTGGTACAGCAGCTCCAGGAAGCGGCCCAACTCTCATCTATGACATTAACAAGC 223
DB 226 GCTGGTACAGCAGACCCAGCGCCAGGCTCCAGCAGCTCATATACGGCACAAGTGTTCC 285
QY 224 GACCTTCAGAAATTTTGACCGATTTCTTGGCTCCAAGTCTGGTACCGCGGCTCCCTGG 283
DB 286 GTTCTTCTGGAGTCCCTGTATGCTCTCTGTGGCTCATCTTGGGAACAAGCGGCTCA 345
QY 284 CCATCACTGGCTCCAGTCACTAGGATGAGGTGATATTAAGTCCAGTCTTATGACCA 343
DB 346 CCATCACTGGGCGCCAGGAGGATGATGAATCTGATTAATTTGTGTCTCTATAT---AGGC 402
QY 344 GCCTGAATCTCAGGTATTCGGAGGAGGACCCGCTGACCGTCTCTAGTTCAGGCCAAGG 403
DB 403 GTAGTGGCTCTTGGGTGTTCCGCGGAGGACCAAGCTGTCTAGTTCAGGCCAAGG 462

QY 404 CTGCCCCCTCGGTCACTCTGTTCCTCGCGCCCTCTCTGAGGAGCTTCAAGCCACAAGGCCA 463
DB 463 CTGCCCCCTCGGTCACTCTGTTCCTCGCGCCCTCTCTGAGGAGCTTCAAGCCACAAGGCCA 522
QY 464 CACTGGTGTGTCTCATTAAGTACCTTCTACCCGGGAGCGGTGACAGTGGCTTGAAGGCAG 523
DB 523 CACTGGTGTGTCTCATTAAGTACCTTCTACCCGGGAGCGGTGACAGTGGCTTGAAGGCAG 582
QY 524 ATAGCAGCCCGTCAAGCGGAGTGGAGACCAACACCCCTCCAAACAAGCAACAACA 583
DB 583 ATAGCAGCCCGTCAAGCGGAGTGGAGACCAACACCCCTCCAAACAAGCAACAACA 642
QY 584 AGTACGGCGCCAGCAGCTACCTGAGCTGAGCGCTGAGCAGTGGAGTCCACAGAGCT 643
DB 643 AGTACGGCGCCAGCAGCTACCTGAGCTGAGCGCTGAGCAGTGGAGTCCACAGAGCT 702
QY 644 ACAGCTGCCAGGTCAACGATGAAGGAGACCCGTGGAAGAGACAGTGGCGCCCTTACAGAAT 703
DB 703 ACAGCTGCCAGGTCAACGATGAAGGAGACCCGTGGAAGAGACAGTGGCGCCCTTACAGAAT 762
QY 704 GTTCAT 709
DB 763 GTTCAT 768

RESULT 11
US-09-152-060-46/c
; Sequence 46, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins.
; FILE REFERENCE: P2003PI.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (78)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (148)

Qy	437	CTGAGGAGCTTCAAGCCCAACAAGCGCACACTGGTGTGTTCTCATAAAGTGACTTCTACCCGG	496
Db	443	TCGAGAGAGCTTCAAGCCCAACAAGCGCACACTAGTGTGTTCTGATCAGTGACTTCTACCCGG	502
Qy	497	GAGCGGTGACAGTGGCTTGGAAGGCAGATAGCAGCCCGTCAAGGGGGGAGTGAGACCA	556
Db	503	GAGCTGTGACATTGGCTTGGAAGGCAGATGCGAGGCCGTCAAGCGGGAGTGGAGACCA	562
Qy	557	CCACACCTCTCAAAACAAGGCAACAACAGTACGGGCCACGACGTACTCTGAGCCTCAGCG	616
Db	563	ACAAACCTCTCAACAGCAGCAACAAGTACGGGGCCAGCAGCTACTTGAGCCTCAGCG	622
Qy	617	CTGAGCAGTGGAAAGTCCCAANGAGCTACAGCTGCGCAGGTCAAGCATGAAGGGAGCAGCG	676
Db	623	CCGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCCAGGTCAAGCATGAAGGGAGCAGCTG	682
Qy	677	TGGAGAAGACAGTGGCCCTTACAGAATGTTTCAT	709
Db	683	CAGAGAAGACGGTGGCCCTTGCAGAATGTTTCAT	715

QY 299 AGACTGAGGATGAGGCTGATTATTACTGACAGTCCCTATGACAGCAGCCTGAATGCTCAGG 358
Db 268 AGGCTGAGGACGAGGCTGATTATTACTGACGCTCATATACAGCAGC---AGCACTCTCG 212
QY 359 TATTGGGAGGAGCCCGCTGACCGTCTAGGTGAGCCCAAGGCTGCCCTCGGTCA 418
Db 211 TGTGTTGGCGGAGGAGCAAGCTGACCGTCTAGGTGAGCCCAAGGCTGCCCTCGGTCA 152
QY 419 CTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCA 478
Db 151 CTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCA 92
QY 479 TAAAGTGACTTCTACCGGAGCCGTGACAGTGGCTGGAAGCAGATAGCAGCCCGTCA 538
Db 91 TAAAGTGACTTCTACCGGAGCCGTGACAGTGGCTGGAAGCAGATAGCAGCCCGTCA 32
QY 539 AGCGGGAGTGGAGACCAACCAC 560
Db 31 AGCGGGAGTGGAGACCACTAC 10

RESULT 15
US-09-062-451-241/C
; Sequence 241, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,451
; FILING DATE: 04-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.419C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 241:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-062-451-241

Query Match 43.1%; Score 306.2; DB 4; Length 771;
Best Local Similarity 83.7%; Pred. No. 1.6e-75;
Matches 370; Conservative 0; Mismatches 66; Indels 6; Gaps 2;

QY 122 CTGTGACCTGGGAGCAGCCTCCAACTGGAGGTTA---TGATCTACATTGGTACCAAGCAGC 178
Db 448 CCTGCANTGGAACCAAGCAGCAGTGGTGGTGTATTAATATGTCNTGTGGTACCAACAGC 389

QY 179 TCCAGGAAGCGGCCCCAAACTCTCATCTATGACATTAAACAAGCAGCCTCAGGAATTT 238
Db 388 ACCAGGCAAGCCCCCAATTCATGATTTATGAGGTGCGTATCGGCCCTCAGGGGTTT 329
QY 239 CTGACCGATTTCTCTGGGTCCAACTCTGGGTACCGCGGCTCCCTTGGCCATCATCTGGGCTCC 298
Db 328 CTAATCGCTTCTCTGGGTCCAAAGTNTGGCAACACAGCGCTCCCTGACCATCTCTGGGCTCC 269
QY 299 AGACTGAGGATGAGGCTGATTATTACTGCGAGTCTCTATGACAGCAGCCTGAATGCTCAGG 358
Db 268 AGGTGAGGACGAGGCTGATTATTACTGACAGCTCATATACAAGCAGC---AGCACTCTCG 212
QY 359 TATTTCGGAGGAGGAGCCCGGCTGACCGTCTTAGGTGACGCCAAAGGCTGCCCTCGGTCA 418
Db 211 TGTGTTGGCGGAGGAGCAAGCTGACCGTCTTAGGTGACGCCAAAGGCTGCCCTCGGTCA 152
QY 419 CTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCA 478
Db 151 CTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCA 92
QY 479 TAAAGTGACTTCTACCGGAGCCGTGACAGTGGCTGGAAGCAGATAGCAGCCCGTCA 538
Db 91 TAAAGTGACTTCTACCGGAGCCGTGACAGTGGCTGGAAGCAGATAGCAGCCCGTCA 32
QY 539 AGCGGGAGTGGAGACCAACCAC 560
Db 31 AGCGGGAGTGGAGACCACTAC 10

Search completed: April 6, 2003, 06:26:26
Job time : 35.3734 secs

QY 541 GCGGAGTGGAGACACACACACACCTCCAAACAAAGCAACAAAGTACGCGCCAGCAGC 600
DB 535 GCGGAGTGGAGACACACACACCTCCAAACAAAGCAACAAAGTACGCGCCAGCAGC 594
QY 601 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTACG 660
DB 595 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTACG 654
QY 661 CATGAAGGAGCAGCAGCTGAGAGACAGTGGCCCTACAGATGTTTCATGA 711
DB 655 CATGAAGGAGCAGCAGCTGAGAGACAGTGGCCCTACAGATGTTTCATGA 705

RESULT 13

AAV35484
ID AAV35484 standard; DNA; 705 BP.

XX AAV35484;

XX 29-SEP-1998 (first entry)

XX Macaque primatized 7C10 light chain DNA.

XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation; ss.
XX Macaca fascicularis.

XX Key Location/Qualifiers

FH 1..705

FT CDS /tag= a

FT /product= 7C10 light chain

XX WO9819706-A1.

XX 14-MAY-1998.

XX 29-OCT-1997; 97WO-US19906.

XX 08-NOV-1996; 96US-0746361.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Brams P, Hanna N;

XX WPI; 1998-286601/25.

DR P-PSDB; AAW63760.

XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PT cells, e.g. graft rejection or tumours

XX Example 7; Fig 3a; 87pp; English.

XX This sequence encodes a primatized form of the antibody 7C10 light chain
CC from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC MAB's are specific immunosuppressants for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC MAB can be conjugated to a drug or toxin. MAB's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotypic reagents. MAB's are optionally combined with other proteins

CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.

XX Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

QY Query Match 76.0%; Score 540.2; DB 19; Length 705;

DB Best Local Similarity 86.1%; Pred. No. 3.2e-128;

XX Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGGTCCCGCTCAGCTCTCTGGGGCTCTCTGCTCTCTGCTCCAGGTGACCATGT 60

DB 1 ATGAGGGTCCCGCTCAGCTCTCTGGGGCTCTCTGCTCTCTGCTCCAGGTGACCATGT 60

QY 61 GAGTCTGTCTGTACACAGCGCCCTCAGTGTCTGGGGCCCGGAGGAGGTACCATC 120

DB 61 GCCTATGAACCTGACTCAGCCACCTCGGTGTCTGCTCTCTGCTCCAGGACGCGGAGATC 120

QY 121 TCGTGCACCTGGGAGACACCTCCCAACATTGGAGGTATGATCTACATTTGGTACACAGCATC 180

DB 121 ACCTGTGGGG-----AGACAACAGTAGAATGATATGTCCACTGGTACACAGCAAG 174

QY 181 CAGGGAACGGCCCCCAAACTCTCTATGATGATTAACAAGCGACCTCAGGAATTTCT 240

DB 175 CCAGCGCGGGCCCTTACTTGGTCTATGATGATGATGACCGGCCCTCAGGGATCCCT 234

QY 241 GACCGATTCTCTGGCTCCCAAGTCTGTCGCGGCTCTCTGCTCCAGGTGACCATC 300

DB 235 GACGGAATCTCTGGCTCCCAATCAGGGAACACCGCCACCTGACCATCAACGGGTGAG 294

QY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGAGCCTGAATGCTCAGGTA 360

DB 295 GCCGGGATGAGGCTGACTATTACTGTGAGGTGTGGACAGGGCTAGTATCATCCGGTC 354

QY 361 TTCGAGGAGGAGACCGGCTGACCGTCTCTAGTGTACGCCCAAGGCTGCCCTCGGTCACT 420

DB 355 TTCGAGGAGGAGACCGGCTGACCGTCTCTAGTGTACGCCCAAGGCTGCCCTCGGTCACT 414

QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCATA 480

DB 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCATA 474

QY 481 AGTGACTTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGAGCCCCGCTCAAG 540

DB 475 AGTGACTTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGAGCCCCGCTCAAG 534

QY 541 GCGGAGTGGAGACACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600

DB 535 GCGGAGTGGAGACACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 594

QY 601 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTGACG 660

DB 595 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTGACG 654

QY 661 CATGAAGGAGCAGCAGCTGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711

DB 655 CATGAAGGAGCAGCAGCTGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705

RESULT 14

AAAS17242

ID AAAS17242 standard; DNA; 705 BP.

XX AAAS17242;

XX 12-MAR-2002 (first entry)

XX DNA sequence of a primatized form of the light chain of 7C10 antibody.

XX Human; macaque monkey; light chain; primatized antibody; 7C10 antibody;
KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;

KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW graft-vs-host disease; immunosuppression; organ rejection;
KW interleukin-2; IL-2; mutant; ds.

XX Chimeric - Homo sapiens.
OS Chimeric - Macaca sp.
OS Synthetic.

XX Key Location/Qualifiers
FH 1..705
FT CDS /tag= a
FT /product= "Light chain of 7C10 antibody"

PN WO200189567-A1.

PD 29-NOV-2001.

PF 22-MAY-2001; 2001WO-US16364.

XX 22-MAY-2000; 2000US-0576424.

XX (IDEC-) IDEC PHARM CORP.

PI Anderson DR, Hanna N, Brams P;

XX WPI: 2002-089895/12.

DR P-PSDB; AAU11538.

XX Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT treating cancer, graft-vs-host disease and autoimmune disease as
PT allergy -

XX Example 8; Fig 3a; 89pp; English.

XX The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,
CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host disease. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present nucleic
CC acid sequence encodes the light chain of 7C10, a primatised antibody
CC used in the invention to induce apoptosis and inhibit production of
CC interleukin-2 (IL-2).

SQ Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match 76.0%; Score 540.2; DB 24; Length 705;

Best Local Similarity 86.1%; Pred. No. 3.2e-128;

Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGTCCTCCGCTCAGCTCCTGGGGCTCCTGCTGCTGCTCCAGGTGCACGATGT 60

Db 1 ATGAGGTCCTCCGCTCAGCTCCTGGGGCTCCTGCTGCTGCTCCAGGTGCACGATGT 60

QY 61 GAGTCTGCTGTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAGTCCACATC 120

Db 61 GCCTATGAACCTGACTCAGCCACCTCGGTGTCTAGTGTCCCGAGGACAGACGCCAGGATC 120

QY 121 TCGTGACTGGGAGCCTCCAACTTGAGGTTATGATCTACATTGTTACGAGGATC 180

Db 121 ACCTGTGGGGG-----AGACACAGTAGAATAATGATCTCACTGGTACCAGCAGAG 174

QY 181 CCAGGAACCGCCCCCAAACTCCTCATCTATGACATTAAACAAGCGACCCCTCAGGAATTTCT 240

Db 175 CCAGCGGGGGCCCTATATCTGGTTCATCTATGATAGTAGACCGGGCCCTCAGGGATCCCT 234

QY 241 GACCGATTCTTGGCTCCAAAGTCTGTACCGGGCTCCTCGGCCCATCACTGGGTCCAG 300

Db 235 GAGCGATTCTTGGCTCCAAATCAGGGAAACCGGCCACCTGACCATCAACGGGGTCGAG 294

QY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGCAGCCCTGAATGCTCAGGTA 360

Db 295 GCGGGATGAGGCTGACTTATTCTGAGGTGTGGACAGGGCTAGTATCATCGGTC 354

QY 361 TTCGAGGAGGGACCCGGGTGACCCCTCTAGGTTCAGCCCAAGGCTGCCCTCGGTCACT 420

Db 355 TTCGAGGAGGGACCCGGGTGACCCCTCTAGGTTCAGCCCAAGGCTGCCCTCGGTCACT 414

QY 421 CTGTTCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTCTCATA 480

Db 415 CTGTTCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTCTCATA 474

QY 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAGATAGAGCCCGCTCAAG 540

Db 475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAGATAGAGCCCGCTCAAG 534

QY 541 GCGGGAGTGGAGACCAACACCCCTCCAAACAAGCAACAAGTACCGGGCCAGCAGC 600

Db 535 GCGGGAGTGGAGACCAACACCCCTCCAAACAAGCAACAAGTACCGGGCCAGCAGC 594

QY 601 TACCTGAGCTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTCCAG 660

Db 595 TACCTGAGCTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTCCAG 654

QY 661 CATCAAGGAGGACCCGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCATGA 711

Db 655 CATGAAGGAGGACCCGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCATGA 705

RESULT 15

AAV11293

ID AAV11293 standard; cDNA; 651 BP.

XX AAV11293;

DT 27-AUG-1998 (first entry)

XX Antibody HB4C5 light chain encoding cDNA.

XX Antibody light chain; carboxypeptidase; bovine pancreas; cancer;

XX porcine pancreas; radioimmunoinaging; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FH 1..651

FT /tag= a

FT /product= "Antibody HB4C5 light chain"

FT /note= "the start and stop codons are not indicated"

XX JF10075791-A.

PN 24-MAR-1998.

XX 30-AUG-1996; 96JP-0246825.

XX 30-AUG-1996; 96JP-0246825.

XX (MOMI) MORINAGA & CO LTD.

XX WPI; 1998-244364/22.

XX P-PSDB; AA40533.

XX New antibody light chain or its fragment - useful for preparation of

PT therapeutic(s) or cancer radio-immuno-imaging agent(s)

XX		
PS	Claim 12; Fig 9; 20pp; Japanese.	
XX		
CC	This cDNA encodes a antibody HB4G5 light chain. This antibody light chain or its fragment is specific for carboxypeptidase from bovine or porcine pancreas and is reactive with human cancer tissue. The antibody light chain and its fragment can be used for preparation of a cancer radioimmunimaging reagent and therapeutic compositions.	
CC		
XX		
SQ	Sequence 651 BP; 160 A; 207 C; 164 G; 120 T; 0 other;	
Query Match	75.0%; Score 533.2; DB 19; Length 651;	
Best Local Similarity	89.8%; Pred. No. 1.9e-126;	
Matches 584; Conservative	0; Mismatches 63; Indels 3; Gaps 1;	
QY	62 AGTCTGTCTGTGACAGCGCGCCTCAGTGTCGTGGGGCCCCAGGCGCAAGGTCAACCATCT 121	
Db	2 AGTCTGTGTGACGAGCGGCCCTCAGTGTCGTGGGCCCCAGGACAGAAGTCACCATCT 61	
QY	122 CGTGCACTGGGAGCACCTCCAATTGGAGGTTATGATCTACATTTGGTACCAAGACTCC 181	
Db	62 CTGTGCTCTGGAAACAAGCTCCAACATTGGGAATAATTATGTATCTGTGCAGCACTCC 121	
QY	182 CAGGAACGGCCCCAAAATCTCATCTATGACATTACAGCGGACCTCAGGAATTTCTG 241	
Db	122 CAGGAACAGCCCCCAAATCTCTCATTTATGACAATAAAGCGGACCTCAAGTATTTCTTG 181	
QY	242 ACCGATTTCTTGGCTTCCAAGTCTGGTAGCGGGCCTCCCTGGCCATCCTCTGGGCTCCAGA 301	
Db	182 ACCGATTTCTTGGCTTCCAAGTCTGGCACGTCTGCCACCTGGGCATCACGGACTCCAGA 241	
QY	302 CTGAGATGAGGCTGATTTATCTGCCAGTCTTAATGACAGAGCCTGAATG---CTCAGG 358	
Db	242 CTGGGACAGGCGCATATTACTCGCAACAATGGAATAGCATCTCCGTGTCAATTGSC 301	
QY	359 TATTTCGGAGGAGGACCGGCTGACCGTCTAGCTGACGCCAACAGGCTGCCCTCGGTCA 418	
Db	302 TGTTCCGGAGGGAGCTAAACTGACCGTCTTAGTTCAGGCCAAGGCTGCGCCCTCGGTCA 361	
QY	419 CTCGTGTTCCGCCCTCTCTTGAGGAGCTTCAAGGCCAACAGGCCACACTGGTGTCTCA 478	
Db	362 CTCGTGTTCCGCCCTCTCTTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTCTCA 421	
QY	479 TAAGTGACTTTACCGGGAGCCGTGACAGTGGCTCTGGAAGGACAGATAGCAGGCCCGTCA 538	
Db	422 TRAAGTGACTTCTACCGGGAGCCGTGACAGTGGCTCTGGAAGGACAGATAGCAGGCCCGTCA 481	
QY	539 AGCGGGAGTGAGACACCAACCCCTCCAAACAAGCAACACAGTACCGGGCCAGCA 598	
Db	482 AGCGGGAGTGAGACACCAACCCCTCCAAACAAGCAACAAAGTACGGGGCCAGCA 541	
QY	599 GCTACTGTGAGCTGACGCTCTGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTGCCAGGTCA 658	
Db	542 GCTACTGTGAGCTGACGCTCTGAGCAGTGGAAAGTCCCACAGAGCTACAGCTGCCAGGTCA 601	
QY	659 CGCATGACGGAGCAACCGTGGAGAAAGACAGTGGCCCCCTACAGAAATGTCA 708	
Db	602 CGCATGACGGAGCAACCGTGGAGAAAGACAGTGGCCCCCTACAGAAATGTCA 651	

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:54 ; Search time 1353.28 Seconds
(without alignments)
8508.978 Million cell updates/sec

Title: US-09-758-173-9

Perfect score: 711

Sequence: 1 ATGAGGTCCCGCTCAGCT.....CCCTACAGAATGTTTCATGA 711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_estba:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estro:*

9: gb_est1:*

10: gb_est2:*

11: gb_hrc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_othr:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569.2	80.1	956	14	BQ711292
2	562.6	79.1	913	14	BQ708635
3	559	78.6	894	14	BQ708570
4	558.6	78.6	819	12	BQ708564
5	557.8	78.5	873	14	BQ712653
6	555.6	78.1	755	12	BQ755185

7	552.2	77.7	1007	14	BM920020
8	552.2	77.7	1060	14	BM906351
9	551.6	77.6	910	12	BQ757147
10	549.4	77.3	857	14	BQ890529
11	549	77.2	764	12	BQ755548
12	546	76.8	817	13	B1835917
13	545.4	76.7	896	12	BQ685967
14	544.8	76.6	823	12	BQ686957
15	544.6	76.6	849	12	BQ756887
16	544.6	76.6	1124	14	BM918688
17	541.8	76.2	900	12	BQ663927
18	541.6	76.2	936	14	BQ709123
19	539.8	75.9	832	13	B1819072
20	539	75.8	774	12	BQ398461
21	538.6	75.8	948	12	BQ757977
22	538.4	75.7	870	12	BQ684025
23	538.2	75.7	873	12	BQ686011
24	537.4	75.6	935	12	BQ755314
c	537	75.5	868	12	BQ745909
25	537	75.5	701	12	BQ398176
26	535.6	75.3	947	13	B1819216
27	535.4	75.3	964	12	BQ758242
28	532.2	74.9	902	14	BQ883560
29	532.2	74.9	792	12	BQ760202
30	529.6	74.5	813	12	BQ755102
31	529.6	74.5	783	13	BM007830
32	529.4	74.5	783	13	BM007830
33	527	74.1	894	14	BQ709510
34	519.8	73.1	911	12	BQ398014
35	519.6	73.1	767	13	B1836367
36	519	73.0	695	14	BM831144
37	517.8	72.8	886	12	BQ758124
38	517.2	72.7	617	10	BE140138
39	517.2	72.7	1030	14	BM921377
40	516.6	72.7	856	10	BE561313
41	515.4	72.5	918	13	B1823305
42	514.2	72.3	823	13	B1819711
43	510.2	71.8	842	12	BF338856
44	510	71.7	718	12	BQ759998
45	509.8	71.7	869	10	BE562370

ALIGNMENTS

RESULT 1
BQ711292
LOCUS AGENCOURT_8353826 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278335
DEFINITION 5', mRNA sequence.
ACCESSION BQ711292
VERSION BQ711292.1 GI:21850191
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 956)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LLCN2466 row: c column: 08
High quality sequence start: 10
High quality sequence stop: 655.

FEATURES

Location/Qualifiers

[illegible]

LOCUS	913 bp	mRNA	EST 16-JUL-2002
BQ708635			
BQ708635	913 bp	mRNA	EST 16-JUL-2002


```
QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCGCACACTGGTGTCTCATA 480
Df 456 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCGCACACTGGTGTCTCATA 515
QY 481 AGTGACTTCTACCCGGGAGCGGTGACAGTGGCGCTTGAAGGCGAGATAGCAGCCCGTCAAG 540
Df 516 AGTGACTTCTACCCGGGAGCGGTGACAGTGGCGCTTGAAGGCGAGATAGCAGCCCGTCAAG 575
QY 541 GCGGAGTGGAGACACACACACCTCCAAACAAAGCAACAAAGTACGCGCGCAGCAGC 600
Df 576 GCGGAGTGGAGACACACACACCTCCAAACAAAGCAACAAAGTACGCGCGCAGCAGC 635
QY 601 TACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCACAGTCAAG 660
Df 636 TACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCACAGTCAAG 695
QY 661 CATGAAGGGAGCAGCGTGGAGAGACAGTGG-CCCTCAGAGTGTTCAT 709
Df 696 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTCAGAGTGTTCAT 745

RESULT 3
B0708570
LOCUS B0708570 894 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT.7976221 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214845
5', mRNA sequence.
ACCESSION B0708570
VERSION B0708570.1 GI:21847469
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 894)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2382 row: m column: 22
High quality sequence start: 11
High quality sequence stop: 654.
FEATURES
Location/Qualifiers
source 1..894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6214845"
/clone.lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 209 a 291 c 217 g 168 t 9 others
ORIGIN
Query Match 78.6%; Score 559; DB 14; Length 894;
Best Local Similarity 90.2%; Pred. No. 2.3e-139;
Matches 598; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 47 CAGGTGCAGGATGTGAGTCTGCTTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
```

```
Df 65 CAGGGCTCTGGGGCCAGTCTGTGCTGACTCAGCCACCTCAGCGCTGGAGCCCGGGC 124
QY 107 AGAAGGTCAACATCTCTGTCACCTGGGAGCACCTCCAAACATTGGAGGTATGATCTACATT 166
Df 125 AGAGGTCAACATCTCTGTTCTGGAAGCAGCTCCAAACATCGGAAGTATCTCTAACT 184
QY 167 GGTACCAAGCAGCTCCAGGAACCGCCCCCAAACTCTCTATATGACATTAACAAGCGAC 226
Df 185 GGTACCAAGCAGCTCCAGGAACCGCCCCCAAACTCTCTATATGATTAATAACAGCGGC 244
QY 227 CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCTCTCCCTGGCCA 286
Df 245 CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCAGCTCAGCGCTCCCTGGCCA 304
QY 287 TCACTGGGCTCCAGAGTGAAGTGAAGTGAATTTATTTACTGCCAGTCTCTATGACAGCGC 346
Df 305 TCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTTATTTACTGTGCAGCATGGGATGACAGC 364
QY 347 TGAATGCTCAGGTATTTCCGAGGAGGACCGCGCTGACCGTCTCTAGTTCAGCCCAAGGCTG 406
Df 365 TGAATGCTGTGTTATTTCCGCGAGGAGCAAGCTGACCGTCTCTAGTTCAGCCCAAGGCTG 424
QY 407 CCCCTCGGTCACTCTGTTCCCGCTCTCTGAGGAGCTTCAAGCCAAAGGCCACAC 466
Df 425 CCCCTCGGTCACTCTGTTCCCGCTCTCTGAGGAGCTTCAAGCCAAAGGCCACAC 484
QY 467 TGGTGTGCTCTATAAGTGAATCTACCGGGAGCGCTGACAGTGGCTTGAAGGCGAGATA 526
Df 485 TGGTGTGCTCTATAAGTGAATCTACCGGGAGCGCTGACAGTGGCTTGAAGGCGAGATA 544
QY 527 GCAGCCCCGTCAAGGGCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGT 586
Df 545 GCAGCCCCGTCAAGGGCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGT 604
QY 587 ACAGGGCGCAGCAGCTACCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAGCTTACA 646
Df 605 ACAGGGCGCAGCAGCTATCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAGCTTACA 664
QY 647 GCTGCCAGGTCAAGCATGAGGAGGAGCAGCTGGAGAGACAGTGGCCCTTACAGATGTT 706
Df 665 GCTGCCAGGTCAAGCATGAGGAGGAGCAGCTGGAGAGACAGTGGCCCTTACAGATGTT 724
QY 707 CAT 709
Df 725 CAT 727

RESULT 4
B0685644
LOCUS B0685644 819 bp mRNA linear EST 01-MAY-2001
DEFINITION B0685644
mRNA sequence.
ACCESSION B0685644
VERSION B0685644.1 GI:13917041
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
```


Db	322	5CTGAGGATGAGGCTGATTATTA	CTTCGCGAGTCTCTTA	TGACAGCAGCGCTGAGTGGGGTGATG	381
Qy	361	TTGCGAGGAGGACCGCGCTGACCGCTCT	AGGTGAGCCCAAGGCTGCCCCCTCGGTCACT	420	
Db	382	TTGCGCGAGGAGCAAGCTGACCGTCT	AGGTGAGCCCAAGGCTGCCCCCTCGGTCACT	441	
Qy	421	CTGTTCCCGCCCTCTCTTGAGAGGCTT	CAAGCCAAACAAGGCCACACTGGTGTGTCATA	480	
Db	442	CTGTTCCCGCCCTCTCTTGAGAGGCTT	CAAGCCAAACAAGGCCACACTGGTGTGTCATA	501	
Qy	481	AGTGACTTCTACCCGGGAGCCGTGACAGT	GCCTTGGAGGCGAGTAGCAGCCCGGTCAAG	540	
Db	502	AGTGACTTCTACCCGGGAGCCGTGACAGT	GCCTTGGAGGCGAGTAGCAGCCCGGTCAAG	561	
Qy	541	GCGGAGTGGAGACCAACACACACCTCT	CCAAACAAGGCCAAACAAGTACGCGGCAGCAGC	600	
Db	562	GCGGAGTGGAGACCAACACACACCTCT	CCAAACAAGGCCAAACAAGTACGCGGCAGCAGC	621	
Qy	601	TACCTGAGCTTGACCGCTGAGAGTGGAA	GTGCCACAGAAGCTACAGTGCAGGTCAAG	660	
Db	622	TATCTGAGCCTGACGCTTGAGCAGTGG	AAATCCCA-AAAGCTACAACTGGCAGGTCAAG	680	
Qy	661	CATGAAGGAGCACCGCTGCGAAGACAGT	GCCCTACAGATGTTTCAT	709	
Db	681	CATGAAGGAGCACCGCTGCGAAGACAGT	GCCCTACAGATGTTTCAT	729	
RESULT	6				
LOCUS	BG755185		755 bp	linear	EST 15-MAY-2001
DEFINITION	602714114F1 NIH_MGC_48 Homo sapiens		cdna clone IMAGE:4854290 5',		
ACCESSION	BG755185		mRNA sequence.		
VERSION	BG755185.1		GI:14065838		
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbe@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cdna Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LUCM1701 row: 1 column: 03 High quality sequence stop: 753.				
FEATURES	Location/Qualifiers				
source	1. 755 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4854290" /clone_lib="NIH_MGC_48" /tissue_type="Primary B-cells from tonsils (cell line)" /lab_host="DH10B (phage-resistant)" /note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."				
BASE COUNT	165 a	249 c	203 g	138 t	
ORIGIN					

[illegible]

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12779 row: o column: 14
High quality sequence stop: 712.

FEATURES

source
1. .1007
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5749861"
/lab_host="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH MGC Library."
BASE COUNT 253 a 336 c 232 g 173 t 13 others
ORIGIN

Query Match 77.7%; Score 552.2; DB 14; Length 1007;
Best Local Similarity 86.2%; Pred. No. 1.6e-137;
Matches 611; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCGCTCAGCTCTCTGGGGCTCTGCTGCTCCAGGTCCAGATGT 60
DB 29 ATCATGACTGTCTCCCTCTCTCTCCACCTTCTCATTTACTGCACAGGGTCTGGGCC 88
QY 61 GAGTCTGTCTGACACAGCGCGCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCCACCATC 120
DB 89 CAGTCTGTGTGAGCGCAGCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCCACCATC 148
QY 121 TCGTGACCTGGGAGCAGCTCCAACTTGAAGGTTATGATCTACATTTGTACAGCAGCTC 180
DB 149 TCGTGTCTGGAAGGAGCTCCAACTTGAAGGTTATGATTTATGTCTCTGGTATCAGCAGTTC 208
QY 181 CCAGGAACGGCCCCAACTCTCATTTATGACATTTAAACAGCGACCTTCAGGAATTTCT 240
DB 209 CCAGGAGCAGCCCCCACTCTCATTTAAGATGATGACGACCTTCAGGATTTCT 268
QY 241 GACCGATTCTCTGGCTCCAAAGTCTGGTACCGGGCTCTCTGGCCATCAGTGGGTCACG 300
DB 269 GACCGATTCTCTGGCTCCAAAGTCTGGCAGCTCAGCCACCTTCGCCATCAGCGGACTCCAG 328
QY 301 ACTGAGATGAGGTGATTTATTCTGCCAGTCTGTATGACAGCAGCGCTGATGCTCAGGTA 360
DB 329 ACTGAGGAGGAGCGGCGAATCTACTTCGGAACATGGGATACCGAGCTGACTCTGGGGT 388
QY 361 TTCGAGGAGGAGCGCGGTGACCGCTTAGTTCAGCCCAAGGCTGCCCTCGGTCTACT 420
DB 389 TTCGGCGGTGGACCAACTGACCGTTCCTAAGTACGCCCAAGGCTGCCCTTCGGTCTACT 448
QY 421 CTGTTCGCCCTCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCAT 480
DB 449 CTGTTCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCAT 508
QY 481 AGTGACTTCAACCGGAGCGGTGACAGTGGCTTGAAGGAGATAGACGCCCTCGCAAG 540
DB 509 AGTGACTTCAACCGGAGCGGTGACAGTGGCTTGAAGGAGATAGACGCCCTCGCAAG 568
QY 541 GCGGAGTGGAGACCAACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
DB 569 GCGGAGTGGAGACCAACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 628
QY 601 TACCTGAGCTGACGCTGAGCAGTGGAAAGTCCCAAGAGGTACAGCTGCGAGGTACG 660

Db 629 TATCTGAGCTGACGCTGAGCAGTGGAAAGTCCACAGAGCTTACAGTGCACAGGTCAAG 688
QY 661 CATCAAGGGAGCACCCTGGAGAGACAGTGGCCCTTACAGAATGTTTCAT 709
Db 689 CATCAAGGGAGCACCCTGGAGAGACAGTGGCCCTTACAGAATGTTTCAT 737

RESULT 8

LOCUS BM906351 1060 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6620012 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590299
5', mRNA sequence.
ACCESSION BM906351
VERSION BM906351.1 GI:19356730
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1060)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12364 row: g column: 04
High quality sequence stop: 729.

FEATURES

source
1. .1060
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5590299"
/clone_lib="NIH_MGC_125"
/lab_host="DH10B"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
BASE COUNT 257 a 338 c 259 g 204 t 2 others
ORIGIN

Query Match 77.7%; Score 552.2; DB 14; Length 1060;
Best Local Similarity 86.2%; Pred. No. 1.6e-137;
Matches 611; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCGCTCAGCTCTCTGGGGCTCTGCTGCTCCAGGTCCAGGTGACCATGT 60
DB 49 ATCATGACTGTCTCCCTCTCTCTCCACCTTCTCATTTACTGCACAGGGTCTCTGGGC 108
QY 61 GAGTCTGTCTGACACAGCGCGCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTTCACCATC 120
DB 109 CAGTCTGTGTGAGCAGCGCGCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTTCACCGTC 168
QY 121 TCGTGACCTCGGAGCAGCTCCAACTTGAAGGTTATGATCTACATTTGGTACCAAGCAGCTC 180
DB 169 TCCTGTCTCGAAGCAGTGCACATTTGGAGTAATTTAGTTTCTCTGGTACCAACACCTC 228
QY 181 CCAGGAACGGCCCCAACTCTCATTTATGACATTTAAACAGCGACCTTCAGGAATTTCT 240
DB 229 CCAGGGGCGACGCCCCCTACTCTCATTTATGACAAATAAAGCGACCCCTCAGGAATTCCT 288

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM2520 row: c column: 19
 High quality sequence stop: 552.

FEATURES
 source
 1. 857
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6302538"
 /clone_lib="NIH MGC 113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 183 a 286 c 235 g 153 t
 ORIGIN

Query Match 77.3%; Score 549.4; DB 14; Length 857;
 Best Local Similarity 91.0%; Pred. No. 8.5e-137;
 Matches 607; Conservative 0; Mismatches 56; Indels 4; Gaps 2;

Qy 47 CAGGTGCACGATGTGAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGCG 106
 Db 72 CAGGGTCTTGGGCCCATCTGTGCTGACGAGCGCCCTCAGTGTCTGGGGCCCCAGGCG 131
 Qy 107 AGAAGTCCACATCTCGTGCATCTGGAGCAGCTCCACATTTGG---AGTTATGATCTAC 163
 Db 132 AGAGGGTCCACCATCTCTGTCACATGGGAGCAGGTCCACATCTGGGGCAGGTTATGATGTAC 191
 Qy 164 ATTGGTACACGAGCTCCGAGGAGCGGCCCAACTCCTCATCTATGACATTAACAAGC 223
 Db 192 AGTGTACACGACATTCACAGGACAGCCCCCAACTCCTCATCTGCTAGCAGCAATC 251
 Qy 224 GACCCCTCAGGAATTTCTGACCGATTTCTCTGCTCCAAAGTCTGGTACCGCGCTCCCTCGG 283
 Db 252 GGCCCTCAGGGTCCCTGACCGATTTCTCTGCTCCAAAGTCTGGCAGCTCAGCCTCCCTCGG 311
 Qy 284 CCATCATCTGGGCTCAGCATGAGATGAGGTGATTATTACTGCCAGTCTCTATGACAGCA 343
 Db 312 CCATCATCTGGGCTCCAGGCTGACATGAGGTGATTATTACTGCCAGTCTCTATGACGGCA 371
 Qy 344 GCCTGATGCTCAGGTATTTCGAGAGAGGAGCCCGGCTGACCGTCTTAGTTCAGCCCAAG 403
 Db 372 GCCTGAGTGTGTGGTATTTCGGCGGAGGACCAAGCTGACCGTCTTAGTTCAGCCCAAG 431
 Qy 404 CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCTCTGTAGGAGCTTCAAGCAACAAGGCCA 463
 Db 432 CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAAGGCCA 491
 Qy 464 CACTGGTGTCTCATTAAGTGACTTCTACCGGGAGCGGTGACAGTGGCTTGGAGGCGAG 523
 Db 492 CACTGGTGTGTCTCATAAGTGAATTTCTACTGGGAGCGGTGACAGTGGCTTGGATGGCAA 551
 Qy 524 ATAGCAGCCCGGTCAAGGGCGGAGTGGAGACCAACACACCCTCCAAACAAGCAACAACA 583
 Db 552 ATAGCAGCCCGGTCAAGGGCGGAGTGGAGACCAACACACCCTCCAAACAAGCAACAACA 611
 Qy 584 AGTACGCGGCGCAGCAGCTACTCCTGAGCCTGACCGCTGAGCAGTGGAAAGTCCCAAGAGCT 643

159	Db	159	YCTGCTCTGGAAGCAGGTC	CAACATTGGGGAATAATATGTCCTGGTACAGACGCTC	218
181	Qy	181	CCAGGAACGCGCCCAACAT	CTCATCTATGACATTAAACAAGCGACCCCTCAGGAATTTCT	240
219	Db	219	CCAGGTACAGCCCGGAAC	TCTCATCTATGANAATAGTAAGCGACCTCCTCAGGGAATCTT	278
241	Qy	241	GACCGATTCTCTGGCTCCA	AGTCTGTGTAACGCGGCGCTCCTCGTGCCATCACTCGGCGTCCAG	300
279	Db	279	GACCGATTCTCTGGCTCCA	AGTCTGTGCACTGACGCGCCCTCGGCCATCACCGCACTCCAG	338
301	Qy	301	ACTGAGGATCAGCGTGATT	AATTACTGCCAGTCTCTATGACAGCAGCGCTGAATGCTCAGTA	360
339	Db	339	ACTGGGACGAGGCGCGATT	AATTACTGCGGAACATGGATGACAGCGCTCGTGCTGGGGTG	398
361	Qy	361	TTCCGAGGAGGAGCCCGG	CTGACGCTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT	420
399	Db	399	TTCCGCGAGGAGCCAAAC	TGACCGTCTGAGTCAGCCCAAGGCTGCCCCCTCGGTCACT	458
421	Qy	421	CTGTTCCCGCCCTCTCTG	TAGGAGCTTCAAGCCAAACAAGGCCACACTGCTGTGTCTCAT	480
459	Db	459	CTGTTCCCGCCCTCTCTG	TAGGAGCTTCAAGCCAAACAAGGCCACACTGCTGTGTCTCAT	518
481	Qy	481	AGTGACTTCTACCGGGAG	CCGTGACAGTGGCTCGAAGCAGATAGCAGCCCCGTCAAG	540
519	Db	519	AGTGACTTCTACCGGGAG	CCGTGACAGTGGCTCGAAGCAGATAGCAGCCCCGTCAAG	578
541	Qy	541	GCGGGAGTGGAGACCA	CCACCTCCAAACAAGCAACAACAAGTACGCGCCACGACG	600
579	Db	579	GCGGGAGTGGAGACCA	CCACCTCCAAACAAGCAACAACAAGTACGCGCCACGACG	638
601	Qy	601	TACCTGAGCCTTGACG	CTTGAGCAGTGGAGTCCCAACAAGAGCTTACAGCTGCCAGGTCCAG	660
639	Db	639	TACCTGAGCCTTGACG	CTTGAGCAGTGGAGTCCCAACAAGAGCTTACAGCTGCCAGGTCCAG	698
661	Qy	661	CATGAAGGAGACCGCTG	GAGAGACAGTGGCCCTCTACGAATGTTTCAT	709
699	Db	699	CATGAAGGAGACCGCTG	GAGAGACAGTGGCCCTCTACGAATGTTTCAT	747

BI835917	BI835917	817 bp	linear	EST 04-OCT-2001
LOCUS	603085650F1 NIH_MGC_120	Homo sapiens	cdna clone	IMAGE:5224645 5',
DEFINITION	603085650F1 NIH_MGC_120	Homo sapiens	cdna clone	IMAGE:5224645 5',
				RNA sequence.

ACCESSION BI835917

ACCESSION
VERSION
BI835917.1
GT:15947467

VERSION
KEYWORDS
EST
BIBS

KEYWORDS	EST.
SOURCE	human

SOURCE	ORGANISM	HOMO PARIENTIS	MILLER
1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
8	8	8	8
9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
13	13	13	13
14	14	14	14
15	15	15	15
16	16	16	16
17	17	17	17
18	18	18	18
19	19	19	19
20	20	20	20
21	21	21	21
22	22	22	22
23	23	23	23
24	24	24	24
25	25	25	25
26	26	26	26
27	27	27	27
28	28	28	28
29	29	29	29
30	30	30	30
31	31	31	31
32	32	32	32
33	33	33	33
34	34	34	34
35	35	35	35
36	36	36	36
37	37	37	37
38	38	38	38
39	39	39	39
40	40	40	40
41	41	41	41
42	42	42	42
43	43	43	43
44	44	44	44
45	45	45	45
46	46	46	46
47	47	47	47
48	48	48	48
49	49	49	49
50	50	50	50
51	51	51	51
52	52	52	52
53	53	53	53
54	54	54	54
55	55	55	55
56	56	56	56
57	57	57	57
58	58	58	58
59	59	59	59
60	60	60	60
61	61	61	61
62	62	62	62
63	63	63	63
64	64	64	64
65	65	65	65
66	66	66	66
67	67	67	67
68	68	68	68
69	69	69	69
70	70	70	70
71	71	71	71
72	72	72	72
73	73	73	73
74	74	74	74
75	75	75	75
76	76	76	76
77	77	77	77
78	78	78	78
79	79	79	79
80	80	80	80
81	81	81	81
82	82	82	82
83	83	83	83
84	84	84	84
85	85	85	85
86	86	86	86
87	87	87	87
88	88	88	88
89	89	89	89
90	90	90	90
91	91	91	91
92	92	92	92
93	93	93	93
94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

ORGANISM HOMO SAPIENS
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

REFERENCE 1 (bases 1 to 817)
Mammalia; Eutheria;

REFERENCE
1 (bases 1 to 817)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institute

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cdNA Library Preparation: Life Technologies, Inc.

cdNA Library Arrayed by: The I.M.A.G.E.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M

<http://image.llnl.gov>

plate: L1AM11565 row: c column: 7

High quality sequence stop:

FEATURES

FEATURES	LOCATION/Qualifiers
SOURCE	1 817

[illegible]

```

db ref="taxon"
organism="Homo sapiens"

```

```
/ab_xref="taxon:9606"
/align="IMAGE-5234645"
```

```
/clone="IMAGE:5224645"
```

RESULT 13

RESUL 13
RG685967

100110
100000

LOCUS
DEFINITION

DEFINITION

ACKNOWLEDGMENTS

ACCESSION
NUMBER

PC695967 996 bp mpNA Linear EST 01-MAY-2001

BG68596 / NTH MCC 48 Homo sapiens CDNA clone IMAGE:4766335 5', 896 bp mRNA linear ESI UI-MAY-2001

602638530FI NI
mRNA 602638530FI NI

mRNA sequ

BG685967

8968

/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

human.
homo sapiens
• Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 896)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC1626 row: k column: 08
High quality sequence stop: 878.
Location/Qualifiers
1..896
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:476635"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally, cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 213 a 287 C 231 g 164 t 1 others
ORIGIN

Query Match 76.7% Score 545.4; DB 12; Length 896;
Best Local Similarity 88.2%; Pred. No. 1e-135;
Matches 628; Conservative 0; Mismatches 77; Indels 7; Gaps 3;

Db	459	ACTCTGTTCCGGCCCTCTCTGAGGAGCTTCAAGCCCAACAAAGCCCACTGGTGTCTC	518
Qy	478	ATAAGTGACTTCTACCGGGAGCCGTGACAGTGGCTTGGAAAGCAGATAGACGCCCGTC	537
Db	519	ATAAGTGACTTCTACCGGGAGCCGTGACAGTGGCTTGGAAAGCAGATAGACGCCCGTC	578
Qy	538	AAGCGGGAGTGAGAGACCACACACCTTCAAACAAGCAACAAACAAAGTACGGGGCCAGC	597
Db	579	AAGCGGGAGTGAGAGACCACACCTTCAAACAAGCAACAAACAAAGTACGGGGCCAGC	638
Qy	598	AGCTACTGAGCTGAGCGCTGAGCAGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT	657
Db	639	AGCTATCTGAGCGCTGAGCGCTGAGCAGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT	698
Qy	658	ACGCATGAAGGGAGCACCGCTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT	709
Db	699	ACGCATGAAGGGAGCACCGCTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT	749
RESULT 14			
LOCUS	BG686957	823 bp mRNA linear	EST 01-MAY-2001
DEFINITION	602650951F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763148 5',		
ACCESSION	BG686957	mRNA sequence.	
VERSION	BG686957.1	GI:13918354	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://imgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs@mail.nih.gov		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLC1618 row: f column: 13		
	High quality sequence stop: 808.		
FEATURES	Location/Qualifiers		
source	1..823		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4763148"		
	/clone_lib="NIH_MGC_48"		
	/tissue_type="primary B-cells from tonsils (cell line)"		
	/lab_host="DH10B (phage-resistant)"		
	/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;		
	Site 2: EcoRI; cDNA made by oligo-dT priming.		
	Directionally cloned into EcoRI/XhoI sites using the		
	following 5' adaptor: GGCACGAG(G). Size-selected >500bp		
	for average insert size 1.8kb. Library constructed by Ling		
	Hong in the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: this is a NIH_MGC Library.		
BASE COUNT	198 a 261 c 213 g 151 t		
ORIGIN			
Query Match	76.6%;	Score 544.8;	DB 12; Length 823;
Best Local Similarity	91.0%;	Pred. No. 1.4e-135;	
Matches 590; Conservative	0; Mismatches 57; Indels 1; Gaps 1;		
Qy	62	AGTCTGTCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGCGAAGGTCAACCATCT	121
Db	17	AGTCTGTCTGACTTACGCCACCTCAGCGTCTGGACCCCGGCGAGAGGTCAACCATCT	76


```
Qy 122 CGTGACCTGGAGGACCTCCAACTGAGGTTATGATCTTACATTTGTGTACAGCAGCTCC 181
Db 77 CTGTTCTTGGGAAGCAGCTCCAACTCGGAAGTAATATGATATCTGTGTACAGCAGCTCC 136
Qy 182 CAGGAGCGCCCGCCAACTCTCTATGACATTAACAGCGACCTTCAGGAATTTCTG 241
Db 137 CAGGAACGGCCCGCCAACTCTCTATGAGTAATAATCAGCGGCCCTTCAGGGGTCCCTG 196
Qy 242 ACCGATTTCTGGGTCGAAGTCTGTGACCGGGCTCTCCCTGGCCATCACTCGGGTCCAGA 301
Db 197 ACCGATTTCTGGGTCGAAGTCTGGCACTCAGCTCCCTGGCCATCAGTGGGTCCGGT 256
Qy 302 CTGAGGATGAGGCTGATTTACTGCCAGTCTCTATGACAGCAGCTGAATGCTCAGGTAT 361
Db 257 CCGAGGATGAGGCTGATTTACTCTGTGCAGCATGGGATGACAGCTGAGTGGTGTGGTAT 316
Qy 362 TCGGAGGAGGACCGGCTGACCTCTAGTGTACGCTCAGCCAGCCAGCTGCCCTCGGTCACTC 421
Db 317 TCGGCGGAGGACCGAGCTGACCGCTCTAGTGTACGCTCAGCCAGCTGCCCTCGGTCACTC 376
Qy 422 TGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGCTGTGTCTCATAA 481
Db 377 TGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGCTGTGTCTCATAA 436
Qy 482 GTGACTTTACCCGGGAGCCGTGACAGTGGCTCGAAGGCGAGATAGCAGGCCCTCAAGG 541
Db 437 GTGACTTTACCCGGGAGCCGTGACAGTGGCTCGAAGGCGAGATAGCAGGCCCTCAAGG 496
Qy 542 CGGAGTGGAGACCAACACACCTCCAAACAAGCAACAAGTACGCGGCCAGCAGCT 601
Db 497 CGGAGTGGAGACCAACACACCTCCAAACAAGCAACAAGTACGCGGCCAGCAGCT 556
Qy 602 ACCTCAGCTGACGCTGAGCAGTGGAGTCCCAAGAAGCTACAGCTGCCAGGTCAAGC 661
Db 557 ATCTGAGCTGACGCTGAGCAGTGGAGTCCCAAGAAGCTACAGCTGCCAGGTCAAGC 616
Qy 662 ATGAAGGAGCACCGTGGAGAGCAGTGGGCCCTTACAGATGTTTCAT 709
Db 617 ATGAAGGAGCACCGTGGAGAGCAGTGG-CCCTACAGATGTTTCAT 663
```

```
RESULT 15
BG756887 849 bp mRNA linear EST 15-MAY-2001
LOCUS 602710380F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850923 5',
DEFINITION mRNA sequence.
```

```
ACCESSION BG756887
VERSION BG756887.1 GI:14067540
KEYWORDS EST.
SOURCE human.
```

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 849)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCW1692 row: 0 column: 20

High quality sequence stop: 841.

Location/Qualifiers

1..849

/organism="Homo sapiens"

/db_xref="taxon:9606"

FEATURES

source

```
/clone="IMAGE:4850923"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
```

```
BASE COUNT 202 a 280 c 213 g 154 t
ORIGIN
```

```
Query Match 76.6%; Score 544.6; DB 12; Length 849;
Best Local Similarity 87.2%; Pred. No. 1.6e-135;
Matches 620; Conservative 0; Mismatches 89; Indels 2; Gaps 2;
```

```
Qy 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTCTGCTCCAGGTGCAGATGT 60
Db 29 ATCATGACCTGTCCCTCTCTCTCTCACCCTTCTCATTCACGACAGGTCTCTGGGCC 88
Qy 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGGCAGAGGTCCACATC 120
Db 89 CAGTCTGTCTGACGAGCGCCCTCAGTGTCTGGGGCCCGAGGACAGAAAGGTCCACATC 148
Qy 121 TCGTGACATGGGAGACCTCCAACTTGGAGGTATGATCTACATTTGGTACCAGCAGCTC 180
Db 149 TCTGTCTCTGGAAGCAGTCCAACTTGGGAATATATGATCTCTGGTACCAGCACTC 208
Qy 181 CCAGGAACCGGCCCAAACTCTCTCATCTATGACATTAACAAGCGACCTTCAGGAATTTCT 240
Db 209 CCAGGAACAGCCCCCAAACTCTCTCATCTATGAAATAATAAGCGACCTTCAGGATTTCT 268
Qy 241 GACCGATTTCTTGGCT-CCAAGTCTGGTACCGGGGCTCCCTGGCCATCAGTGGGGTCCA 299
Db 269 GACCGATTTCTTGGCTCCCAAGTCTGCCACGTCAGCCACCTGGGCATCACCGGACTCCA 328
Qy 300 GACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTCAATGCTCAGGT 359
Db 329 GACTGGGAGCAGGGCCGATTTACTTGGGAACATGGGATAGCAGCTGAGTGTGGGT 388
Qy 360 ATTTCGAGGAGGACCGGGCTGACCGCTCCTAGTTCAGCCCAAGGCTGCCCTCGGTTCAC 419
Db 389 GTTCGGCGGAGGACCAAGTGCAGCTGACCGTCTAGTTCAGCCCAAGGCTGCCCTCGGTTCAC 448
Qy 420 TCTGTTCCCGCCCTCTCTGAGGAGTTTCAAGCCAAAGAGCCACACTGGTGTCTCAT 479
Db 449 TCTGTTCCCGCCCTCTCTGAGGAGTTTCAAGCCAAAGAGCCACACTGGTGTCTCAT 508
Qy 480 AAGTGACTTCTACCCGGAGCGTGACAGTGGCTGGAAGGAGATAGCAGCCCGCTCAA 539
Db 509 AAGTGACTTCTACCCGGAGCGGTGACAGTGGCTGGAAGGAGATAGCAGCCCGCTCAA 568
Qy 540 GCGGGAGTGAGACCAACCAACCTCCAAAACAAAGCAACAAGTACGCGGCCAGAG 599
Db 569 GCGGGAGTGAGACCAACCAACCTCCAAAACAAAGCAACAAGTACGCGGCCAGAG 628
Qy 600 C-TACCTGAGCTTACCGCTGAGCAGTGAAGTCCACAGAGCTACAGTGCAGGTCA 658
Db 629 CTTTACCTGAGCTTACCGCTGAGCAGTGAAGTCCACAAAAGCTACAGTGCAGGTCA 688
Qy 659 CGCATGAAGGAGCAGCGTGGAGAGCAGTGGCCCTTACAGATGTTTCAT 709
Db 689 CGCATGAAGGAGCAGCGTGGAGAGCAGTGGCCCTTACAGATGTTTCAT 739
```

Search completed: April 6, 2003, 06:20:40

Job time : 1357.28 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 18:12:24 ; Search time 195.124 Seconds
(without alignments)

8205.894 Million cell updates/sec

Title: US-09-758-173-9

Perfect score: 711

Sequence: 1 ATCAGGTCGCCGCTCAGCT.....CCCTACAGAAATGTTTCATGA 711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N Geneseq_101002.*

```

1: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	711	19 AAV35488	Macaque primatized DNA sequence of a
2	711	100.0	711	24 AAS17246	Primate anti-hu
3	709.4	99.8	711	18 AAT62512	Human immune syste
4	582.6	81.9	935	22 AAC6525	Sequence encoding
5	571.4	80.4	884	11 AAQ03609	Plasmid Glambda-1B
6	565.2	78.5	762	22 AAC84209	Plasmid Glambda-1A
7	558.8	78.6	5679	22 AAC84207	Monoclonal antibod
8	552.6	77.7	768	20 AAX06953	Monoclonal antibod
9	552.6	77.7	768	20 AAX06954	

10	547	76.9	654	14	AAQ49835	Anti-HIV-1 recombi
11	546.2	76.8	810	23	AAS87270	DNA encoding novel
12	540.2	76.0	705	18	AAT62509	Primate anti-hu
13	540.2	76.0	705	19	AAV35484	Macaque primatized
14	540.2	76.0	705	24	AAS17242	DNA sequence of a
15	533.2	75.0	651	19	AAV11293	Antibody HB4C5 lig
16	533.2	75.0	708	22	AAH47902	Human type antiHum
17	532.2	74.9	915	24	ABN97248	Gene #3746 used to
18	532.2	74.9	915	24	ABK64815	Human benign prost
19	532.2	74.9	915	24	ABL65478	Lung cancer relate
20	530.2	74.6	895	22	AAC66530	Human immune syste
21	523.6	73.6	708	22	AAH47904	Human type antiHum
22	522.8	73.5	1845	24	ABL49526	Plasmid scFv(CC046
23	518.8	73.0	708	22	AAH47898	Human type antiHum
24	510.6	71.8	891	22	AAC66528	Human immune syste
25	509.2	71.6	763	23	AAS83480	DNA encoding novel
26	502.6	70.7	902	14	AAQ35100	Antibody D lambda
27	499.4	70.2	889	23	AAS77073	DNA encoding novel
28	498.6	70.1	906	22	AAK51914	Human polynucleoti
29	496.4	69.8	951	23	AAS90539	DNA encoding novel
30	494.4	69.5	783	23	AAS83483	DNA encoding novel
31	494.4	69.5	876	23	AAS83478	DNA encoding novel
32	493.8	69.5	888	21	AA95786	Human immune syste
33	487.4	68.6	1636	23	ABV22585	Human prostate exp
34	487.4	68.6	1636	23	ABV22585	Human prostate exp
35	486.6	68.4	756	23	AAS83477	DNA encoding novel
36	484.2	68.1	885	19	AAV34321	Human secreted pro
37	482.6	67.9	879	19	AAV34304	Human secreted pro
38	480.6	67.6	1636	23	ABV22585	Human prostate exp
39	480.6	67.6	1636	23	ABV22585	Human prostate exp
40	477	67.1	926	20	AAZ24427	Human bladder tumo
41	475.2	66.8	807	23	AAS83484	DNA encoding novel
42	470.4	66.2	872	9	AAH81655	VDJC regions of hu
43	468.4	65.9	702	18	AAT62867	Ant-CD4 monkey-hum
44	466	65.5	1027	24	ABQ54438	Human ovarian anti
45	465.6	65.5	849	22	AAH98186	Human EST-derived

ALIGNMENTS

```

RESULT 1
AAV35488
ID AAV35488 standard; DNA; 711 BP.
AC AAV35488;
XX
XX
DT 29-SEP-1998 (first entry)
XX
DE Macaque primatized 16C10 light chain DNA.
XX
XX
KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation; ss.
XX
XX
OS Macaca fascicularis.
XX
FH Key Location/Qualifiers
FT CDS 1..711
FT /tag= a
FT /product= 16C10 light chain
FT
XX
PN WO9819706-A1.
XX
PD 14-MAY-1998.
XX
PF 29-OCT-1997; 97WO-US19906.
XX
PR 08-NOV-1996; 96US-0746361.
XX
PA (IDEC-) IDEC PHARM CORP.

```

XX Anderson DR, Brams P, Hanna N;
XX WPI: 1998-286601/25.
DR P-PSDB; AA63764.
XX
PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PT cells, e.g. graft rejection or tumours
PT
PS Example 7; Fig 5a; 87pp; English.
XX
CC This sequence encodes a primatized form of the antibody'16C10 light chain
CC from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC Mab's are specific immunosuppressants for treatment of diseases involving
CC T cell/BA cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotype reagents. Mab's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (Il-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
SQ Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match 100.08; Score 711; DB 19; Length 711;
Best Local Similarity 100.08; Pred. No. 8.5e-172;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCCGCTCAGCTCTCGGGGCTCTGCTGCTCTGGCTCCAGGTGCACGATGT 60
DB 1 ATGAGGGTCCCCGCTCAGCTCTCGGGGCTCTGCTGCTCTGGCTCCAGGTGCACGATGT 60
QY 61 GAGTCTGTCTGACACAGCGCGCTCAGTGTCTGGGGCCCGCAGGCGACAAGGTCAACATC 120
DB 61 GAGTCTGTCTGACACAGCGCGCTCAGTGTCTGGGGCCCGCAGGCGACAAGGTCAACATC 120
QY 121 TCGTGCACTGGGAGCACCTCCAACTTGGAGGTATGATCTACATTGGTACCAGCAGCTC 180
DB 121 TCGTGCACTGGGAGCACCTCCAACTTGGAGGTATGATCTACATTGGTACCAGCAGCTC 180
QY 181 CCAGGAACGGCCCCCAAACTCTCTATCTATGACATTAACAAGCGACCTTCAGGAATTCT 240
DB 181 CCAGGAACGGCCCCCAAACTCTCTATCTATGACATTAACAAGCGACCTTCAGGAATTCT 240
QY 241 GACCGATTCTTGGCTCCAACTGCTGGTACCGGGCTCCCTGGGCCATCAGTGGGCTCCAG 300
DB 241 GACCGATTCTTGGCTCCAACTGCTGGTACCGGGCTCCCTGGGCCATCAGTGGGCTCCAG 300
QY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGCAGCTGAATGCTCAGGTA 360
DB 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGCAGCTGAATGCTCAGGTA 360
QY 361 TTCGAGGAGGACCCGGCTGACCGCTCTAGGTACAGCCAAAGGCTGCCCTCGGTCACT 420
DB 361 TTCGAGGAGGACCCGGCTGACCGCTCTAGGTACAGCCAAAGGCTGCCCTCGGTCACT 420
QY 421 CTGTTCCCGCCCTCTCTGAGGAGTTCAGCCACACAGGCGCACCTGGTGTGTCTATA 480
DB 421 CTGTTCCCGCCCTCTCTGAGGAGTTCAGCCACACAGGCGCACCTGGTGTGTCTATA 480
QY 481 AGTGACTTCTACCCGGGAGCCGTGACGTGGCTTGGAGGCGAGATAGCAGCCCCGTCAAG 540
DB 481 AGTGACTTCTACCCGGGAGCCGTGACGTGGCTTGGAGGCGAGATAGCAGCCCCGTCAAG 540

QY 541 GCGGGAGTGGAGACCAACCACTCCAAACAAAGCAACAAGTACGCGGCCAGCAGC 600
DB 541 GCGGGAGTGGAGACCAACCACTCCAAACAAAGCAACAAGTACGCGGCCAGCAGC 600
QY 601 TACTGAGGCTGAGCGCTGAGCAGTGGAAAGTCCCAAGCTTACAGCTGCCAGGTCACG 660
DB 601 TACTGAGGCTGAGCGCTGAGCAGTGGAAAGTCCCAAGCTTACAGCTGCCAGGTCACG 660
QY 661 CATGAAGGGAGCACCTGGAGAGACAGTGGCCCTTACAGAATGTTTCATGA 711
DB 661 CATGAAGGGAGCACCTGGAGAGACAGTGGCCCTTACAGAATGTTTCATGA 711

RESULT 2
AAS17246
ID AAS17246 standard; DNA; 711 BP.
XX
AC AAS17246;
XX
DT 12-MAR-2002 (first entry)
XX
DE DNA sequence of a primatized form of the light chain of 16C10 antibody.
XX
KW Human; macaque monkey; light chain; primatized antibody; 16C10 antibody;
KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW graft-vs-host disease; immunosuppression; organ rejection;
KW interleukin-2; IL-2; mutant; db.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Macaca sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..711
FT /tag= a
FT /product= "Light chain of 16C10 antibody"
XX
PN WO200189567-A1.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16364.
XX
PR 22-MAY-2000; 2000US-0576424.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Hanna N, Brams P;
XX
WPI: 2002-089895/12.
DR P-PSDB; AAU11845.
XX
PT Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT treating cancer, graft-vs-host disease and autoimmune disease such as
PT allergy
XX
PS Example 8; Fig 5a; 89pp; English.
XX
CC The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus,
CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host diseases. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or

CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present nucleic
CC acid sequence encodes the light chain of 16C10, a primatised antibody
CC used in the invention to induce apoptosis and inhibit production of
CC interleukin-2 (IL-2).
XX
SQ Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;
Query Match 100.0%; Score 711; DB 24; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.5e-172;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGCTCCAGGTGCACGATGT 60
Db 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGCTCCAGGTGCACGATGT 60
Qy 61 GAGTCTGTCTGACACAGCGGCTCAGTGTCTGGGGCCCGAGGCGAGAGGTCAACATC 120
Db 61 GAGTCTGTCTGACACAGCGGCTCAGTGTCTGGGGCCCGAGGCGAGAGGTCAACATC 120
Qy 121 TCGTCACCTGGGAGCAGCTCCAACTTGGAGTTATGATCTACATTTGGTACCAGAGCTC 180
Db 121 TCGTCACCTGGGAGCAGCTCCAACTTGGAGTTATGATCTACATTTGGTACCAGAGCTC 180
Qy 181 CCAGGAACGGCCCCAACTCTCATCTATGACATTAACAAGCGACCTCAGGAATTTCT 240
Db 181 CCAGGAACGGCCCCAACTCTCATCTATGACATTAACAAGCGACCTCAGGAATTTCT 240
Qy 241 GACCAATTTCTGGTCTCAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCCAG 300
Db 241 GACCAATTTCTGGTCTCAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCCAG 300
Qy 301 ACTGAGGATGAGGCTGATTTACTGCGAGTCTTATGACAGCAGGCTGAATGCTCAGGTA 360
Db 301 ACTGAGGATGAGGCTGATTTACTGCGAGTCTTATGACAGCAGGCTGAATGCTCAGGTA 360
Qy 361 TTCGAGGAGGAGACCGGCTGACCTCTAGGTACAGCCCAAGGCTGCCCTCCGTCACCT 420
Db 361 TTCGAGGAGGAGACCGGCTGACCTCTAGGTACAGCCCAAGGCTGCCCTCCGTCACCT 420
Qy 421 CTGTTCCCGCTCTCTTGAGAGCTTCAAGCCCAAGGCTGCTGTGCTCATATA 480
Db 421 CTGTTCCCGCTCTCTTGAGAGCTTCAAGCCCAAGGCTGCTGTGCTCATATA 480
Qy 481 AGTGACTTCTACCGGGAGCCGTGACAGTGGCTGGAGGAGATAGAGCCCGTCAAG 540
Db 481 AGTGACTTCTACCGGGAGCCGTGACAGTGGCTGGAGGAGATAGAGCCCGTCAAG 540
Qy 541 GCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
Db 541 GCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
Qy 601 TACTGAGCTGACCGCTGAGAGTGGAGTCCCAAGAGCTACAGTGCAGGTCAAG 660
Db 601 TACTGAGCTGACCGCTGAGAGTGGAGTCCCAAGAGCTACAGTGCAGGTCAAG 660
Qy 661 CATGAGGAGGACCGTGGAGAGACAGTGGCCCTTACAGATGTTCTATGA 711
Db 661 CATGAGGAGGACCGTGGAGAGACAGTGGCCCTTACAGATGTTCTATGA 711

RESULT 3

AAT62512

ID AAT62512 standard; DNA; 711 BP.

XX AAT62512;

XX

DT 25-MAY-1997 (first entry)

XX

DE Primatised anti-human B7.1 antigen antibody 16C10 light chain DNA.

XX Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
XX hetero-hybridoma; transfectoma; ss.
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N, Sheetowsky WS;
XX
XX WPI; 1997-108638/10.
DR P-PSDB; AAW01821.
XX
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
PS Claim 11; Fig 10A; 81pp; English.
XX
CC 2 DNA sequences (AAT62512 and AAT62513) respectively code for
CC primatised forms (AAW01821 and AAW01822) of the light and heavy chains
CC of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC 16C10. Cloned 16C10 light and heavy variable genes are inserted
CC into an expression vector (pref. NEOSPLA) which contains human light
CC and heavy chain constant region genes to allow prodn. of primatised
CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC antibodies have also been produced (see also AAW01817-20). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.
XX
SQ Sequence 711 BP; 161 A; 226 C; 193 G; 131 T; 0 other;
Query Match 99.8%; Score 709.4; DB 18; Length 711;
Best Local Similarity 99.9%; Pred. No. 2.2e-171;
Matches 710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGCTCCAGGTGCACGATGT 60
Db 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGCTCCAGGTGCACGATGT 60
Qy 61 GAGTCTGTCTGACACAGCGGCTCAGTGTCTGGGGCCCGAGGCGAGAGGTCAACATC 120
Db 61 GAGTCTGTCTGACACAGCGGCTCAGTGTCTGGGGCCCGAGGCGAGAGGTCAACATC 120
Qy 121 TCGTGACCTGGGAGCACCTCCAACTTGGAGTTATGATCTACATTTGGTACCAGAGCTC 180
Db 121 TCGTGACCTGGGAGCACCTCCAACTTGGAGTTATGATCTACATTTGGTACCAGAGCTC 180
Qy 181 CCAGGAACGGCCCCAACTCTCATCTATGACATTAACAAGCGACCTCAGGAATTTCT 240
Db 181 CCAGGAACGGCCCCAACTCTCATCTATGACATTAACAAGCGACCTCAGGAATTTCT 240
Qy 241 GACCGATTTCTTGGCTCCAAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCCAG 300
Db 241 GACCGATTTCTTGGCTCCAAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCCAG 300
Qy 301 ACTGAGGATGAGGCTGATTTACTGCCAGTCTTATGACAGCAGGCTGAATGCTCAGGTA 360
Db 301 ACTGAGGATGAGGCTGATTTACTGCCAGTCTTATGACAGCAGGCTGAATGCTCAGGTA 360


```
Matches 610; Conservative 0; Mismatches 53; Indels 3; Gaps 1;
QY 47 CAGGTGCAGATGTGAGTCTGCTCTGACACAGCCGCTCAGTGTCTGGGGCCCGAGGC 106
DB 70 CAGGTGTCACTCCAGTCTGTGTTAGACGACGCCGCTCAGTCTCTGGGGCCCGAGGC 129
QY 107 AGAAGGTCAACCATCTCTGCTCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTAC 163
DB 130 AGAAGGTCAACCATCTCTGCTCACTGGGAGCACCTCCAACATTGGTTATGATGTTTC 189
QY 164 ATTGGTACAGCAGTCTCCAGAACGGCCCCCAAACTCTCTCATCTATGACATTAACAAGC 223
DB 190 ACTGGTACCGGCAACTTCCAGGACAGCCCCCAAACTCTCATCTATGATAACAACAATC 249
QY 224 GACCTCAGGAATTTCTGACCGATCTCTGGCTCCAAGTCTGGTACCGGCTCCCTCGG 283
DB 250 GGCCCTCAGGGTCTCTGACCGATCTCTGGCTCCAAGTCTGGCCCTCAGCCTCCCTGG 309
QY 284 CCATCACTGGGCTCCAGATGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCA 343
DB 310 CCATCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCA 369
QY 344 GCTGAATGCTCAGGTATTCGAGGAGGAGCCCGGCTGACCGTCTAGGTGAGCCCAAGG 403
DB 370 GCTGAATGTTATGTTCTTCGGAATTCGGAGCCAGCTCACCGTCTTAGGTGAGCCCAAGG 429
QY 404 CTGCCCTCTCGTCACTCTGTTCCCGCTCTCTCTGAGGAGCTTCAAGCCCAACAGGCCA 463
DB 430 CTGCCCTCTCGTCACTCTGTTCCCGCTCTCTCTGAGGAGCTTCAAGCCCAACAGGCCA 489
QY 464 CACTGTGTGTCTCATAGTACTTCTACCCGGAGCGCTGACAGTGGCTGGAGGCGAG 523
DB 490 CACTGTGTGTCTCATAGTACTTCTACCCGGAGCGCTGACAGTGGCTGGAGGCA 549
QY 524 ATAGCAGCCCCGTAAAGCGGAGTGGAGACACACACCTTCCAAAACAAAGCAACACA 583
DB 550 TTAGCAGCCCCGTAAAGCGGAGTGGAGACACACACCTTCCAAAACAAAGCAACACA 609
QY 584 AGTACGGCGCCAGCAGTACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAACT 643
DB 610 AGTACGGCGCCAGCAGTATCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAACT 669
QY 644 ACAGTGTCCAGGTCAAGCATGAGGAGGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAA 703
DB 670 ACAGTGTCCAGGTCAAGCATGAGGAGGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAA 729
QY 704 GTTCAT 709
DB 730 GTTCAT 735

RESULT 7
AAC84207
ID AAC84207 standard; DNA; 5679 BP.
XX
AC AAC84207;
XX
XX 19-MAR-2001 (first entry)
XX
XX Plasmid Glambda-lapcn DNA sequence.
XX
XX Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
KW Glambda-1; human; virucide; RSV propagation; ds.
XX
XX Homo sapiens.
XX
XX WO200069462-A1.
XX
XX 23-NOV-2000.
XX
XX 18-MAY-2000; 2000WO-US13694.
XX
XX 18-MAY-1999; 99US-0134702.
XX
```

```
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Gross MS, Sweet RW, Taylor G;
XX
XX WPI; 2001-024947/03.
XX
XX Human monoclonal antibody and functional fragments, useful for
PT therapeutic and/or prophylactic treatment of respiratory syncytial
PT virus infection, is specifically reactive with the F protein epitope of
PT the virus -
XX
XX Claim 6; Fig 9A-E; 102pp; English.
XX
XX The invention provides a human monoclonal antibody (I) and its functional
CC fragments specifically reactive with an F protein epitope of respiratory
CC syncytial virus (RSV), and capable of neutralising infection by the virus
CC such as Glambda-1A or Glambda-1B. The antibody can be expressed by
CC standard recombinant methodology. (I) is useful for detecting RSV by
CC contacting a source suspected of containing RSV with (I) and determining
CC whether (I) binds to the source. (I) is also useful for providing passive
CC immunotherapy prophylactically, to RSV disease in a human. (I) is useful
CC for therapeutic and/or prophylactic treatment of RSV infection in human
CC patients, particularly infants and young children. (I) is also useful
CC as a diagnostic reagent for the determination of RSV mediated disorders
CC or for tracking progress of treatment of the disorders. The present
CC sequence represents the continuous DNA sequence of the expression plasmid
CC Glambda-lapcn containing the RSV neutralising human Glambda-1 mAb for the
CC light chain.
XX
SQ Sequence 5679 BP; 1339 A; 1489 C; 1483 G; 1368 T; 0 other;
Query Match 78.6%; Score 558.8; DB 22; Length 5679;
Best Local Similarity 91.0%; Pred. No. 9.4e-133;
Matches 606; Conservative 0; Mismatches 57; Indels 3; Gaps 1;
QY 47 CAGGTGCAGATGTGAGTCTGCTCTGACACAGCCGCTCAGTGTCTGGGGCCCGAGGC 106
DB 1052 CAGCTACAGGTGTCCACTCCGAGTCTCAGCAGCGCGCTCAGTCTCTGGGGCCCGAGGC 1111
QY 107 AGAAGTCAACCATCTCTGCTCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTAC 163
DB 1112 AGAAGTCAACCATCTCTGCTCACTGGGAGCACCTCCAACCTTCGGGGCAGGTATGATGTTTC 1171
QY 164 ATTGGTACCAAGCAGTCTCCAGGAAACGGCCCCCAAACTCTCTCATCTATGACATTAACAAGC 223
DB 1172 ACTGGTACCGGCAACTTCCAGGAGCAGCCCCCAAACTCTCTCATCTATGATAACAACAATC 1231
QY 224 GACCTCAGGAATTTCTGACCGATTTCTTGGCTCCAAGTCTGGTACCGGCGCTCCCTCGG 283
DB 1232 GGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCCCTCAGCCTCCCTCGG 1291
QY 284 CCATCACTGGGCTCCAGACCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCA 343
DB 1292 CCATCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCA 1351
QY 344 GCCTGAATGCTCAGGTATTTCGAGAGGAGGACCCCGGTGAGCCGCTCCTAGGTTCAGCCCAAGG 403
DB 1352 GCCTGAATGTTATGTTCTTCGGAACCTGGGACCCAGCTCACCGTCTTAGGTTCAGCCCAAGG 1411
QY 404 CTGCCCTCTCGGTCACTCTGTTCCCGCTCTCTCTGAGGAGCTTCAAGCCCAACAGGCCA 463
DB 1412 CTGCCCTCTCGGTCACTCTGTTCCCGCTCTCTCTGAGGAGCTTCAAGCCCAACAGGCCA 1471
QY 464 CACTGGTGTGTCTCATAGTACTTCTACCCGGAGCGCTGACAGTGGCTGGAAGCGAG 523
DB 1472 CACTGGTGTGTCTCATAGTACTTCTACCCGGAGCGCTGACAGTGGCTGGAAGCGAA 1531
QY 524 ATAGCAGCCCCGTCAAGCGGAGTGGAGACCAACACCTTCCAAAACAAAGCAACACA 583
DB 1532 TTAGCAGCCCCGTCAAGCGGAGTGGAGACCAACACCTTCCAAAACAAAGCAACACA 1591
QY 584 AGTACGGCGCCAGCAGTACTCTGAGCTGAGCGCTGAGCAGTGGAGTCCACAGAGCT 643
```


DT 10-MAY-1999 (first entry)
 XX Monoclonal antibody 4B5 light chain variable region DNA.
 DE
 XX
 KW Antigen binding fragment 4B5; monoclonal antibody; cancer;
 KW neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
 KW sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
 KW GD2 antigen; human; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT CDS complement (43..750)
 FT /*tag= a
 XX
 PN WO9902545-A2.
 XX
 XX 21-JAN-1999.
 PD
 XX 08-JUL-1998; 98WO-IB01046.
 PF
 XX 08-JUL-1997; 97US-0051945.
 PR
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 PA
 XX Dan MD;
 PI
 XX WPI; 1999-120769/10.
 DR P-PSDB; AAW88465.
 XX
 XX New antibody 4B5 polynucleotides and polypeptides - used to develop
 PT products for the diagnosis and treatment of cancers and for
 PT prophylactic therapy to reduce risk of recurrence
 XX
 XX Claim 6; Page 80; 83pp; English.
 PS
 XX This is the complementary strand of a DNA sequence (see also
 CC AAX06953) that encodes the light chain variable region (see AAW88465)
 CC of the recombinant human monoclonal antibody (MAB) 4B5. 4B5. 4B5
 CC recognises antibodies specific for GD2 antigen antibodies. Such
 CC antibodies recognise various cancers including glioblastoma,
 CC neuroblastoma, malignant and/or metastatic melanoma, breast
 CC adenocarcinoma, lung adenocarcinoma, small cell lung carcinoma,
 CC colon adenocarcinoma and prostate adenocarcinoma. The invention
 CC encompasses 4B5 derivatives with immunologic specificity for
 CC antibodies specific for GD2. These derivatives, or antigen binding
 CC fragments, may comprise regions of the 4B5 VDJ junction and regions
 CC spanning the 4B5 CDRs. Other derivatives include Fab, F(ab')₂,
 CC Fab', scFv and isolated heavy and light chains. Polynucleotide
 CC fragments (see AAX06951-54), both coding and complementary strands,
 CC encoding 4B5 antibody V regions are also provided, as well as
 CC therapeutic plasmids and vectors, including vaccinia virus vectors,
 CC comprising these polynucleotides. 4B5 mimics GD2, and is useful in
 CC generating a host immune response to cancer. Products of the
 CC invention can be used in the detection and treatment of e.g.
 CC astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
 CC primitive neural ectodermal tumour (PNET), pancreatic ductal
 CC adenocarcinoma, small and large cell lung adenocarcinomas,
 CC squamous cell carcinoma, bronchoalveolar carcinoma, epithelial
 CC adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
 CC breast tumours such as ductal and lobular adenocarcinoma, squamous
 CC and adenocarcinomas of the uterine cervix, uterine and ovarian
 CC epithelial carcinomas, prostatic adenocarcinoma, transitional
 CC squamous cell carcinoma of the bladder, B and T cell lymphoma
 CC (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
 CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
 XX
 SQ Sequence 768 BP; 141 A; 202 C; 256 G; 169 T; 0 other;
 Query Match 77.7%; Score 552.6; DB 20; Length 768;
 Best Local Similarity 89.6%; Pred. No. 2.2e-131;
 Matches 594; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 47 CAGGTGCACGATGTGAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGCG 106
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 707 CAGGGTCCTGGGGCCAGTCTGTGCTGACTCAGCCACCTCAGCGTCTGGGACCCCGGGC 648
 QY 107 AGAAGTCAACATCTCTGTCGATCGGAGCAGCTTCCAACTTGGAGGTTATGATCTACATT 166
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 647 AGAGGGTCAACATCTCTGTTCTGGAAGCAACTCCAACTCGGAAGTAAAGACTGTAAACT 588
 QY 167 GTTACCAGCAGCTCCAGGACGGGCCCAAACTCCTCATCTATGACATTAAACAGCGAC 226
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 587 GTTACCAGCAACTCCAGGAAGGGCCCCCAAAATTTCTCATCTATAGTAAATACAGCGGC 528
 QY 227 CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGGGCTCCCTCGGCCA 286
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 527 CCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCA 468
 QY 287 TCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCGCAGTCTTATGACAGCGCC 346
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 467 TCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCGAGCATGGGATGACAGCC 408
 QY 347 TGAATGCTCAGGTATTTCGGAGGAGGACCGGCTGACCGTCTAGTTCAGCCCAAGGGCTG 406
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 407 TGAATGCTCAGGTATTTCGGCGGAGGACCAAGCTGACCGTCTCTGGTTCAGCCCAAGGGCTG 348
 QY 407 CCCCTTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGGCCACAC 466
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 347 CCCCTTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGGCCACAC 288
 QY 467 TGTGTGTCTCAATGACTTCTACCCGGGAGCGGTGACAGTGGCCTCGAAGGCGAGATA 526
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 287 TGTGTGTCTCATAAGTACTTCTACCCGGGAGCGGTGACAGTGGCCTCGAAGGCGAGATA 228
 QY 527 GCAGCCCGCTCAAGCGGGAGTGGAGACCACCACTCCAAACAAAGGCAACCAACT 586
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 227 GCAGCCCGCTCAAGCGGGAGTGGAGACCACCACTCCAAACAAAGGCAACCAACT 168
 QY 587 ACCGGCCAGCAGCTACCTGAGCTGAGCCTGAGCAGTGGAGTCCCAAGAGCTACA 646
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 167 ACCGGCCAGCAGCTACCTGAGCCTGAGCAGTGGAGTGGAGTCCCAAGAGCTACA 108
 QY 647 GTCGCCAGTTCACGATGAGGAGCAGCCTGCGGAGAGACACAGTGGCCTTACAGATGTT 706
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 107 GCTGCCAGTTCACGATGAGGAGCAGCCTGCGGAGAGACACAGTGGCCTTACAGATGTT 48
 QY 707 CAT 709
 DB |||||
 47 CAT 45
 RESULT 10
 AAQ49835
 ID AAQ49835 standard; cDNA; 654 BP.
 XX
 XX AAQ49835;
 AC
 XX 27-APR-1994 (first entry)
 DT
 XX Anti-HIV-1 recombinant antibody 447-52D light chain coding sequence.
 DE
 XX Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
 KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
 KW acquired immune deficiency syndrome; chimeric antibody;
 KW surface glycoprotein gp120; V3 loop; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 1..654
 FT /*tag= a
 FT /note= "encodes recombinantly modified 447-52D
 light chain"
 XX
 PN WO9319785-A.

```
XX PD 14-OCT-1993.
XX XX
XX PF 23-MAR-1993; 93WO-US02629.
XX XX
XX PR 01-APR-1992; 92US-0861701.
XX XX
XX PA (MERI ) MERCK & CO INC.
XX PA (JOHN/) JOHNSON L S.
XX PA (PFAR/) PFARR D S.
XX XX
XX PI Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;
XX XX
XX DR WPI; 1993-336600/42.
XX DR P-PSDB; AAR42163.
XX XX
XX PT New recombinant human antibody - with HIV neutralising activity
XX PT against at least two isolates, useful for preventing or treating
XX PT infection in diagnosis, etc.
XX XX
XX PS Example 9; Fig 2B; 154pp; English.
XX XX
XX CC EBV-transformed cell lines and mouse-human heterohybridomas
XX CC producing human MAbs specific for the gp120 V3 loop of HIV-1 MN
XX CC isolate were obtained. MAb 447-52D was found to recognise the
XX CC tetrapeptide motif GPR, i.e. the Principal Neutralising
XX CC Determinant common to the V3 loop of different HIV isolates.
XX CC A recombinant Ab was produced in which the L chain V region was
XX CC derived from 447-52D and to which a signal sequence and a L chain
XX CC intronic sequence are appended, fused to a fragment contg. a short
XX CC intronic segment of the human lambda 2 C region and the human
XX CC lambda 2 constant encoding domain.
XX XX
XX SQ Sequence 654 BP; 156 A; 199 C; 178 G; 121 T; 0 other;

Query Match 76.9%; Score 547; DB 14; Length 654;
Best Local Similarity 91.1%; Pred. No. 5,7e-130;
Matches 593; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

QY 62 AGTCGTCTGACACAGCGCCCTCAGTGTCTGGGCCCCAGGCGCAGAGTCAACCATCT 121
Db 2 AGTCGTCTGACGAGCGCCCTCAGTGTCTGGGCCCCAGGCGCAGAGTCAACCATCT 61
QY 122 CQTGACCTGGGAGCACCTCCAACTGAGTGTATGATCTACATTGGTACCAGCAGTCC 181
Db 62 CTTGCTCTGGAAGCAGCTCCAACTGAGTGTATGATCTACATTGGTACCAGCAGTCC 121
QY 182 CAGGAACGGCCCCCAAACTCTCTATGATGATTAACAAGGACCCCTCAGGAATTTCTG 241
Db 122 CAGGAACAGCCCCCAAACTCTCTATGATGATTAACAAGGACCCCTCAGGAATTTCTG 181
QY 242 ACCGATTCTCTGGCTTCAAGTCTGATCGCGGCTCCCTGGCCATCATCTGGGCTCCAGA 301
Db 182 ACCGATTCTCTGGCTTCAAGTCTGATCGCGGCTCCCTGGCCATCATCTGGGCTCCAGA 241
QY 302 CTGAGGATGAGGCTGATTATTACTCCAGTCTCTATGACAGCAGCTGGAATCTCA---GG 358
Db 242 CTGGGAGAGGCGCGATTATTCTTCTGGCAACATGGATAGCGGCTGAGTCTGATTGGG 301
QY 359 TATTGCGAGGAGGAGCCCGGCTGACCGTCTAGGTGACGCCAAGGCTGCCCTCCGCTCA 418
Db 302 TGTTCGGGAGGAGGAGCAAGTCTGACCGTCTTAAGTTCAGCCCAAGGCTGCCCTCCGCTCA 361
QY 419 CTCTGCTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGTGTGTCTCA 478
Db 362 CTCTGCTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGTGTGTCTCA 421
QY 479 TAAGTGACTTCTACCCGGAGCCGTGACAGTGGCCCTGGAAGGCAGATAGCAGCCCCGTCA 538
Db 422 TAAGTGACTTCTACCCGGAGCCGTGACAGTGGCCCTGGAAGGCAGATAGCAGCCCCGTCA 481
QY 539 AGGCGGGAGTGAGACCAACCACTCCAAACAAAGCAACAAAGTACGCGGCCAGCA 598
|||||
```

Db 482 AGCGGGAGTGGAGACCACACACCCCTCAAACAAGCAACAAGTACGCGGCCAGCA 541

QY 599 GCTACTCTGAGCTGACGCTGAGCAGTGGAAAGTCCACAGAGCTACAGCTGCCAGGTCA 658

Db 542 GCTATCTGAGCCTGACGCTGAGCAGTGGAAAGTCCACAGAGCTACAGCTGCCAGGTCA 601

QY 659 CGCATGAAGGGAGCACCCGTGGAGAAAGACAGTGGCCCCCTACAGAATGTTTCAT 709

Db 602 CGCATGAAGGGAGCACCCGTGGAGAAAGACAGTGGCCCCCTACAGAATGTTTCAT 652

RESULT 11

AAS87270

ID AAS87270 standard; cDNA; 810 BP.

XX AC AAS87270;

XX XX

DT 13-FEB-2002 (first entry)

XX XX

DE DNA encoding novel human diagnostic protein #23074.

XX XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX XX

PF 30-MAR-2001; 2001WO-US08631.

XX XX

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX XX

PA (HYSE-) HYSEQ INC.

XX XX

PI Drmanac RT, Liu C, Tang YT;

XX XX

DR WPI: 2001-639362/73.

DR P-PSDB; ABG23083.

XX XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX XX

PS Claim 1; SEQ ID No 23074; 103pp; English.

XX XX

CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human

CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX XX

SQ Sequence 810 BP; 176 A; 275 C; 211 G; 148 T; 0 other;

Query Match 76.8%; Score 546.2; DB 23; Length 810;
Best Local Similarity 89.0%; Pred. No. 9.7e-130;
Matches 590; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 47 CAGGTGACGATGAGTCTGCTCTACACAGCGCGCTCAGTGTCTGGGGCCCGAGGGC 106
DB 49 CAGGGTCTGGGCCCCAGTCTGTACTACGACGACCCCTCAGCGTCTGGGACCCCGGGC 108

QY 107 AGAAGTCCACATCTCGTGCACCTGGGAGCACCTCCAAACATTTGAGGTTATGATCTACATT 166
DB 109 AGAGGGTCAATCTCTGTTCTGGAGCAGCTCCAAATCGGCATTAATGATGATACT 168

QY 167 GTACACAGAGCTCCAGGAAGCGCCCCAAACTCTCTATGACATTAACAAGCCAC 226
DB 169 GTTACAGCAACTCACAGGAAGCGCCCCAAACTCTCTATAGGAATAATCAGCGC 228

QY 227 CTTACAGAAATTTGACCAATCTCTGGCTCCAAAGTCTGGTACCGGGCTCCCTGGGCA 286
DB 229 CTTACAGGGTCCCTGACCAATCTCTGGCTCCAAAGTCTGGCTCCCTCAGCCTCCCTGGCA 288

QY 287 TCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCCTATGACAGCACC 346
DB 289 TCACTGGGCTCCAGTCCGAGATGAGGCTGATTATTACTGCCAGTGGGATGACGCC 348

QY 347 TGAATGCTCAGGTATTCGAGGAGGACCCGCTGACCGTCTTAGGTGAGCCCAAGGCTG 406
DB 349 TCACTGGTCCGGTGTTCGGCGGAGGACCAAGCTGACCGTCTTAGGTGAGCCCAAGGCTG 408

QY 407 CCCCCTCGGTCACTCTGTTCCGCGCTCTCTGAGGAGTTCAGGCAACAAGGCCACAC 466
DB 409 CCCCCTCGGTCACTCTGTTCCGCGCTCTCTGAGGAGTTCAGGCAACAAGGCCACAC 468

QY 467 TGGTGTGTCTCAATAGTGAATCTTACCCGGGAGCGTGACGTGGCTGGAAGGCAGATA 526
DB 469 TGGTGTGTCTCAATAGTGAATCTTACCCGGGAGCGTGACGTGGCTGGAAGGCAGATA 528

QY 527 GCAGCCCCGTCAAGGCGGAGTGGAGACCAACACACCTTCCAAAACAAAGCAACAAGT 586
DB 529 GCAGCCCCGTCAAGGCGGAGTGGAGACCAACACACCTTCCAAAACAAAGCAACAAGT 588

QY 587 AGCGGCGCAGCAGCTACCTGAGCTGAGCGCTGAGCGTGGAGTGGAGTCCACAGAGCTACA 646
DB 589 AGCGGCGCAGCAGCTATCTGAGCGCTGAGCGCTGAGCGTGGAGTGGAGTCCACAGAGCTACA 648

QY 647 GCTGCCAGTTCAGCATGAAGGAGCACCGTGGAGAGACAGTGGCGCCCTACAGAAATGTT 706
DB 649 GCTGCCAGTTCAGCATGAAGGAGCACCGTGGAGAGACAGTGGCGCCCTACAGAAATGTT 708

QY 707 CAT 709
DB 709 CAT 711

RESULT 12

AAT62509

ID AAT62509 standard; DNA; 705 BP.

XX AC

AAT62509;

XX AC

25-MAY-1997 (first entry)

XX DT

DE Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA.

XX KW

KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;

KW autoimmune disease; idiopathic thrombocytopenia purpura;

KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;

KW type 1 diabetes mellitus; graft versus host disease;

KW hetero-hybridoma; transfectoma; ss.

XX KW

OS Chimeric Macaca cynomolgus;

OS Chimeric Homo sapiens.

XX OS

PN W09640878-A1.
XX PD 19-DEC-1996.
XX PF 06-JUN-1996; 96WO-US10053.
XX PR 07-JUN-1995; 95US-0487550.
XX PA (IDEC-) IDEC PHARM CORP.
XX PI Anderson DR, Brans P, Hanna N, Shestowsky WS;
XX WPI; 1997-108638/10.
XX P-PSDB; AAW01817.
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
XX useful for treating autoimmune disease or graft-versus-host disease
XX Claim 7; Fig 8A; 81pp; English.
XX 2 DNA sequences (AAT62509 and AAT62510) respectively code for
XX primatised forms (AAW01817 and AAW01818) of the light and heavy chains
XX of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
XX 7C10. Cloned 7C10 light and heavy variable genes are inserted into
XX an expression vector (pref. NEOSPLA) which contains human light and
XX heavy chain constant region genes to allow prodn. of primatised
XX antibody in e.g. CHO cells. Primatised 786 and 16C10 anti-B7.1
XX antibodies have also been produced (see also AAW01819-22). The
XX primatised antibodies inhibit the B7:CD28 pathway, making them
XX useful immunosuppressants for the treatment of autoimmune disorders
XX and graft-versus-host disease.

SQ Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match 76.0%; Score 540.2; DB 18; Length 705;

Best Local Similarity 86.1%; Pred. No. 3.2e-128;

Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGTTCCCGCTCAGTCTCCGCGGCTCTGCTGCTCTGGCTCCAGGTGACCATGT 60

DB 1 ATGAGGTTCCCGCTCAGTCTCCGCGGCTCTGCTGCTCTGGCTCCAGGTGACCATGT 60

QY 61 GAGTCTGTCTGACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACATC 120

DB 61 GCCTATGAATGACTGACGACCCCTCGGTGTCACTGTCTCCAGGACAGCGCCAGGATC 120

QY 121 TCTGTACTGGGAGCAGCTCCAAACATTTGGAGGTATGATCTACATTTGGTACGACGATC 180

DB 121 ACCTGTGGGG-----AGACACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAG 174

QY 181 CCAGGAACGSCCCCCCAAACTCCTCATCTATGACATTAACAAGGACCCCTCAGGAATTTCT 240

DB 175 CCAGCGGGGCCCCCTATCTGTTGATCTATGATGATGACCGGCCCTCAGGGATCCCT 234

QY 241 GACCGATTCTCTGGCTCCAAAGTCTGGTACCGGGCTCTCCCTGGCCATCATCTGGGTCCAG 300

DB 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCACCTTGACCATCAACGGGGTCGAG 294

QY 301 ACTGAGATGAGCTGATTTACTGCCAGTCTTATGACAGAGCCTGAATGCTCAGGTA 360

DB 295 GCCGGGATGAGCTGACTATTACTGTCAAGTGTGGGAGTAGTGTATCATCCGGTC 354

QY 361 TTCGAGGAGGAGCCCGGCTGACCGTCTAGGTTCAGCCCAAGGCTGCCCTCGGTCACT 420

DB 355 TTCGAGGAGGAGCCCGGCTGACCGTCTAGGTTCAGCCCAAGGCTGCCCTCGGTCACT 414

QY 421 CTGTTCCCGCTCTCTCAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCATA 480

DB 415 CTGTTCCCGCTCTCTCAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCATA 474

QY 481 AGTGACTTCTACCCGGAGCCGTGACAGTGGCTGGAAGGAGATAGACGCCCGTCAAG 540

DB 475 AGTGACTTCTACCCGGAGCCGTGACAGTGGCTGGAAGGAGATAGACGCCCGTCAAG 534

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 32.1002 Seconds
(without alignments)
6735.375 Million cell updates/sec

Title: US-09-758-173-1

Perfect score: 705

Sequence: 1 ATGAGGTCCCGCTCAGCT.....CCCTACAGAATGTTTCATGA 705

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	US-08-487-550-1	Sequence 1, Appli
2	585.2	83.0	702	US-08-523-894-5	Sequence 5, Appli
3	540.2	76.6	711	US-08-487-550-9	Sequence 9, Appli
4	473	67.1	935	US-09-049-672A-20	Sequence 20, Appli
5	457	64.8	902	US-08-378-939-11	Sequence 11, Appli
6	456	64.7	895	US-09-049-672A-25	Sequence 25, Appli
7	455.4	64.6	891	US-09-049-672A-23	Sequence 23, Appli
8	435.6	61.8	885	US-09-152-060-47	Sequence 47, Appli
9	434	61.6	879	US-09-152-060-29	Sequence 29, Appli
c 10	432.2	61.3	928	US-09-152-060-46	Sequence 46, Appli
11	425.4	60.3	919	US-09-049-672A-24	Sequence 24, Appli
12	407.4	57.8	716	US-08-793-450-5	Sequence 5, Appli
c 13	306.6	43.5	584	US-09-404-879A-268	Sequence 268, App
c 14	273.2	38.8	771	US-08-991-789A-241	Sequence 241, App
c 15	273.2	38.8	771	US-09-062-451-241	Sequence 241, App
c 16	273.2	38.8	771	US-09-598-326-241	Sequence 241, App
17	267.2	37.9	387	US-08-379-072A-20	Sequence 20, Appli
18	267.2	37.9	387	US-08-478-039-109	Sequence 109, App
19	267.2	37.9	387	US-08-481-869-20	Sequence 20, Appli
20	267.2	37.9	387	US-08-476-349A-109	Sequence 109, App
21	267.2	37.9	387	US-08-476-237-16	Sequence 16, Appli
22	267.2	37.9	387	US-08-523-894-3	Sequence 3, Appli
23	260.4	36.9	327	US-09-202-181-1	Sequence 1, Appli
24	259.4	36.8	408	US-09-025-769B-169	Sequence 169, App
25	249.8	35.4	642	US-08-634-783A-4	Sequence 4, Appli
26	249.8	35.4	642	US-09-070-817-4	Sequence 4, Appli
27	246.2	34.9	346	US-08-761-277A-50	Sequence 50, Appli

28	246	34.9	333	2	US-08-477-553A-44	Sequence 44, Appli
29	244.2	34.6	324	1	US-08-259-372A-9	Sequence 9, Appli
30	244.2	34.6	324	1	US-08-468-671-9	Sequence 9, Appli
31	242.4	34.4	318	2	US-08-646-981-4	Sequence 4, Appli
32	237.4	33.7	431	2	US-08-345-321-7	Sequence 7, Appli
33	226.4	32.1	318	1	US-08-436-463-9	Sequence 9, Appli
34	226.4	32.1	318	1	US-08-024-253-9	Sequence 9, Appli
35	212	30.1	324	1	US-08-360-125-10	Sequence 10, Appli
36	212	30.1	324	2	US-08-450-578-10	Sequence 10, Appli
37	212	30.1	324	2	US-09-017-628-10	Sequence 10, Appli
38	212	30.1	324	2	US-09-014-880-10	Sequence 10, Appli
39	212	30.1	324	4	US-08-450-363-10	Sequence 10, Appli
40	202.2	28.7	314	4	US-09-370-838-13	Sequence 13, Appli
41	200.2	28.4	831	4	US-09-260-527-2	Sequence 2, Appli
42	200.2	28.4	840	4	US-09-260-527-4	Sequence 4, Appli
43	199.4	28.3	930	4	US-09-079-029-6	Sequence 6, Appli
44	199.4	28.3	939	4	US-09-079-029-7	Sequence 7, Appli
45	187.6	26.6	318	1	US-08-259-372A-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-487-550-1
; Sequence 1, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..705
US-08-487-550-1

Query Match 100.0%; Score 705; DB 3; Length 705;

```
Best Local Similarity 100.0%; Pred. No. 3.4e-186;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGGTCCCCGCTCAGCTCTCTGGGGCTCTCTGGCTCCAGGTGCAGATGT 60
Db 1 ATGAGGGTCCCCGCTCAGCTCTCTGGGGCTCTCTGGCTCCAGGTGCAGATGT 60
QY 61 GCCTATGAATGACTCAGCACCCTCGTGTGTCAGTGTCCCAAGGACAGACGCCAGGATC 120
Db 61 GCCTATGAATGACTCAGCACCCTCGTGTGTCAGTGTCCCAAGGACAGACGCCAGGATC 120
QY 121 ACCTGTGGGGGAGACACAGTGAATGAATATGTCCTGCTACAGCAGAGCCAGCG 180
Db 121 ACCTGTGGGGGAGACACAGTGAATGAATATGTCCTGCTACAGCAGAGCCAGCG 180
QY 181 CGGGCCCTTATCTGCTGCTATCTATGATGATAGTACCGGCCCTCAGGGATCCTGAGGA 240
Db 181 CGGGCCCTTATCTGCTGCTATCTATGATGATAGTACCGGCCCTCAGGGATCCTGAGGA 240
QY 241 TTCTCTGGCTCCAAATCAGGGAACACCGCCCTGACCATCAACGGGGTCGAGCCGGG 300
Db 241 TTCTCTGGCTCCAAATCAGGGAACACCGCCCTGACCATCAACGGGGTCGAGCCGGG 300
QY 301 GATGAGGCTGACTATTAATCTCAGGTGGGACAGGGCTAGTATCATCCGTCTTCGGA 360
Db 301 GATGAGGCTGACTATTAATCTCAGGTGGGACAGGGCTAGTATCATCCGTCTTCGGA 360
QY 361 GGAGGACCCGGGTGACCTCTAGTGTAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 420
Db 361 GGAGGACCCGGGTGACCTCTAGTGTAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 420
QY 421 CGCCCTCTCTGAGGAGTTCACAGCAACAGGCAACACTGGTGTGTCTCATAGTGAC 480
Db 421 CGCCCTCTCTGAGGAGTTCACAGCAACAGGCAACACTGGTGTGTCTCATAGTGAC 480
QY 481 TTCTACCCGGGAGCGTGACGTGGCTGGAGGAGAGATAGCAGCCCGCTCAGCGGGA 540
Db 481 TTCTACCCGGGAGCGTGACGTGGCTGGAGGAGAGATAGCAGCCCGCTCAGCGGGA 540
QY 541 GTGGAGACCCACACACCTCTAGTGTAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 600
Db 541 GTGGAGACCCACACACCTCTAGTGTAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 600
QY 601 AGCTGACCCCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTCAAGCATGAA 660
Db 601 AGCTGACCCCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTCAAGCATGAA 660
QY 661 GGGAGACCTGGAGAGACAGTGGCCCTCAGAAATGTTATGA 705
Db 661 GGGAGACCTGGAGAGACAGTGGCCCTCAGAAATGTTATGA 705
```

RESULT 2

```
US-08-523-894-5
; Sequence 5, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; City: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: lambda variable and constant domains in
; CHROMOSOME/SEGMENT: CE9.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..702
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..702
; US-08-523-894-5
;
; Query Match 83.0%; Score 585.2; DB 3; Length 702;
; Best Local Similarity 89.6%; Pred No. 5e-153;
; Matches 629; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 4 AGGGTCCCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGCTCCCAAGGTGCACGATGTGCC 63
Db 1 ATGGCTTGGGCTCTGCTGCTCTCTGGGCTCTCTGCTCACTTTACAGACTCTGCGGCTCC 60
QY 64 TATGAATGACTCAGCACCCTCGGTGTCAGTGTCCCAAGGACAGACGGCCAGGATCACC 123
Db 61 TATGAGTTGAGTCAGCCTCGCTCAGTGTCCGTCCTCCAGGACAGACGGCCGGTTTACC 120
QY 124 TGTGGGGAGACAACTAGTAATATGTCCACTGTGTACAGAGAGCCAGCGCGG 183
Db 121 TGTGGGGAGACAACTTGGAGGAAAAGTGTACAGTGTACAGCAGAGAACCCAG 180
QY 184 GCCCCTATCTGCTCATCTATGATGATGATGACCGGCCCTCAGGGATCCTGAGCATTC 243
Db 181 GCCCCTGTGCTGCTCATCTATGCTGACAGGAAGGCCCTCAGGGATCCTGCGGATTC 240
QY 244 TCTGGCTCCAAATCAGGGAACACCGCCACCTTGACCATCAACGGGGTCAGGCGGGGAT 303
Db 241 TCTGGCTCCAACTCAGGGAACACCGCCACCTTGACCATCAGCGGGTCAGGCGGGGAT 300
QY 304 GAGGCTGACTATTACTGTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCCGAGGA 363
Db 301 GAGGCTGACTATTACTGTGTCAGGTGTGGGACAGTACTGTGATCATTTGGGTCTTCCGCGGA 360
QY 364 GGGACCCGGGTGACCGTCTCTAGGTGACGCCAAGGTCGCCCTCCGGTCACTCTGTFTCCCG 423
Db 361 GGGACCCGGGTGACCGTCTCTAGGTGACGCCAAGGTCGCCCTCCGGTCACTCTGTFTCCCG 420
QY 424 CCCTCTCTGAGGAGCTTCAAGCAACAGGGCCACACTGGTGTGTCTCATAGTGNCTTC 483
Db 421 CCCTCTCTGAGGAGCTTCAAGCAACAGGGCCACACTGGTGTGTCTCATAGTGNCTTC 480
QY 484 TACCCGGGAGCCGTGACAGTGGGCTGGAAGGAGAGATAGCAGCCCGCTCAAGCGGGAGTG 543
Db 481 TACCCGGGAGCCGTGACAGTGGGCTGGAAGGAGAGATAGCAGCCCGCTCAAGCGGGAGTG 540
```


RESULT 6
 US-09-049-672A-25
 / Sequence 25, Application US/09049672A
 / Patent No. 6135941
 / GENERAL INFORMATION:
 / APPLICANT: Hillman, Jennifer L.
 / APPLICANT: Lai, Preeti
 / APPLICANT: Tang, Y. Tom
 / APPLICANT: Yue, Henry
 / APPLICANT: Au-Young, Janice
 / APPLICANT: Corley, Neil C.
 / APPLICANT: Guegler, Karl J.
 / APPLICANT: Baughn, Mariah R.
 / TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
 / NUMBER OF SEQUENCES: 28
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Incyte Pharmaceuticals, Inc.
 / STREET: 3174 Porter Drive
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94304
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FASTSEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/049,672A
 / FILING DATE: HEREWITH
 / CLASSIFICATION: 536
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Cerrone, Michael C

Db 147 GGGAAACAACAATGTTGGGCAACAGGAGCAGCTTGGCTGCAGCAGCACCAGGCGCCAC 206
Qy 184 GCCCTATACCTGCTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTTC 243
Db 207 CTCTCCAAACTCTCTCTACAGGATTAATAACCGGCCCTCAGGGATCTCAGAGAGATT 266
Qy 244 TCTGGCTCAAAATCAGGAAACACCGCCACCTTGACCAATCAACCGGGTTCAGGCGCGGAT 303
Db 267 TCTGATCCAGGTGAGGAGCAGATCTCTCCCTGACCAATTAAGTCTCCAGGCTGAGGAC 326
Qy 304 GAGGCTGACTATTACTGTCAGGTGGGACAGGAGCTAGTATCATCCGCTCTTCGAGGA 363
Db 327 GAGGCTGACTATTACTGTCGAGCATATGACAGAGCTTCGAGTTGGATGTTTCGGCGA 386
Qy 364 GGGACCGGGTGACCGTCTTAGGTGAGCCCAAGGCTGCCCGCTCGGTCTACTGTTCCGG 423
Db 387 GGGACCAAGCTGACCGTCTTAGGTGAGCCCAAGGCTGCCCGCTCGGTCTACTGTTCCCA 446
Qy 424 CCTCTCTGAGGAGCTTCAAGCCAAAGGCAACAGGCTGCTGATGATGATGATGATGATGAT 483
Db 447 CCTCTCTGAGGAGCTTCAAGCCCAAGGCTGCTGATGATGATGATGATGATGATGATGAT 506
Qy 484 TACCGGAGCGGTGACAGTGGCTGAGGAGCAGATGAGAGCCCGCTCAAGCGCGGAGTG 543
Db 507 TACCGGAGCGGTGACAGTGGCTGAGGAGCAGATGAGAGCCCGCTCAAGCGCGGAGTG 566
Qy 544 GAGACACACACCTCTCAAAAGGCAACAGGCTGAGGAGCAGATGAGAGCCCGCTCAAGCGCGGAGTG 603
Db 567 GAGACACACACCTCTCAAAAGGCAACAGGCTGAGGAGCAGATGAGAGCCCGCTCAAGCGCGGAGTG 626
Qy 604 CTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTACGATGAGAGG 663
Db 627 CTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTACGATGAGAGG 686
Qy 664 AGCAGCGTGGAGAGACAGTGGCGCCCTACAGATGTTTCAT 703
Db 687 AGCAGCGTGGAGAGACAGTGGCGCCCTACAGATGTTTCAT 726

RESULT 9

US-09-152-060-29
; Sequence 29, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-29
Query Match 61.6%; Score 434; DB 4; Length 879;
Best Local Similarity 81.1%; Pred. No. 4e-111;
Matches 519; Conservative 0; Mismatches 115; Indels 6; Gaps 1;
Qy 70 CTGACTCAGCCACCTCCGCTGTCAGTGTCCCGGACAGACGAGGATCACTCTGTGGG 129
Db 79 CTGACTCAGCCACCTCCGCTGTCAGTGTCCCGGACAGACGAGGATCACTCTGTGGG 138
Qy 130 GGAGACAACAGTAGAATG-----AATATGTCCACTGGTACCAAGAGAGGAGGAGGAGG 183
Db 139 GGAACAACAACAATGTTGGGCAACAGGAGCAGCTTGGCTGCAGCAGCAGCAGGCGCCAC 198
Qy 184 GCCCTATACCTGCTCATCTATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGATTTC 243
Db 199 CTTCCTCAACTCTGCTCTACAGGATTAATAACCGGCCCTCAGGGATCTCAGAGAGATT 258
Qy 244 TCTGGCTCAAAATCAGGAAACACCGCCACCTTGACCAATCAACCGGGTTCGAGGCGCGGAT 303
Db 259 TCTGATCCAGGTGAGGAGCAGATCTCTCCCTGACCAATTAAGTCTCCAGCTCCAGCTGAGGAC 318
Qy 304 GAGGCTGACTATTACTGTCAGTGTGGGACAGGAGCTAGTATCATCCGCTCTTCGAGGA 363
Db 319 GAGGCTGACTATTACTGTCGAGCATATGACAGAGCCTCGCAGTTTGGATGTTTCGGCGGA 378
Qy 364 GGAACCGGGTGACCGTCTTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCG 423
Db 379 GGAACCAAGCTGACCGTCTTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCA 438
Qy 424 CCTCTCTGAGGAGCTTCAAGCCAAAGGCAACAGGCTGCTGATGATGATGATGATGATGAT 483
Db 439 CCTCTCTGAGGAGCTTCAAGCCAAAGGCTGCTGATGATGATGATGATGATGATGATGAT 498
Qy 484 TACCGGAGCGGTGACAGTGGCTGAGGAGCAGATGAGAGCCCGCTCAAGGCGGAGTG 543
Db 499 TACCGGAGCGGTGACAGTGGCTGAGGAGCAGATGAGAGCCCGCTCAAGGCGGAGTG 558
Qy 544 GAGACACACACCTCCAAAGGCAACAGGCTGAGGAGCAGATGAGAGCCCGCTCAAGGCGGAGTG 603
Db 559 GAGACACACACCTCCAAAGGCAACAGGCTGAGGAGCAGATGAGAGCCCGCTCAAGGCGGAGTG 618
Qy 604 CTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTACGATGAGAGG 663
Db 619 CTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTACGATGAGAGG 678
Qy 664 AGCAGCGTGGAGAGACAGTGGCGCCCTACAGATGTTTCAT 703
Db 679 AGCAGCGTGGAGAGACAGTGGCGCCCTACAGATGTTTCAT 718

RESULT 10

US-09-152-060-46/c
; Sequence 46, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100

Qy	145	AATGAATATGTCAC	TGGTACCAAGCAAGCAGCGCGGGCCCCAT	ATGTGTCACTCA	203
Db	900	AAGAAATATGTWTAT	TGGTACCAACGAAGTCAGGCCAGGCCCTGTGGCTGTGTCACTCA	841	
Qy	204	TGATGATAGTACCGG	CCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGAA	263	
Db	840	TCAGGACAAACAAAC	CGACCTCC-GGATCCCTSAGAGATTCTYGGCTCCAGYTCAGGGAC	782	
Qy	264	CACCCGCCCTGACCA	TCATCAACGGGTTCAGCGCGGGATGAGGTGACTATTACTTGTC	323	
Db	781	AGTGGCCACCTTGAC	TATCATAGTGGGCCCAAGGTGAGAGATGGGCTGACTACTACTTGTT	722	
Qy	324	GGTGTGGGACAGGC	TAGTGATCATCGGTCTTCGAGAGGGACCCGGGTGACCGTCCT	383	
Db	721	CTCAACAGACAGAGT	GGTAATCATGGKGTCTTCGGAACCTGGGACCAAGGTCAACGTCCT	662	
Qy	384	AGGTGAGCCCAAGG	TGCGCCCTCGGTCACTCTGTTCCGCGCTCTCTTGAGAGCTTCA	443	
Db	661	AGGTGAGCCCAAGG	CCYRMCCKGTCACTCTGTTCCGCGCTCTCTGAGGAGCTYCA	602	
Qy	444	AGCCACAGGCGCAC	TGCTGTGTCTCTAAGTGNCATCTTACCGGGAGCCGTGACGT	503	
Db	601	AGCCACAGGCGCAC	TRGTGTGTCTSATMAGTGACTTCTACCGGGAGCTGTGACGT	542	
Qy	504	GGCCTGGAAGCAGA	TAGCAGCCCGTCAAGCGGGAGTGGAGACCACACACCTCCAA	563	
Db	541	GGCCTGGAAGCAG	ATRGAGCCCGCTCAAGCGGGAGTGGAGACCACCAACCTCCAA	482	
Qy	564	ACAAAGCAACAAAG	TACGGCCAGCAGCTACTTGAGCCTGACGCTGAGCAGTGGA	623	

Qy	66	TGA	CTG	ACT	CAG	CC	CC	CT	CG	GT	G	T	C	A	G	T	G	T	C	C	C	C	A	G	A	C	A	G	C	C	A	G	A	C	A	C	T	G	125				
Db	125	TG	T	G	T	G	A	C	C	C	A	G	A	G	C	A	T	C	G	T	T	C	A	G	T	G	T	C	C	C	T	G	A	G	G	A	C	A	C	A	C	T	184
Qy	126	TG	G	-----	-----	GGG	A	C	A	A	C	A	G	T	A	G	A	A	T	G	A	T	T	T	C	C	A	T	G	T	G	T	A	C	C	A	G	A	A	G	C	176	

D _b	185	TGGCTTGAGCTCTGGGCTCAGTCTCTACTAGTAGTAATCCACAGCTGGGTACCAGACAGCCCC	244
Q _y	177	AGCGGGGCCCTATACTGGTCATCTATGATGATAGTACCGGCOCCTCAGGGAATCCCCTGA	236
D _b	245	AGGCCAGGCTCCAACGACGCTCATATACGGACAAGTTGTTGCTTTCTTGAGTCCCTGA	304
Q _y	237	GCGATTCTCTGGCTCCAAATCAGGSMAACCGCACCCCTGACCAATCACAGGGGTCGAGGC	296
D _b	305	TCGCTTCTCTGGCTCCATCTCTTGGGNAAGAAGCCGGCTCAACATCACGGGGGCCAAGGC	364
Q _y	297	CGGGGATGAGGCTGATATTACTGTCAAGTGTGGGACAGGGCTAGTGATCATCCGGTCTT	356
D _b	365	AGATGATGAATCTGATTATTATTGT---GTCCTATATAGSCGTAGTGCTCTTGGGTGTT	421
Q _y	357	CGAGAGGAGGACCCGGGTGACCGGTCTTAGTACGCCAACAGGTGCCCCCTCGGTCACTCT	416
D _b	422	CGCGGAGGGAACAAGCTGTCCGTCTTAGTACGCCAACAGGTGCCCCCTCGGTCACTCT	481
Q _y	417	GTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGGTGTCCTCATAG	476
D _b	482	GTTCACCACTCTCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTGTCTCATAG	541
Q _y	477	TGACTTCTACCCGGAGCGGTGA CAGTGGCTGGAAAGCAGATAGCACCCCGGTCAAGGC	536
D _b	542	TGACTTCTACCCGGGAGCGGTGA CAGTGGCTTGGAGGCCAGATAGCACCCCGGTCAAGGC	601
Q _y	537	GGGAGTGGAGACCAACACACCTCCAAACAAGCAACAACATGATACGGCCGACAGCTA	596
D _b	602	GGAGTGGAGACCAACACCTCCAAACAAGCAACAACATGATACGGCCGACAGCTA	661
Q _y	597	CTTGAGCTTGACGCTGAGCAGTGGAAAGTCCCACAGAGCTACAGTCCGACAGGTCAAGCA	656
D _b	662	CCTGAGCTTGACGCTGAGCAGTGGAAAGTCCCACAAAAGCTACAGTCCGACAGGTCAAGCA	721
Q _y	657	TGAAGGGAGCACCGTGGAGAGACAGTGGGCCCTCAGAAATGTTCAT	703
D _b	722	TGAAGGGAGCACCGTGGAGAGACAGTGGGCCCTCAGAAATGTTCAT	768

RESULT 12

US-08-793-450-5
: Sequence 5, Application US/08793450
: Patent No. 6312690
: GENERAL INFORMATION:
: APPLICANT: EDELMAN, LENA
: APPLICANT: MARGARITTE, CHRISTEL
: APPLICANT: KACZOREK, MICHEL
: APPLICANT: CHABUHI, HASSAN
: TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
: TITLE OF INVENTION:
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
: ADDRESSEE: P.C.
: STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/793,450
: FILING DATE: 03-MAR-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94/10566
: FILING DATE: 02-SEP-1994
: ATTORNEY/AGENT INFORMATION:

QY 677 AGACAGTGGCCCTACAGAAATGTTTAT 703
|||||
Db 689 AGACGGTGGCCCTGCAGAAATGTTTAT 715

RESULT 13

US-09-404-879A-268/c
; Sequence 268, Application US/09404879A

; Patent No. 6468546

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.462C2

; CURRENT APPLICATION NUMBER: US/09/404,879A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 393

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 268

; LENGTH: 584

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)....(584)

; OTHER INFORMATION: n = A,T,C or G

US-09-404-879A-268

Query Match 43.5%; Score 306.6; DB 4; Length 584;
Best Local Similarity 85.0%; Pred. No. 6.7e-76;
Matches 367; Conservative 0; Mismatches 57; Indels 8; Gaps 2;

QY 215 ACCGGCCCTCAGGATCCCTGAGCAATCTCTGGCTCCAAATCAGGG-----AACACCGC 269

Db 449 AGCGGCCCTCAGGGTCCCTGATCGCTTCTGCTTCCAAATCAGGG-----AACACCGC 390

QY 270 CACCTGTACCATCAACGGGGTCCAGGGGATGAGGCTGACTATTACTGTCTCAGGTGTG 329

Db 389 TCCCTTGACNGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTACTGCACTATA 330

QY 330 GACAGGGCTAGTATGATCCCGTCTTCGAGAGGAGGACCCGGGTGACCGTCTAGGTCA 389

Db 329 TGCAGGCAACA---ACAATTGGGTGTTCGGCGGAGGACCAAGCTGACCGTCTAGGTCA 273

QY 390 GCCCAAGGCTGCCCTCGGTCACTCTGTTCGCCCTCTCTGAGGAGCTTCAAGCAA 449

Db 272 GCCCAAGGCTGCCCTCGGTCACTCTGTTCGCCCTCTCTGAGGAGCTTCAAGCAA 213

QY 450 CAAGGCCACACTGGTGTCTCATAGTGAATTTTACCCGGAGCCGTTGACAGTGGCTG 509

Db 212 CAAGGCCACACTGGTGTCTCATAGTGAATTTTACCCGGAGCCGTTGACAGTGGCTG 153

QY 510 GAAGGCAGATACAGCCCGTCAAGCGGAGTGGAGACCAACACCTCCAAACAAAG 569

Db 152 GAAGGCAGATACAGCCCGTCAAGCGGAGTGGAGACCAACACCTCCAAACAAAG 93

QY 570 CAACAAAGTACCGGGCCAGCAGTACTGAGCTGACGCTGACGCTGAGAGTGGAAAGTCCCA 629

Db 92 CAACAAAGTACCGGGCCAGCAGTACTGAGCTGACGCTGACGCTGAGAGTGGAAAGTCCCA 33

QY 630 CAGAGCTACAG 641

Db 32 CAGAGCTACAG 21

RESULT 14

US-09-991-789A-241/c

; Sequence 241, Application US/08991789A

; Patent No. 6225054

; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 292

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed IP Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/991,789A

FILING DATE: 11-Dec-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 210121.419C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 241:

SEQUENCE CHARACTERISTICS:

LENGTH: 771 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 241:

US-08-991-789A-241

Query Match 38.8%; Score 273.2; DB 4; Length 771;
Best Local Similarity 79.2%; Pred. No. 1.3e-66;
Matches 336; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

QY 131 GAGACAAACAGTAGAAATATCTCCACTGGTACCAAGAGAGCCAGCGCGGGCCCCCTA 190

Db 430 GTGAGTTGGTGTATATAATCTCTCTGTTGTTACCAACAGCACCAGGCAAGCCCCCA 371

QY 191 TACTGGTCACTATGATGATAGTACCGGGCCCTCAGGGATCCCTGAGCGATTCTTGGCT 250

Db 370 AATTCAATTTATGAGTCCGTTAATCGGGCCCTCAGGGGTTTCTAATCGCTTCTTGGCT 311

QY 251 CCAAAATCAGGAAACACCGCCACCTGACCATCAACGGGGTCCGAGGCGGGGATGAGGCTG 310

Db 310 CCAAGTNTGGCAACCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAGGCTG 251

QY 311 ACTATTACTGTAGGTGGGACAGGCTGTATCATCCGGTCTTCGAGGAGGAGGACCC 370

Db 250 ATTATTTACTG---CAGCTCATATACAAGCAGCAGCACTCTCGTGTTCGCGGAGGACCA 194

QY 371 GGGTGACCGCTCTAGGTGAGGCTGCGCCCTCGGCTCACTCTGTTCGCGGCTTCTTCCCT 430

Db 193 AGCTGACCGCTCTAGGTGAGGCTGCGCCCTCGGCTCACTCTGTTCGCGGCTTCTTCCCT 134

QY 431 CTGAGGAGCTTCAAGGCCAACAGGCCACACTGTGTGTCTCATTAAGTGAATTTTACCCGG 490

Db 133 CTGAGGAGCTTCAAGGCCAACAGGCCACACTGTGTGTCTCATTAAGTGAATTTTACCCGG 74

QY 491 GAGCGGTGACAGTGGCGCTGGAAGGACAGATAGCAGCCCGCTCAAGGGGGAGTGGAGACCA 550

Db 73 GAGCGGTGACAGTGGCGCTGGAAGGACAGATAGCAGCCCGCTCAAGGGGGAGTGGAGACCA 14

QY 551 CCAC 554
Db 13 CTAC 10

RESULT 15

US-09-062-451-241/c
; Sequence 241, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,451
; FILING DATE: 04-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.419C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 241:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-062-451-241

Query Match 38.8%; Score 273.2; DB 4; Length 771;
Best Local Similarity 79.2%; Pred. No. 1.3e-66;
Matches 336; Conservative 0; Mismatches 85; Indels 3; Gaps 1;
QY 131 GAGACACAGTAGAATCAATATCTCCACTGGTACACAGACAGCCGCGGGCCCTTA 190
Db 430 GTGACGTTGGTGTAAATATCTCTGTTGTTACCAACAGACCCAGGCAAGCCCTCA 371
QY 191 TACTGGTCATCTATCATGATAGTAGCCGCGCCTCAGGGATCCCTGAGCGATTCTCTGGCT 250
Db 370 AATTCATGATTTATGAGGTCGGTAATCGGCCCTCAGGGTTTCTAATCGCTTCTCTGGCT 311
QY 251 CCAATACGGGAACACCGCCACCTGACCATCAACCGGGGTGAGGGCCGGGGATGAGGCTG 310
Db 310 CCAAGTNTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGACGAGGCTG 251
QY 311 ACTATTACTGTTCAGGTGGGACAGGGCTAGTGNATCATCGGTTCTCGGAGGAGGACCC 370
Db 250 ATTATTACTG---CAGCTCATATACAAGACGACACTCTCGTGTGTTGGCGGAGGACCA 194
QY 371 GGGTGACCGTCTTAGGTGAGGCTGAGGCTGCGCCCTCGGTCACTCTGTTCCCGCCCTCCT 430
Db 193 AGCTGACCGTCTTAGGTGAGGCTGAGGCTGCGCCCTCGGTCACTCTGTTCCCAACCTCCT 134

QY 431 CTGAGGAGCTTCAAGCCCAACAGGCCACACTGCTGTGTCTCATAAGTACTTCTACCCGG 490
Db 133 CTGAGGAGCTTCAAGGCCCAACAGGCCACACTGCTGTGTCTCATAAGTACTTCTACCCGG 74
QY 491 GAGCCGTGACAGTGGGCTTGAAGGCGAGATAGCAGCCCGCTCAAGGCGGGAGTGGAGACCA 550
Db 73 GAGCCGTGACAGTGGGCTTGAAGGCGAGATAGCAGCCCGCTCAAGGCGGGAGTGGAGACCA 14
QY 551 CCAC 554
Db 13 CTAC 10

Search completed: April 6, 2003, 06:25:10
Job time : 34.1002 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:05 ; Search time 2231 Seconds
(without alignments)
9274.790 Million cell updates/sec

Title: US-09-758-173-9
Perfect score: 711
Sequence: 1 ATGAGGTCCCGCTCAGCT.....CCCTACAGAATGTTTCATCA 711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: gb_ba.*	GenEmbl.*
2: gb_htg.*	
3: gb_in.*	
4: gb_om.*	
5: gb_ov.*	
6: gb_pat.*	
7: gb_ph.*	
8: gb_pl.*	
9: gb_pr.*	
10: gb_ro.*	
11: gb_sts.*	
12: gb_sy.*	
13: gb_un.*	
14: gb_vi.*	
15: em_ba.*	
16: em_fun.*	
17: em_hum.*	
18: em_in.*	
19: em_mu.*	
20: em_om.*	
21: em_or.*	
22: em_ov.*	
23: em_pat.*	
24: em_ph.*	
25: em_pl.*	
26: em_ro.*	
27: em_sts.*	
28: em_un.*	
29: em_vi.*	
30: em_htg_hum.*	
31: em_htg_inv.*	
32: em_htg_other.*	
33: em_htg_mus.*	
34: em_htg_pln.*	
35: em_htg_rod.*	
36: em_htg_mam.*	
37: em_htg_vrt.*	
38: em_sy.*	
39: em_htgo_hum.*	
40: em_htgo_mus.*	
41: em_htgo_other.*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	711	100.0	711	6	AR108866	AR108866 Sequence
2	582.6	81.9	935	6	ARI35362	ARI35362 Sequence
3	575.4	80.9	790	9	AB064208	AB064208 Homo sapi
4	573	80.6	870	9	HSIGLV	X14583 Human mRNA
5	571.2	80.3	903	9	BC020233	BC020233 Homo sapi
6	570.6	80.3	827	9	AB064143	AB064143 Homo sapi
7	566.6	79.7	800	9	AB064188	AB064188 Homo sapi
8	566.4	79.7	919	9	BC022098	BC022098 Homo sapi
9	566	79.6	815	9	AB064149	AB064149 Homo sapi
10	562.8	79.2	812	9	AB064148	AB064148 Homo sapi
11	562.4	79.2	816	9	AB064147	AB064147 Homo sapi
12	562.4	79.1	827	9	AB064219	AB064219 Homo sapi
13	562.2	79.1	750	9	HSIGVL027	XS7817 Human rearr
14	560	78.8	747	9	HSIGVL006	XS7806 Human rearr
15	558	78.5	821	9	AB064141	AB064141 Homo sapi
16	558	78.5	824	9	AB064227	AB064227 Homo sapi
17	557.6	78.4	804	9	AB064172	AB064172 Homo sapi
18	556.4	78.3	790	9	AB064206	AB064206 Homo sapi
19	556.4	78.3	824	9	AB064226	AB064226 Homo sapi
20	555.4	78.1	827	9	HSIGVL021	XS7811 Human rearr
21	554.8	78.0	816	9	AB064150	AB064150 Homo sapi
22	554.4	78.0	790	9	AB064169	AB064169 Homo sapi
23	554.4	78.0	803	9	AB064166	AB064166 Homo sapi
24	553.2	77.8	829	9	AB064203	AB064203 Homo sapi
25	552.8	77.7	788	9	AB064171	AB064171 Homo sapi
26	552.8	77.7	789	9	AB064170	AB064170 Homo sapi
27	552.8	77.7	819	9	AB064151	AB064151 Homo sapi
28	551.6	77.6	781	9	AB064216	AB064216 Homo sapi
29	550	77.4	828	9	AB064222	AB064222 Homo sapi
30	548.4	77.1	827	9	AB064218	AB064218 Homo sapi
31	548.4	77.1	831	9	AB064224	AB064224 Homo sapi
32	547.8	77.0	802	9	HSIGVL032	XS7822 Human rearr
33	546.2	76.8	810	9	HSIGVL025	XS7815 Human rearr
34	546.2	76.8	816	9	AB064178	AB064178 Homo sapi
35	545.6	76.7	9472	6	AX287808	AX287808 Sequence
36	545	76.7	789	9	AB064205	AB064205 Homo sapi
37	541	76.1	927	9	BC012876	BC012876 Homo sapi
38	540.8	76.1	648	9	AF191795	AF191795 Homo sapi
39	540.4	76.0	824	9	AB064228	AB064228 Homo sapi
40	540.2	76.0	705	6	ARI08862	ARI08862 Sequence
41	538.8	75.8	823	9	AB064142	AB064142 Homo sapi
42	534.8	75.2	651	9	AB027448	AB027448 Homo sapi
43	533.8	75.1	818	9	AB064146	AB064146 Homo sapi
44	533.2	75.0	651	6	E15551	E15551 cDNA encodi
45	533.2	75.0	708	6	BD013339	BD013339 Novel pep

ALIGNMENTS

RESULT 1
LOCUS AR108866
DEFINITION Sequence 9 from patent US 6113898.
ACCESSION AR108866
VERSION AR108866.1 GI:12825142
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 711)
AUTHORS Anderson,D.R., Brame,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transectomas
expressing said antibodies
JOURNAL Patent: US 6113898-A 9 05-SEP-2000;

Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: Isolation of therapeutic human antibodies and application to functional genomics
Unpublished
2 (bases 1 to 790)
Kurosawa,Y.
Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;
Kurusake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.

FEATURES
Source
1..790
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="L68"
/clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
1..790
/gene="IGL"
1..>790
/gene="IGL"
/codon_start=1
/product="immunoglobulin lambda light chain VLJ region"
/protein_id="BAC01836.1"
/db_xref="GI:2169623"
/translation="MKYLLPTAAAGLLLAQPMASQSVLTQPPSVSGPQGVITSL
TGSNNICAGDYVHWYQOLPCTAPKLLIYGNRNPSGPDPRFSGSKSGTSASLAIATGL
QADEADYQCVDSLSLGVFGGWTLVLGQPKAASVTLPFPPSEELQANKATLV
CLISDFYPGATVAWKADSPVAGVETTPSQSNKNKYAASLYSLTPEQWKSHSY
SCQVTHGSTEKTVAPTECSARQSTPFVCEYQGQSDLPQPPVN"
1..66
/gene="IGL"
/note="pe1B signal peptide"
BASE COUNT 176 a 250 c 213 g 151 t
ORIGIN
|||||
62 AGTCTGCTCTGACAGCGCCCTCAGTGTCTGGGCCCCAGGCAGAGTCAACATCT 121
|||||
68 AGTCTGTGTTGACGAGCGCCCTCAGTGTCTGGGCCCCAGGCAGAGTCAACATCT 127
|||||
122 CGTGCACCTGGGAGCACCTCCCAACATTGG- --AGTTATGATCTACATTGGTACCAGCAGC 178
|||||
128 CTGCACTGGGAGCAGCTCCAACTCGGGCAGGTTATGATGATACATGTTACAGCAGC 187
|||||
179 TCCAGGAACCGCCCCCAAACTCTCTATGATGATTAACAGCGACCTTCAGGAATTT 238
|||||
188 TTCCAGGAACAGCCCCCAAACTCTCTATGATGATTAACAGCAATCGGCCCTCAGGGGTCC 247
|||||
239 CTGACCGATTCTGGCTCCAGTCTGATACCGGGCTCTCCCTGGCCATCACTGGGCTCC 298
|||||
248 CTGACCGATTCTGGCTCCAGTCTGATACCGGGCTCTCCCTGGCCATCACTGGGCTCC 307
|||||
299 AGACTGAGGATCAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTGAATCTCAGG 358
|||||
308 AGGCTGAGGATCAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTGATGTTGTTGG 367
|||||
359 TATTCGAGGAGGACCGGCTGACCGTCTAGTACGCCCAAGCTGCCCTTCGGTCA 418
|||||
368 TATTTCGGCGGAGGACCAAGCTGACCGTCTAGTACGCCCAAGCTGCCCTTCGGTCA 427
|||||
419 CTCTGTTCCCGCCCTCTCTAGGAGCTTCAAGCAACAGGCCACACTGGTGTGTTCTCA 478
|||||

Query Match 80.9%; Score 575.4; DB 9; Length 790;
Best Local Similarity 94.0%; Pred. No. 8.3e-139;
Matches 610; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

Db 428 CTCTGTTCCACCCCTCTCTGAGGAGCTTTCAAGCCAAACAGGCCACACTGGTGTGTCTCA 487
QY 479 TAAGTCACTTCTACCCGGGAGCGGTGACAGTGGCTTGGAAAGCAGATAGCAGCCCGTCA 538
Db 488 TAAGTCACTTCTACCCGGGAGCGGTGACAGTGGCTTGGAAAGCAGATAGCAGCCCGTCA 547
QY 539 AGCGGAGTGGAGACCAACACACCTCCAAAACAAAGCAACAAAGTACGCGGCCAGCA 598
Db 548 AGCGGAGTGGAGACCAACACACCTCCAAAACAAAGCAACAAAGTACGCGGCCAGCA 607
QY 599 GCTACCTGAGCCTGAGCCTGAGCAGTGAAGTCCACAGAAAGCTACAGTGCAGGTCA 658
Db 608 GCTACCTGAGCCTGAGCCTGAGCAGTGAAGTCCACAAAGCTACAGTGCAGGTCA 667
QY 659 CGCATCAAGGAGCAGCCGTGGAGAGACAGTGGCCCTACAGAATGTTTC 707
Db 668 CGCATCAAGGAGCAGCCGTGGAGAGACAGTGGCCCTACAGAATGTTTC 716

RESULT 4
HSIGLV
LOCUS Human mRNA for Ig lambda-chain.
DEFINITION
ACCESSION X14583
VERSION X14583.1 GI:33394
KEYWORDS Ig light chain; immunoglobulin; lambda-immunoglobulin.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS Kishimoto,T.
TITLE Direct Submission
JOURNAL Submitted (03-Mar-1989) Kishimoto T., Yoshitomi Pharmaceutical Industries Ltd, Research Labs, 7-25 Koyata 3-chome, Iruma Shi, Saitama, 358 Japan
REFERENCE 2 (bases 1 to 414)
AUTHORS Kishimoto,T., Okajima,H., Okumoto,T. and Taniguchi,M.
TITLE Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells
JOURNAL Nucleic Acids Res. 17 (11), 4385 (1989)
MEDLINE 89296497
PUBMED 2500644
COMMENT hybridoma: clones 4G12 L6
Data kindly reviewed (03-JUL-1989) by Kishimoto T.
FEATURES
source
Location/Qualifiers
1..870
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="4G12"
/cell_type="lymphocyte"
/tissue_type="lymph node"
25..732
/codon_start=1
/product="lambda-chain precursor (AA -20 to 215)"
/protein_id="CAA32725.1"
/db_xref="GI:33395"
/translation="MTCSPLLLLIHCTGSAOSVLTPSPVSAAPQKQVITSCSGS
SSNINNYVSWYQQLPGTAPKLLIYDNNRPSGIPDRFSGSKSGTSATLGTGLQTGD
EADYTCGTWDSLSAGVFGGKTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS
DFYPGATVAWKADSPVAGVETTPSQSNKNKYAASLYSLTPEQWKSHRSYSCQV
THEGSTVBKTVAPTECS"
25..84
sig_peptide
misc_feature 85..375
/note="V region"
misc_feature 376..414
/note="J region"
misc_feature 415..729
/note="C region"
BASE COUNT 206 a 285 c 213 g 166 t
ORIGIN


```
QY 358 GTATTTCGGAGGAGGACCGGCTGACCGTCTCTAGGTCTAGCCCAAGGTCGCCCTCGGTTC 417
Db 395 GTATTTCGGAGGAGGACCAAGCTACCGTCTCTAGGTCTAGCCCAAGGTCGCCCTCGGTTC 454
QY 418 ACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTCTC 477
Db 455 ACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTCTC 514
QY 478 ATAAGTACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGCAGCCCGTTC 537
Db 515 ATAAGTACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGCAGCCCGTTC 574
QY 538 AAGCGGAGGTGGAGACACACACACCTCCAAACAAGCAACAAGTACGCGGCCAGC 597
Db 575 AAGCGGAGGTGGAGACACACACACCTCCAAACAAGCAACAAGTACGCGGCCAGC 634
QY 598 AGCTACCTGAGCCTGACGCCCTGAGCAGTGGAGTCCCAACAAGCTACAGCTGCCAGGTC 657
Db 635 AGCTATCTGAGCCTGACGCCCTGAGCAGTGGAGTCCCAACAAGCTACAGCTGCCAGGTC 694
QY 658 ACGCATGAAGGAGACACCGTGGAGAGACAGTGGCCCTTACAGAATGTTTCAT 709
Db 695 ACGCATGAAGGAGACACCGTGGAGAGACAGTGGCCCTTACAGAATGTTTCAT 746

RESULT 6
AB064143 827 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
DEFINITION region, partial cds, clone:L3.
ACCESSION AB064143
VERSION AB064143.1 GI:21669492
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L3.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 827)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
COMMENT (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/
FEATURES
source Location/Qualifiers
1..827
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="L3"
/clone_lib="AIMS4"
/notes="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
1..827
/gene="IGL"
1..>827
/gene="IGL"
/codon_start=1
/product="immunoglobulin lambda light chain VLJ region"
/protein_id="BAC01771.1"
/db xref="GI:21669493"
/translations="MKVLLPTAAAGLLLLAOPAMAQSVLTQPPSLSGAPGQRTVISC
TGSNNIGAGDVHWYQQLPGTAPKLLIYGDINRPSGVDKSGKTSASLAITGL
QAEDEADYYCQSYDSSLSGVSFGGGLKLVLGQPKAAPSVTLFPPSSEELQANKATLV
```

```
CLISDFYPGAVTVAWKADSSPVKAGVETTTPTSKSNKKVAASSYLSLTPEOWKSHRSY
SQOVTHEGSTVEKTVAPTECSARQSTPFVCEYQGSSDLPPQPPVNAAGSGSGSGSGS
"
sig_peptide 1..66
/ gene="IGL"
BASE COUNT 174 a 260 c 231 g 162 t
ORIGIN
Query Match 80.3%; Score 570.6; DB 9; Length 827;
Best Local Similarity 93.5%; Pred. No. 1.5e-137;
Matches 607; Conservative 0; Mismatches 39; Indels 3; Gaps 1;
QY 62 AGTCTCTCTGACACAGCCGCTCAGTCTCTGGGCCCCCAGGGCAAGAGTCCACCATCT 121
Db 68 AGTCTCTGTTGACGAGCGCCCTCACTGTCTGGGGCCCCAGGGCAAGAGTCCACCATCT 127
QY 122 CGTGCACTGGGAGACCTCCAAACATTTGG---AGGTTATGATCTACATTGGTACCAGCAGC 178
Db 128 CTTGCACTGGGAGCAGCTCCAAACATCGGGCAGGTTATGATGTACACTGGTACCAGCAGC 187
QY 179 TCCAGGAACGGCCCCCAAACTCTCATCTATGACATTAACAAGCGACCTCAGGAATTT 238
Db 188 TTCAGGAACAGCCCCCAAACTCTCATCTATGGTGACATCAATCGGCCCTCAGGGGTC 247
QY 239 CTGACCGATTCTCTGGCTCCAAAGTCTGGTACCGCGCCCTCCCTGGCCATCACTGGGCTCC 298
Db 248 CTGACCGATTCTCTGGCTCCAAAGTCTGGGACCTCAGCCTCCCTGGCCATCACTGGGCTCC 307
QY 299 AGACTGAGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCCTGGAATGCTCAGG 358
Db 308 AGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCCTGAGTGGTTCGG 367
QY 359 TATTCCGAGGAGGACCGGCTGACCGTCTTAGTTCAGCCCAAGGTCGCCCTCGGTCA 418
Db 368 TATTCCGAGGAGGACCGGCTGACCGTCTTAGTTCAGCCCAAGGTCGCCCTCGGTCA 427
QY 419 CTCTGTTCCTCCGCTCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTCTCA 478
Db 428 CTCTGTTCCTCCGCTCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTCTCA 487
QY 479 TAAGTGACTTCTACCGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGCAGCCCGTCA 538
Db 488 TAAGTGACTTCTACCGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGCAGCCCGTCA 547
QY 539 AGCGGGAGTGAGACACACACCTCCAAACAAGCAACAAGTACGCGGCCAGCA 598
Db 548 AGCGGGAGTGAGACACACACCTCCAAACAAGCAACAAGTACGCGGCCAGCA 607
QY 599 GCTACTGAGCCTGACCGCTGAGCAGTGGAGTCCCAACAAGCTACAGCTGCCAGGTCA 658
Db 608 GCTACTGAGCCTGAGCCTGAGCAGTGGAGTCCCAACAAGCTACAGCTGCCAGGTCA 667
QY 659 CGCATGAAGGAGACCGGTGGAGAAAGACAGTGGCCCTTACAGAATGTTTC 707
Db 668 CGCATGAAGGAGACCGGTGGAGAAAGACAGTGGCCCTTACAGAATGTTTC 716

RESULT 7
AB064188 800 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
DEFINITION region, partial cds, clone:L48.
ACCESSION AB064188
VERSION AB064188.1 GI:21669582
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L48.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
```

Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics

JOURNAL
REFERENCE

2 (bases 1 to 800)

AUTHORS

Kurosawa,Y.

JOURNAL

Submitted (25-JUN-2001) Yoshitazu Kurosawa, Institute for

Comprehensive Medical Science, Fujita Health University;

Kutsukake-cho, Toyosake 470-1192, Japan

(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)

Please visit our web site

URL:http://www.fujita-hu.ac.jp/immunity/.

COMMENT

FEATURES

source

1..800

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="L48"

/clone_lib="AIMS4"

/note="mixture of tissues:tonsils, umbilical cords,

peripheral blood and bone marrow"

1..800

/gene="IGL"

1..->800

/gene="IGL"

/codon_start=1

/product="immunoglobulin lambda light chain VLJ region"

/protein_id="BAC01816.1"

/db_xref="GI:21669583"

/translation="WKYLLPTAAAGLLLAQPMAMHVLTPPSVSGAPQRTVTC

TGSSNIGAGYDVHWYQOLPGTAPKLLIYGNRPSGVPDRFSGSKGTSASLAITGL

QAEEDYVYQSDYSLSGWFGGKTLTVGPQKAPSVTLFPSSSELOANKATLV

CLISDPYQAVTVANKADSPVKAGVETTPSKQGNKYAASSVLSLTPQWKSHKSY

SCQVTHGTVETKTVAPTECSARQSTPFVCEYQGQSSDLPFPVNAAGG"

1..66

/gene="IGL"

/note="pelB signal peptide"

176 a 256 c 217 g 151 t

BASE COUNT

ORIGIN

Query Match 79.7%; Score 566.6; DB 9; Length 800;

Best Local Similarity 93.5%; Pred.No.1.6e-136;

Matches 603; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 66 TGTCTCAGACAGCGCCCTCAGTGTCTGGGGCCCGAGGACAGAGTCCACATCTCGTG 125

DB 72 TATACTGACTCAACCGCCCTCAGTGTCTGGGGCCCGAGGACAGAGTCCACATCTCGTG 131

QY 126 CACTGGGAGCAGCTCCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTCCC 182

DB 132 CACTGGGAGCAGCTCCCAACATTGGGGGCGAGGTATGATGTACCTGGTACCAGCAGCTTC 191

QY 183 AGGAACGGCCCCCAAACTCTCATATGACATTAAACAGCGACCCCTCAGGAATTTCTGA 242

DB 192 AGGAACAGCCCCCAAACTCTCATATGTTAAACAGCAATCGGCCCTCAGGGTCCCTGA 251

QY 243 CCGATTCTTGCTCCAGTGTGTACCGGGCTCCCTCGGCATCACTGGGCTCCAGAC 302

DB 252 CCGATTCTTGCTCCAGTGTGTACCGGGCTCCCTCGGCATCACTGGGCTCCAGAC 311

QY 303 TGAGGATGAGGCTGATTATTACTCCAGTCTCTATGACAGCAGGCTTGAATGCTCAGGTATT 362

DB 312 TGAGGATGAGGCTGATTATTACTCCAGTCTCTATGACAGCAGGCTTGAATGCTCAGGTATT 371

QY 363 CGGAGGAGGACCGCGCTGACCGTCTTAGGTGACCCCAAGGCTGCCCTCCGCTCACTCT 422

DB 372 CGGCGGAGGACCAAGCTGACCGTCCAGGTTCAGCCCAAGGCTGCCCTCCGCTCACTCT 431

QY 423 GTTCCCGCCCTCTCTCAGGAGCTTCAAGCCCAAGGCTGCCCTCCGCTCACTCAAG 482

DB 432 GTTCCCGCCCTCTCTCAGGAGCTTCAAGCCCAAGGCTGCCCTCCGCTCACTCAAG 491

QY 483 TGACTTCTACCCGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCCTCAAGGC 542

DB 492 TGACTTCTACCCGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCCTCAAGGC 551

QY 543 GGGAGTGGAGACACACACCCCTCCAAACAAACACACACACACACACACACACACACAC 602

DB 552 GGGAGTGGAGACACACACACCCCTCCAAACAAACACACACACACACACACACACACAC 611

QY 603 CTTGAGCTCAGCGCTGAGCAGTGGAGTCCACAGAGCTCCACAGAGCTACAGCTGCCAGGTCA 662

DB 612 CTTGAGCTCAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTCA 671

QY 663 TGAAGGAGCAGCCGTGGAGAGACAGTGGCCCTCAGAGATGTTTC 707

DB 672 TGAAGGAGCAGCCGTGGAGAGACAGTGGCCCTCAGAGATGTTTC 716

RESULT 8

BC022098

LOCUS

BC022098

DEFINITION

BC022098

ACCESSION

BC022098.1

VERSION

BC022098.1

KEYWORDS

MGC.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa;

Chordata; Craniata;

Vertebrata; Euteleostomi;

Mammalia; Eutheria;

Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 919)

Strausberg,R.

Direct Submission

Submitted (24-JAN-2002)

National Institutes of Health, Mammalian

Gene Collection (MGC),

Cancer Genomics Office,

National Cancer

Institute, 31 Center Drive,

Room 11A03, Bethesda,

MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-x@mail.nih.gov

Tissue Procurement: Louis Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline

Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Scott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 40 Row: n Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomescan gene
prediction, Similarity but not identity to protein.

FEATURES

source

1..919

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="MGC:31944 IMAGE:4878869"

/tissue_type="Primary B-Cells from Tonsils"

/clone_lib="NIH MGC 48"

/lab_host="DH10B-R"

/note="vector: pGB7"

33..746

/codon_start=1

/product="Unknown (protein for MGC:31944)"

/protein_id="AAH22098.1"

/db_xref="GI:18380972"

CDS


```

Db 428 TGTTCCTCCGCTCTCTGAGGAGCTTCAAGCCACACAGGCGCACACTGGTGTCTCATRAA 487
QY 482 GTGACTTTACCCGGGAGCGTGACAGTGGCTGGAGGACAGATAGACGCCCGCTCAAGG 541
Db 488 GTGACTTTACCCGGGAGCGTGACAGTGGCTGGAGGACAGATAGACGCCCGCTCAAGG 547
QY 542 CGGGAGTGGAGACACACACCTTCAACAAAGCAACAAACAGTACGGCGGCGCAGCGT 601
Db 548 CGGGAGTGGAGACACACACCTTCAACAAAGCAACAAACAGTACGGCGGCGCAGCGT 607
QY 602 ACCTGAGCCTGAGCCTGAGCAGTGGAGTCCACAGAAAGCTACAGCTCCAGGTCACGC 661
Db 608 ACCTGAGCCTGAGCCTGAGCAGTGGAGTCCACAGAAAGCTACAGCTCCAGGTCACGC 667
QY 662 ATGAAGGAGCAGCCTGGAGAGCAGTGGCCCTCAGAAATGTC 707
Db 668 ATGAAGGAGCAGCCTGGAGAGCAGTGGCCCTCAGAAATGTC 713

RESULT 10
AB064148 812 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
DEFINITION region, partial cds, clone:L8.
ACCESSION AB064148
VERSION AB064148.1 GI:21669502
KEYWORDS
SOURCE
ORGANISM Homo sapiens
cDNA to mRNA, clone_lib:AIMS4 clone:L8.
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 812)
AUTHORS Kurosawa,Y.
DIRECT SUBMISSION
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyooka 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES
Location/Qualifiers
1..812 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="L8"
/clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
1..812 /gene="IGL"
1..812 /gene="IGL"
/codon_start=1
/product="immunoglobulin lambda light chain VLJ region"
/protein_id="BAC01776.1"
/db_xref="GI:21669503"
/translation="MKYLLPTAAAGLLLLAAQFAMAQSVLTQPPSVSAAPGQKVTISC
SGSSNNINNVSWYQQLPGTAPKLIYDNNKPSGIDPFSGSKSGTSATLIGTLQ
TGEDADYCYGTWSSLSAGVFGGKTLTVLQGPKAAPSVTLFPFSSSEELQANKATLVC
LISDFYPGAVTAWKADSPVKAGVETTPSKOSNNKYAASSVLSLTQPMKSHRSYS
CQVTEGSTVEKTVAPTECSARQSTPVCVYQGSDDLQPPVPVNAAGSGSGGS"
1..66 /gene="IGL"
/note="pe1a signal peptide"
sig_peptide

```

```

BASE COUNT 183 a 253 c 220 g 156 t
ORIGIN
Query Match 79.2%; Score 562.8; DB 9; Length 812;
Best Local Similarity 92.0%; Pred. No. 1.6e-135;
Matches 594; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 62 AGTCTGTCTTGACACAGACGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAAAGGTCAACATCT 121
Db 68 AGTCTGTGTGACGACGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAAAGGTCAACATCT 127
QY 122 CGTGCACGTGGAGAGCACCTCCAAACATTGGAGGTTATGATCTACATTGGTACACAGAGTCC 181
Db 128 CTTCTCTGGAAGCAGCTCCAAACATTGGGAATAATATGTATCTCTGGTACACAGAGTCC 187
QY 182 CAGGAACGGCCCCCAAACTCTCATCTATCAGATTAAACAGGACACCTCAGGAATTTCTG 241
Db 188 CAGGAACAGCCCCCAAACTCTCATTTATGACAAATAAAGACGACCTCAGGGATTTCTG 247
QY 242 ACCGATTTCTTGGCTCCAAAGTCTGGTACCGCGGCTCTCCCTGGCCATCAGTGGGCTCCAGA 301
Db 248 ACCGATTTCTTGGCTCCAAAGTCTGGCAGCTCAGCCACCTTGGGCATCACCGGACTCCAGA 307
QY 302 CTGAGGATGAGGCTGATTTACTTGCAGTCTCTATGACAGCAGCTGAATGCTCAGGTAT 361
Db 308 CTGGGACGAGGCGGATTTACTTCTGCGGAACATGGGATAGCAGCTGAGTGTGCTGGCGTGT 367
QY 362 TCGGAGGAGGACCGCGCTGACCGTCTAGTTCAGCCCAAGGCTGCCCTCGGTCACTC 421
Db 368 TCGGAGGAGGACCAAGCTGACCGTCTAGTTCAGCCCAAGGCTGCCCTCGGTCACTC 427
QY 422 TGTTCCTCCGCTCTCTGAGGAGCTTCAAGCCAAACAGGCGCACACTGTGTGTCTATAA 481
Db 428 TGTTCCTCCGCTCTCTGAGGAGCTTCAAGCCAAACAGGCGCACACTGTGTGTCTATAA 487
QY 482 GTGACTTTACCCGGGAGCGCTGACAGTGGCTGGAGGAGATAGCAGCCCGCTCAAGG 541
Db 488 GTGACTTTACCCGGGAGCGCTGACAGTGGCTGGAGGAGATAGCAGCCCGCTCAAGG 547
QY 542 CGGGAGTGGAGACACACACCTTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCT 601
Db 548 CGGGAGTGGAGACACACACCTTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCT 607
QY 602 ACCTGAGCCTGAGCCTGAGCAGTGGAGTCCACAGAAAGCTACAGTGCAGGTCCAGC 661
Db 608 ACCTGAGCCTGAGCCTGAGCAGTGGAGTCCACAGAAAGCTACAGTGCAGGTCCAGC 667
QY 662 ATGAAGGAGCAGCCTGGAGAGCAGTGGCCCTCAGAAATGTC 707
Db 668 ATGAAGGAGCAGCCTGGAGAGCAGTGGCCCTCAGAAATGTC 713

RESULT 11
AB064147 816 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
DEFINITION region, partial cds, clone:L7.
ACCESSION AB064147
VERSION AB064147.1 GI:21669500
KEYWORDS
SOURCE
ORGANISM Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L7.
REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 816)

```


AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/
FEATURES Location/Qualifiers
source
1. .816
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
gene
1. .816
/gene="IGL"
CDS
1. .>816
/gene="IGL"
/codon_start=1
/product="immunoglobulin lambda light chain VLJ region"
/protein_id="BAC01775.1"
/db_xref="GI:21669501"
/translation="MKYLLPTAAAGLLLAQPMAGSVLTQPPSVSAAPGQKVITSCSGSSNIGNNVYQQLPGTAPKLLIYDNNKRPSPGIPDRFSGSKGTSLGITGLQ TGDADYICGTWDSLSGAVFGGKTLVLGQPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKOSNNKYAASSYLSLTPEQWKSHRS CQVNEGSTVEKTVAPTECSARQSTPFVCEYQGOSSDLPPPPVYVAGGGSGGGSG"
sig_peptide
1. .66
/gene="IGL"
/note="pe1B signal peptide"
BASE COUNT 185 a 252 c 221 g 158 t
ORIGIN
Query Match 79.2%; Score 562.8; DB 9; Length 816;
Best Local Similarity 92.0%; Pred. No. 1.6e-135;
Matches 594; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 62 AGTCGTCTGTACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGTCACCATCT 121
DB 68 AGTCGTGTGACGACGCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGTCACCATCT 127
QY 122 CTGTCACCTGGGAGCACCTCCAACTTGGAGGTTATGATCTACATTGGTACCAGCAGCTCC 181
DB 128 CTGCTCTGGAGCAGCTCCAACTTGGGAATAATTATGTTATCTGGTACCAGCAGCTCC 187
QY 182 CAGGAACGGCCCCCAACTCTCTATGACATTAAACAGCGACCTTCAGGAATTCTG 241
DB 188 CAGGAACAGCCCCCAACTCTCTATGACAAATAAAGCGACCTTCAGGGATTCTGT 247
QY 242 ACCGATTTCTTGGCTCCAACTGCTGTCGCGGCTCCTCGCCATCTACCTGGCTCCAGA 301
DB 248 ACCGATTTCTTGGCTCCAACTGCTGTCGCGGCTCCTCGCCATCTACCTGGCTCCAGA 307
QY 302 CTGAGGATGAGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTGAATGCTCAGGTAT 361
DB 308 CTGGGGACGAGCCGATTTATTCTGGGACATGAGGATAGCAGCTGAGTCCGCTGAT 367
QY 362 TCGGAGGAGGACCGCGCTGACCGTCTAGGTACGCCCAAGGCTGCCCTCGGTCACTC 421
DB 368 TCGGCGGAGGACCAAGCTGACCGTCTAGGTACGCCCAAGGCTGCCCTCGGTCACTC 427
QY 422 TGTTCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCATAA 481
DB 428 TGTTCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCATAA 487
QY 482 GTGACTTCTTACCCGGGAGCCGTGACAGTGGCTGGAAGCAGATAGCAGCCCGTCAAGG 541
DB 488 GTGACTTCTTACCCGGGAGCCGTGACAGTGGCTGGAAGCAGATAGCAGCCCGTCAAGG 547
QY 542 CGGGAGTGGAGACCAACCTCCAAACAAAGCAACAAAGTACCGGCCAGCAGCT 601
|||||

DB 548 CGGAGTGAGGACCAACACACCCCTCCAAACAAAGCAACAAAGTACGGCGCAGCAGT 607
QY 602 ACCTGAGCCTGAGCCTGAGCAGTGAAGTCCACAGAAGCTACAGCTCCAGGTCAAGC 661
DB 608 ATCTGAGCCTGAGCCTGAGCAGTGAAGTCCACAGAAGCTACAGCTCCAGGTCAAGC 667
QY 662 ATGAAGGAGCAGCCTGAGGAGACAGTGGCCCTTACAGAATGTTTC 707
DB 668 ATGAAGGAGCAGCCTGAGGAGACAGTGGCCCTTACAGAATGTTTC 713
RESULT 12
AB064219
LOCUS Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:L79.
ACCESSION AB064219
VERSION AB064219.1 GI:21669644
KEYWORDS
SOURCE
ORGANISM Homo sapiens
cDNA to mRNA, clone_lib:AIMS4 clone:L79.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 827)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyooka 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/
FEATURES Location/Qualifiers
1. .827
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="L79"
/clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
gene
1. .827
/gene="IGL"
CDS
1. .>827
/gene="IGL"
/codon_start=1
/product="immunoglobulin lambda light chain VLJ region"
/protein_id="BAC01847.1"
/db_xref="GI:21669645"
/translation="MKYLLPTAAAGLLLAQPMAGSVLTQPPSVSGVPGORVTISC
TGSSNIGAGYDVHMYQQLPGTAPKLLIYGNRSRSGVPDRFSGSKGTSLAITGF
QBEDADYICQSDLSLGHVFGGKTLVLGQPKAAPSVTLFPSSSEELQANKATL
VCLISDFYPGAVTVAWKADSSPVKAGVETTPSKOSNNKYAASSYLSLTPEQWKSHRS
YSCVTHEGSTVEKTVAPTECSARQSTPFVCEYQGOSSDLPPPPVYVAGGGSGGGSGG"
sig_peptide
1. .66
/gene="IGL"
/note="pe1B signal peptide"
BASE COUNT 175 a 256 c 232 g 164 t
ORIGIN
Query Match 79.1%; Score 562.4; DB 9; Length 827;
Best Local Similarity 93.6%; Pred. No. 2e-135;
Matches 610; Conservative 0; Mismatches 36; Indels 6; Gaps 2;
QY 62 AGTCGTCTGTACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGTCACCATCT 121
|||||

```
Db 68 AGGCTGTGCTCACTCAGCGCTCCTCAGTGTCTGGGGTCCAGGCGAGGGTCAACATCT 127
Qy 122 CFTGCACTGGGAGCAGCTCAACATTTGG--AGTTATGATCTACATTTGGTACAGCAGC 178
Db 128 CFTGCACTGGGAGCAGCTCAACATCGGGCAGGTTATGATGATACACTGGTACAGCAGC 187
Qy 179 TCCCAGGAAGCGGCCCCCAAACTCTCATCTATGACATTAAAGAGGACCTCAGGAATTT 238
Db 188 TTCCAGGAACAGCCCCCAAACTCTCATCTATGTTGTTACAGCAATCGGCCCTCAGGGTCC 247
Qy 239 CTGACCGATTCTCTGGCTCAAGTCTGTGTACCGGGCCCTCCCTGGCCATCATCTGGGCTCC 298
Db 248 CTGACCGATTCTCTGGCTCAAGTCTGTGTACCGGGCCCTCCCTGGCCATCATCTGGGTTCC 307
Qy 299 AGACTGAGATGAGGCTGATTTATTCTGCAGTCTTATGACAGCAGCTGAAATGCTCA-- 356
Db 308 AGGCTGAGGATGAGGCTGATTTATTCTGCAGTCTTATGACAGCAGCTGAGTGGTCTATG 367
Qy 357 -GGTATTTCCGAGGAGGAGCCCGGCTGACCGTCTCTAGGTGAGCCCAAGGCTGCCCTCGG 415
Db 368 TGGTATTTCCGAGGAGGAGCAAGCTGACCGTCTCTAGGTGAGCCCAAGGCTGCCCTCGG 427
Qy 416 TCACTCTGTTCCCGCCCTCTCTGTGAGGAGCTTCAAGCCAAAGGCCACACTGTGTGTC 475
Db 428 TCACTCTGTTCCCGCCCTCTCTGTGAGGAGCTTCAAGCCAAAGGCCACACTGTGTGTC 487
Qy 476 TCATAAGTACTTCTACCGGGAGCGGTGACAGTGGCTTGGAAAGGAGATGACAGCCCGG 535
Db 488 TCATAAGTACTTCTACCGGGAGCGGTGACAGTGGCTTGGAAAGGAGATGACAGCCCGG 547
Qy 536 TCAAGCGGGAGTGGAGACACACACACCTTCAAAACAAAGCAACAAAGTACGCGGCCA 595
Db 548 TCAAGCGGGAGTGGAGACACACACACCTTCAAAACAAAGCAACAAAGTACGCGGCCA 607
Qy 596 GCAGCTACTGTAGCCTTGAGCCTTGAGCAGTGGAAAGTCCACAGAAGCTACAGTCCGAGG 655
Db 608 GCAGCTACTGTAGCCTTGAGCCTTGAGCAGTGGAAAGTCCACAGAAGCTACAGTCCGAGG 667
Qy 656 TCACGATGAAGGAGCAGCGTGGAGAAACAGTGGCCCTCAGAAATGTTT 707
Db 668 TCACGATGAAGGAGCAGCGTGGAGAAACAGTGGCCCTCAGAAATGTTT 719
```

```
RESULT 13
LOCUS HSI0VL027 750 bp mRNA linear PRI 20-JUL-1995
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57817
VERSION X57817.1 GI:33733
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 750)
AUTHORS Kloebeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) H.G. Kloebeck, Inst fuer Physiologische
Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE 2 (bases 338 to 384)
AUTHORS Combrato, G. and Kloebeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
PUBMED 1904362
COMMENT , for overlapping sequences see: X51754-55; J00252-54; M15641-42.
FEATURES
Location/Qualifiers
1..750
/organism="Homo sapiens"
```

```
/isolate="individual ML"
/db xref="taxon:9606"
/chromosome="22"
/clone="cML39"
/cell_type="B-cell"
/tissue_type="spleen"
/clone_lib="phage library cML"
1..702
/gene="immunoglobulin lambda light chain"
<1..702
/gene="immunoglobulin lambda light chain"
/codon_start=1
/protein_id="CAA40954.1"
/db xref="GI:33734"
/translation="SFPLLTLTHCAGSWAQSVLTQPPSASGTGQRTVITSCSSSS
NIGSNTVWYQQLPGTAPKLLIYRNQRPSPGVPDRFSGSKGTSASLSAIGLQSDSEA
DIYCAWDDSLNGVVGSGTKLVIGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YFGAVTAWKADSPVKAGVETTTTPSKSNKYYAASSYLSLTPEQWKSHRSYSCQVTH
EGSTVEKTVAPTECS"
<1..51
/gene="immunoglobulin lambda light chain"
52..382
/gene="immunoglobulin lambda light chain"
/notes="variable region; V(lambda)I"
345..382
/gene="immunoglobulin lambda light chain"
/notes="J-segment"
383..702
/gene="immunoglobulin lambda light chain"
/notes="constant region"
BASE COUNT 168 a 246 c 196 g 140 t
ORIGIN
```

```
Query Match 79.1%; Score 562.2; DB 9; Length 750;
Best Local Similarity 90.5%; Pred. No. 2.2e-135;
Matches 600; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy 47 CAGGTGCACCATGTGAGTCTGCTGTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGGC 106
Db 38 CAGGGTCTGGGGCCAGTCTGTGCTGACTCAGCCACCTCAGGCTCTGGAGCCCCGGGC 97
Qy 107 AGAAGGTCACCATCTCGTGCACTGGGAGCACCTCCAAACATTTGGAGGTTATGATCTACATT 166
Db 98 AGAGGGTCACCATCTCTTGTCTTGAAGCAGCTCCAAACATCGGAAGTAATCTGTAAACT 157
Qy 167 GGTACACAGCAGCTCCAGGAACCGCCCCCAAACTCCTCATCTATGACATTAAACAGGCAC 226
Db 158 GGTACACAGCAGCTCCAGGAACCGCCCCCAAACTCCTCATCTATCGTAATAATCAGCGGC 217
Qy 227 CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAAGTCTGTGTACCGGGCTCCCTCGGCCA 286
Db 218 CCTCAGGGGTCTCTGACCGATTCTCTGGCTCCAAAGTCTGTGTACCGCTCAGCCTCGCTGGCCA 277
Qy 287 TCAGTGGGCTCCAGACTGAGGATGAGGCTGATTTACTGCCAGTCTCTATGACAGCAGCC 346
Db 278 TCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTTACTGTGAGCATGGGATGACAGCC 337
Qy 347 TGAATGCTCAGGATTTCCGAGGAGGAGCCGGCTGACCGTCTTAGTCTAGCCCAAGGCTG 406
Db 338 TGAATGCTGAGTATTCGGCGGAGGAGCACAAGCTGACCGTCTTAGTCTAGCCCAAGGCTG 397
Qy 407 CCCCTCGGTCACCTCTGTTCCCGCTCTCTCAGGAGCTTCAAGCCAAACAGGCCACAC 466
Db 398 CCCCTCGGTCACCTCTGTTCCCGCTCTCTCAGGAGCTTCAAGCCAAACAGGCCACAC 457
Qy 467 TGTGTGCTCTCATAAGTACTTTCTACCGGGAGCCGTGACAGTGGCTTGAAGGAGATA 536
Db 458 TGTGTGCTCTCATAAGTACTTTCTACCGGGAGCCGTGACAGTGGCTTGAAGGAGATA 517
Qy 527 GCAGCCCCCTCAAGCGGGGAGTGGAGACCACACCTCCAAACAAAGCAACAAACAGT 586
Db 518 GCAGCCCCCTCAAGCGGGGAGTGGAGACCACACCTCCAAACAAAGCAACAAACAGT 577
```

QY	587	ACGGGGCAGCAGCTACCTGAGCCTGAGCGCTGAGCAGTGAAGTCCACAGAAAGTACA	646
Db	578	ACGGGGCAGCAGCTATCTGAGCCCTGAGCGCTGAGCAGTGAAGTCCACAGAAAGTACA	637
QY	647	GCTCCAGGTCACGCATGAAGGGAGACCGGTGGAGAGACAGTGGCCCTACAGAAATGTT	706
Db	638	GCTCCAGGTCACGCATGAAGGGAGACCGGTGGAGAGACAGTGGCCCTACAGAAATGTT	697
QY	707	CAT 709	
Db	698	CAT 700	
RESULT 14			
HSIGVL006			
LOCUS		747 bp mRNA linear PRI 20-JUL-1995	
DEFINITION		Human rearranged immunoglobulin lambda light chain mRNA.	
ACCESSION		X57806	
VERSION		X57806.1 GI:33709	
KEYWORDS		Ig lambda light chain; immunoglobulin.	
SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 747)	
JOURNAL		Klobeck,H.G.	
REFERENCE		Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische	
AUTHORS		Chemie, Physiologische Biochemie und Zellbiologie der Universitaet	
TITLE		Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany	
REFERENCE		2 (bases 335 to 381)	
AUTHORS		Combratio,G. and Klobeck,H.G.	
TITLE		V lambda and J lambda-C lambda gene segments of the human	
JOURNAL		immunoglobulin lambda light chain locus are separated by 14 kb and	
MEDLINE		rearrange by a deletion mechanism	
PUBMED		Eur. J. Immunol. 21 (6), 1513-1522 (1991)	
COMMENT		91257162	
FEATURES		1904362	
source		for overlapping sequences see: X51754-55; J00252-54; M15641-42.	
		Location/Qualifiers	
		1. .747	
		/organism="Homo sapiens"	
		/isolate="individual ML"	
		/db xref="taxon:9606"	
		/chromosome="22"	
		/clone="cML115"	
		/cell_type="B-cell"	
		/tissue_type="spleen"	
		/clone_lib="phage library cML"	
gene		1. .747	
		/gene="immunoglobulin lambda light chain"	
mRNA		1. .747	
		/gene="immunoglobulin lambda light chain"	
		/note="cDNA"	
		/evidence="experimental"	
CDS		<1. .699	
		/gene="immunoglobulin lambda light chain"	
		/codon_start=1	
		/protein_id="CAA40944.1"	
		/db xref="GI:33710"	
		/translation="SPILLTLIHCTGWAQSVLTPPPVSAAPGQKVTITSCSGSSN	
		IGNVSWYQOLPGAPKLLIPENKRPSAIPDRFGSKSGTATLIGLAGLQGTGDA	
		YVCGTWSSLTQVVGEGTGLTVLGOPKAPSVTLPPPSSEELQANKATLVCLISDP	
		PGATVAVKADSPVKAGVETTFPSKSNKNYAASSVLSLTPEQWKSHRSYSCQVTHE	
		GSTVEKTVAPTECS"	
		<1. .48	
sig_peptide		/gene="immunoglobulin lambda light chain"	
misc_feature		49. .379	
		/gene="immunoglobulin lambda light chain"	
		/note="variable region; V(lambda)I"	
misc_feature		342. .379	
		/gene="immunoglobulin lambda light chain"	
		/note="J-segment"	

misc_feature		380..699		/gene="immunoglobulin lambda light chain"		/note="constant region"	
BASE COUNT	169 a	244 c	196 g	138 t			
ORIGIN							
Query Match	78.8%; Score 560; DB 9; Length 747;						
Best Local Similarity	87.8%; Pred. No. 8,4e-135;						
Matches 611; Conservative	0; Mismatches 85; Indels 0; Gaps 0;						
Qy	14	CTCAGCTCTGGGCTCTCTGCTCTGGCTCCAGGTGCACGATGTGAGTCTGCTCTGA	73				
Db	2	CCCTCTCTCTCTACCCCTCTCATTCACGTACAGAGTCTCTGGGCCAGTCTGTGTGA	61				
Qy	74	CACAGCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGTCAACATCTCGTGCACCTGGA	133				
Db	62	CGCAGCGCCCTCAGTGTCTGGGCCCCAGGACAGAAGGTCAACATCTCTCTCTCGAA	121				
Qy	134	GCACCTTCAACATTTGAGGTTATGATCTACATTGGTACACGACGCTCCACAGGAACGGCC	193				
Db	122	GCAGCTCAACATTTGGGAAATATATGTATCTCTGGTACACGACGCTCCCGGGAAGGCC	181				
Qy	194	CCAACTCTCATCTATGACATTAACAAGCGCCCTCAGGAATTTCTGACCGATTCTCTG	253				
Db	182	CCAACTCTCATCTTTGAAAAATAAAGCGACCCCTCAGCCATTCCTGACGATTTCTG	241				
Qy	254	GCTCCAAGTCTGCTACCGCGCCCTCCCTGGCCATCACTGGGCTCCAGACTGAGGATGAG	313				
Db	242	GCTCCAAGTCTGCAAGTCAAGCCCTCGGGATCGCGGGCTCCAGACTGGGACGAGG	301				
Qy	314	CTGATTATTAAGTCTGCTATGACACGACGCTGAATCTCAGGTATTCGGAGGAGGA	373				
Db	302	CCGATTATTACTCGGAAACATGGATAGCAGCCTGACTGATGTGGTTTCGGCGGGGGA	361				
Qy	374	CCGGCTGACCGTCTAGTCTGACGCCAAGGCTGCCCTCGGTCACTCTGTCGCCGCT	433				
Db	362	CCAAGTCTGACCGTCTAGTCTGACGCCAAGGCTGCCCTCGGTCACTCTGTCGCCGCT	421				
Qy	434	CTCTGAGGAGCTTCAAGCCAAACAAGCCACACTGGTGTGTCTCATAACTGACTTCTACC	493				
Db	422	CTCTGAGGAGCTTCAAGCCAAACAAGCCACACTGGTGTGTCTCATAACTGACTTCTACC	481				
Qy	494	CGGAGCGCTGACAGTGGCTTGGAAAGCAGATAGCAGCCCGCTCAAGCGGAGTGAGA	553				
Db	482	CGGAGCGCTGACAGTGGCTTGGAAAGCAGATAGCAGCCCGCTCAAGCGGAGTGAGA	541				
Qy	554	CCACCACCCCTCAACAAGACAAACAAGTACGCGGCCAGCAGCTACTGAGCCTGA	613				
Db	542	CCACCACCCCTCAACAAGACAAACAAGTACGCGGCCAGCAGCTACTGAGCCTGA	601				
Qy	614	CGCTGAGCAGTGGAGTCCACAGAGCTACAGCTCCAGGTCACGCATGAAGGGAGCA	673				
Db	602	CGCTGAGCAGTGGAGTCCACAGAGCTACAGCTCCAGGTCACGCATGAAGGGAGCA	661				
Qy	674	CCGTGGAGAGACAGTGGCCCTTACAGAATGTTTCAAT	709				
Db	662	CCGTGGAGAGACAGTGGCCCTTACAGAATGTTTCAAT	697				
RESULT 15							
AB064141							
LOCUS	Homo sapiens IGL mRNA for immunoglobulin lambda light chain VJLJ						
DEFINITION	AB064141.1 GI:21669488						
ACCESSION	AB064141						
VERSION	AB064141.1						
KEYWORDS	Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L1.						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1. Akahori.Y., Iba.Y., Morino.K., Shinozawa.M., Hirono.Y., Kakita.M.,						

Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Unpublished
2 (bases 1 to 821)

Kurosawa,Y.

Direct Submission

Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for

Comprehensive Medical Science, Fujita Health University;

Kutsukake-cho, Toyosake 470-1192, Japan

(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)

Please visit our web site

URL: <http://www.fujita-hu.ac.jp/immunity/>.

Location/Qualifiers

source

1..821

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="L1"

/clone_lib="AIMS4"

/note="mixture of tissues:tonsils, umbilical cords,

peripheral blood and bone marrow"

1..821

/gene="IGL"

1..>821

/gene="IGL"

/codon_start=1

/product="immunoglobulin lambda light chain VLJ region"

/protein_id="BAC01769.1"

/db_xref="GI:21669489"

/translation="WKYLLPTAAAGLLILAAQPAQMAQSVLTQPPSVAAAPQKVTVC

TGSNSNIKNDVSVYQGPAA PKLLISDTRRPSGIPDRFSKSGTSATLAAGIQ

AEDADYVQSHDTLQPIFGGDTLVLGQPKAAPSVTLFPPSSELOANKATLVC

LISDPYPAIVAMKAGSSPTAGVETITPSKNNKYAASSYLSLTPEQWKHRSYS

QVINEGSTVEKTVAPTECSARQSTPFVCEYQGSQSDLPQPPVNAVGGSGGGG"

1..66

/gene="IGL"

/note="pelB signal peptide"

175 a 260 c 228 g 158 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 78.5%; Score 558; DB 9; Length 821;

Matches 591; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 62 AGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGTCAACATCT 121

DB 68 AGTCTGTGTGACGACGCGCCCTCAGTGTCTGCGGCCCCAGGACAGAGGTCAACGCT 127

QY 122 CGTGCACTGGGAGCACCTCCAACTTTGGAGGTATTGATCTACATTGGTACCAGCAGCTCC 181

DB 128 CTGCACTGGAGCAACTCCAACTTTGAGAAGATGATGTTCTCTGGTACCAGCAGGAC 187

QY 182 CAGGAACGGCCCCCAACTCTCATCTATGACATTAAACAAGCAGCCCTCAGGAATTTCTG 241

DB 188 CAGGAGCAGCCCCCAACTCTCATTTCTGACACTGATAGCGACCCCTCAGGATTCCTG 247

QY 242 ACCGATTCTCTGGCTCCAAAGTCTGGTACCGGGCCCTCCCTGGCCATCATCTGGGCTCCAGA 301

DB 248 ACCGATTCTCTGGCTCCAAAGTCTGGCAGCTCAGCCACCCCTGGCCATCATCTGGGCTCCAGG 307

QY 302 CTGAGGATCAGGCTGATTATTACTGCGAGTCTCTATGACAGCAGCCTGAATGCTCAGGTAT 361

DB 308 CTGAGGATCAGGCTGATTATTACTGCGAGTCTCTATGACAGCAGCCTGAATGCTCAGGTAT 367

QY 362 TCGGAGGAGGACCCCGGTGACCGTCTTAGGTACGCCCAAGGCTGCCCCCTCGGTCACTC 421

DB 368 TCGGCGGGGGGACCCAGCTGACCGTCTTAGGTACGCCCAAGGCTGCCCCCTCGGTCACTC 427

QY 422 TGTTCGCCGCCCTCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCTATAA 481

DB 428 TGTTCGCCGCCCTCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCTATAA 487

QY 482 GTGACTTCTTACCCGGGAGCCGTGACAGTGGCCCTGGGAAGGCAGATAGCAGCCCGTCAAGG 541

DB 488 GTGACTTCTTACCCGGGAGCCGTGACAGTGGCCCTGGGAAGGCAGATAGCAGCCCGTCAAGG 547

QY 542 CGGAGTGGAGACCAACACACACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCT 601

DB 548 CGGAGTGGAGACCAACACACACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCT 607

QY 602 ACCTGAGCCTGACGCGCTGAGCAGTGGAGTCCCAAGCAACAAAGTACAGCTGCCAGGTCAAGC 661

DB 608 ACCTGAGCCTGACGCGCTGAGCAGTGGAGTCCCAAGCAACAAAGTACAGCTGCCAGGTCAAGC 667

QY 662 ATGAAGGGAGCACCGTGGGAGACAGACAGTGGCCCTTACAGAAATGTTT 707

DB 668 ATGAAGGGAGCACCGTGGGAGACAGACAGTGGCCCTTACAGAAATGTTT 713

Search completed: April 6, 2003, 01:56:15

Job time : 2233 secs

GenCore version 5.1.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:54 ; Search time 1341.86 Seconds
(without alignments)
8508.978 Million cell updates/sec

Title: US-09-758-173-1
Perfect score: 705
Sequence: 1 ATGAGGTCGCCGCTCAGCT.....CCCTACAGATGTTCTATGA 705

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_estbam:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_nam:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	558.8	79.3	952	14	BQ711447	BQ711447 AGENCOURT
2	555.6	78.8	931	14	BQ709526	BQ709526 AGENCOURT
3	555.2	78.8	931	14	BQ711683	BQ711683 AGENCOURT
4	552	78.3	796	12	BG757730	BG757730 602714835
5	552	78.3	969	14	BQ707953	BQ707953 AGENCOURT
6	551.2	78.2	921	14	BQ708246	BQ708246 AGENCOURT

7	548.8	77.8	920	14	BQ712280	BQ712280 AGENCOURT
8	547.2	77.6	925	14	BQ710672	BQ710672 AGENCOURT
c	546	77.4	832	12	BG746204	BG746204 602723726
10	545.8	77.4	908	14	BQ884067	BQ884067 AGENCOURT
11	545.6	77.4	754	13	BI907909	BI907909 603069019
12	545.2	77.3	924	12	BG756256	BG756256 602713568
13	545	77.3	1086	14	BM924274	BM924274 AGENCOURT
14	544.4	77.2	917	14	BQ711587	BQ711587 AGENCOURT
15	542.4	76.9	949	14	BQ709509	BQ709509 AGENCOURT
16	541.6	76.8	1018	14	BM914338	BM914338 AGENCOURT
17	540.8	76.7	947	14	BQ709579	BQ709579 AGENCOURT
18	540.4	76.7	789	13	BI765865	BI765865 603046058
19	537	76.2	742	13	BI906298	BI906298 603063246
20	533.6	75.7	874	12	BG755301	BG755301 602714044
21	531	75.3	837	12	BG754193	BG754193 602709741
22	530.2	75.2	731	10	AV649126	AV649126 AV649126
23	529	75.0	803	12	BG758687	BG758687 602712935
24	528	74.9	862	12	BF338816	BF338816 602036250
25	527.4	74.8	842	12	BG686249	BG686249 602638157
26	525.6	74.6	788	13	BM007725	BM007725 603617172
27	525	74.5	1010	14	BM914307	BM914307 AGENCOURT
28	520.8	73.9	913	12	BG745387	BG745387 602723726
29	520.2	73.8	871	12	BG398521	BG398521 602439614
30	517.2	73.4	1005	12	BF974359	BF974359 602244026
31	516.6	73.3	883	13	BI760703	BI760703 603044891
32	515.2	73.1	926	13	BI911261	BI911261 603062819
c	513.8	72.9	868	12	BG745881	BG745881 602724051
34	512.8	72.7	923	14	BQ708365	BQ708365 AGENCOURT
35	512.6	72.7	864	12	BG756128	BG756128 602713428
36	508.4	72.1	782	13	BM007795	BM007795 603617259
37	508.2	72.1	801	13	BM007626	BM007626 603617044
38	508	72.1	829	12	BG754011	BG754011 602709539
39	501.8	71.2	688	12	BG745481	BG745481 602724051
c	499.8	70.9	722	14	BQ576097	BQ576097 UT-H-EZ1-
41	499	70.8	872	12	BG757059	BG757059 602710483
42	498.8	70.8	880	13	BI517885	BI517885 603041960
43	497	70.5	895	12	BF975632	BF975632 602246092
44	496.8	70.5	863	13	BI837966	BI837966 603083802
45	495.8	70.3	746	13	BI911011	BI911011 603068731

ALIGNMENTS

RESULT 1
BQ711447
LOCUS BQ711447 952 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8353624 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279618
5', mRNA sequence.
ACCESSION BQ711447
VERSION BQ711447.1 GI:21850346
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 952)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-1@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1CM2469 row: h column: 19
High quality sequence stop: 584.
Location/Qualifiers
source 1..952

SUMMARIES

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6279618"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-
/notes="Organ: spleen; Vector:
ECORI; CDNA made by oligo
into ECORI/XhoI sites using
GGCAGCAG(G). Library con-
laboratory of Gerald M.
Berkeley) using ZAP-cDNA
Superscript II RT (Life
NIH MGC library "
```

BASE COUNT	241 a	282 c	254 g	173 t	2 others
ORIGIN					
Query Match	79.3%;	Score 558.8;	DB 14;	Length 952;	
Best Local Similarity	91.9%;	Pred. No. 4.6e-134;			
Matches 590;	Conservative 0;	Mismatches 52;	Indels 0;	Gaps 0;	
QY	62	CCATGAACTGACTCAGCCACCCCTCGGTGTCTCAGTGTCCCGACGACAGAGCGCCAGGATCA	121		
DB	23	CCATATGCTCTGACTCAGTCAACCCCTCAGTGTCTCAGTGTGGCCCGCCAGGAGAGAGCGCCAGGATTA	82		
QY	122	CCGTGGGGGACACAACAGTATGAATGAATGTCCACTGGTACCACGACAGAACCCAGCGC	181		
DB	83	CCGTGAGAAACAAACATTTGGAGGTAAAGTGTGCACTGTACACGACGAGAGGACGCGCC	142		
QY	182	GGCCCCCTATATCTGTGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTTGAGCGAT	241		
DB	143	AGGCCCTCTGGTGGTCTATGTTTATGATAGGAGACGGCCCTCAGGGATCCCTGAGCGAT	202		
QY	242	TCCTCTGGCTCCAAATCAGGGACACCGCCACCTTGACCATCAACGGGTTCGAGCGCGGG	301		
DB	203	TCCTCTGGCTCCAACTCTGGGAATACGGCACCCCTGACCATCAGCAGGGTTCGAAGCGGGG	262		
QY	302	ATGAGCGCTGACTATTACTGTCTCAGGTGTGGGACAGGGCTAGTGATCATCCGGCTTCCTGGAG	361		
DB	263	ATGAGGCCGACTATTACTGTCTCAGGTGTGGGACAATACTATTGATCACGTGGTATTTCGGCG	322		
QY	362	GAGGACCCGGGTGACCGTCTTAGGTCTAGCCCAAGGCTGCCGCCCTCGTGCTACTCTGTGTCC	421		
DB	323	GAGGACCAAGCTGACCGTCTCTCGGTCTAGCCCAAGGCTGCCGCCCTCGGTCACTCTGTTC	382		
QY	422	CGCCCTCTCTGAGAGCTTCAAGCCAAACAGGCCACACTGGTGTGTCTCATAGTGACT	481		
DB	383	CGCCCTCTCTGAGAGCTTCAAGCCAAACAGGCCACACTGGTGTGTCTCATAGTGACT	442		
QY	482	TCCTACCCGGGACCGTGACAGTGGCTTGGAAAGGCAGATAGCAGCCCCCGTCAAGCGGGAG	541		
DB	443	TCCTACCCGGGACCGTGACAGTGGCTTGGAAAGGCAGATAGCAGCCCCCGTCAAGCGGGAG	502		
QY	542	TGAGACACACACACCTTCCAAACAAAGCAACAAAGTACGGCGCCAGGAGTCACTTGA	601		
DB	503	TGAGACACACACACCTTCCAAACAAAGCAACAAAGTACGGCGCCAGGAGTCACTTGA	562		
QY	602	GCCTGACGCTGAGCAGTGGAAAGTCCCACAGAGCTACAGCTGCCAGGTACACGCATGAAG	661		
DB	563	GCCTGACGCTGAGCAGTGGAAAGTCCCACAGAGCTACAGCTGCCAGGTACACGCATGAAG	622		
QY	662	GGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAATGTTCAAT	703		
DB	623	GGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAATGTTCAAT	664		

RESULT 2	
BQ709526	
LOCUS	
DEFINITION	BQ709526 931 bp mRNA linear EST 16-JUL-2002
	ACENGCOURT_8443486 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281636
	5', mRNA sequence.
ACCESSION	BQ709526
VERSION	BQ709526.1
KEYWORDS	GI:21848425
	EST.

SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 931)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LNCM2474 row: 1 column: 21 High quality sequence stop: 653.

FEATURES
source

```

1. .931
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6281636"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming, directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

```

BASE COUNT	227 a	284 c	245 g	174 t	1 others
ORIGIN					

Query Match	78.8%	Score 555.6	DB 14	Length 931
Best Local Similarity	89.3%	Pred. No. 3.1e-133		
Matches 623	Conservative 0	Mismatches 69	Indels 6	Gaps 2
Qy 11	CCGTCAGCTCCTGGGGCTCTGTGTCCTGTGGCTCCAGGTGCACGATGTGCCTATGAAC	70		
Db 37	CCGTTCTCCTCTGGGCTCCTCTCTCACTG--CACAGGCTCTGTGACCTCTATGTGC	93		
Qy 71	TGACTCAGCCACCCTCGGTGTCACTGTCCCAGAGACAGACGGCCAGGATCACTGTGGGG	130		
Db 94	TGACTCAGCCACCCTCGGTGTCACTGTGCCCTCCAGAGACAGCGGCCAACATTACCTGTGTGG	153		
Qy 131	GAGACAAACAGTAGAAATGAATATGTCCACTGGTACACAGCAGAACCCAGCGGGGCCCTTA	190		
Db 154	GAACAATATTGGAACTAANAAGTGTGCACTGGTACACAGAGGCCAGGCCCTG	213		
Qy 191	TACTGGTCACTATGATGATAGTAGACCGGCCCTCAGGGATCCCTGAGGGATTCCTTGCT	250		
Db 214	TGCTGGTGGTCAATGATGACAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCCTTGCT	273		
Qy 251	CCAAATCAGGGAACACCGCCACCTGACCATCAACGGGTCAGAGCCGGGATCAGGGCTG	310		
Db 274	CCAACTTGGNAACAACGGCCACCTGACCATCGACAGGTCGAAGCCGGGATGAGGCCG	333		
Qy 311	ACTATTACTGTCAAGTGTGGACAGGGCTAGTGATATC---CGGTCTTCGAGGAGAGGA	367		
Db 334	ACTATTACTGTCAAGTGTGGGATACTAGTATTGATCATCATGTGCTGTTTCGCGGAGGGA	393		
Qy 368	CCCGGGTGACCGTCCCTAGGTTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCCGCT	427		
Db 394	CCAAGCTGACCGTCTTAGGTTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCCGCT	453		
Qy 428	CCTCTGAGGAGCTTCAAGCCCAACAAAGGCCACACTGGTGTGTCTCATAGTGACTTCTACC	487		
Db 454	CCTCTGAGGAGCTTCAAGCCCAACAAAGGCCACACTGGTGTGTCTCATAGTGACTTCTACC	513		

RESULT 2	ACCESSION
BQ709526	VERSION
LOCUS	KEYWORDS
DEFINITION	

```

QY 488 CCGGAGCCGTGACAGTGGCCTGGAAGGACAGATAGCAGCCCCCGTCAAGCGGAGTGGA 547
Db 514 CCGGAGCCGTGACAGTGGCCTGGAAGGACAGATAGCAGCCCCCGTCAAGCGGAGTGGA 573
QY 548 CCACCACACCTCCAAACAAAGCAACAAAGTAGCGGCCAGCAGCTACCTGAGCCTGA 607
Db 574 CCACCACACCTCCAAACAAAGCAACAAAGTAGCGGCCAGCAGCTATCTGAGCCTGA 633
QY 608 CGCCTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCCAGGTCCAGCTACGATGAAGGAGCA 667
Db 634 CGCCTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCCAGGTCCAGCTACGATGAAGGAGCA 693
QY 668 CCGTGAGAGAGCAGTGGCCCTTACAGATGTTTCATGA 705
Db 694 CCGTGAGAGAGCAGTGGCCCTTACAGATGTTTCATGA 731

RESULT 3
B0711683
LOCUS AGENCOURT_8485100 NIH_MGC_113 Homo sapiens cdna clone IMAGE:6301194
DEFINITION 5', mRNA sequence.
ACCESSION B0711683
VERSION B0711683.1 GI:21850582
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 931)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: k column: 19
High quality sequence stop: 549.
Location/Qualifiers
1..931
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6301194"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 222 a 286 c 248 g 171 t 4 others
ORIGIN

Query Match 78.8%; Score 555.2; DB 14; Length 931;
Best Local Similarity 89.4%; Pred. No. 3.9e-133;
Matches 622; Conservative 0; Mismatches 66; Indels 6; Gaps 2;

QY 11 CCGCTCAGCTCTCGGGCTCCCTGCTGCTCTCCAGTCCAGATGTCGCTATGAAC 70
Db 39 CCGTTCTCTCTCGGCCCTCTCTCACTG---CACAGGCTCTGTGACCTCTATGTGC 95
QY 71 TGACTCAGCCACCTCGGTGTGAGTGTCCCGCAGGACAGACGCCAGGATCACTGTGGG 130
Db 96 TAACTCAGCCACCTCGGTGTGAGTGTCCCGCAGGACAGACGCCAGGATTAACCTGTGGG 155

```

```

QY 131 GAGACAACAGTAGAAATGAAATATGTCCACTGGTACACAGAGAAAGCCAGCGCGGCCCTTA 190
Db 156 GAAATAAGATTGGAAGTAAAGTGTGCACCTGGTTCACAGAGAGCCAGCGCCCTG 215
QY 191 TACTGGTTCATCTATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGATTTCTGGCT 250
Db 216 TCCTGGTTCGTCTCTGATGATCGGACCGGCCCTCAGGGATCCCTGAGCGAATCTTGCT 275
QY 251 CCAATCAGGGACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGGATGAGGCTG 310
Db 276 CCAACTCTGGGAACAACCGCCACCTGACCATCAGACGCTCGAGGCCGGGATGAGGCCG 335
QY 311 ACTATTACTGTCTAGGTGTGGGACAGGGCTAGTGATCATCC---GGTCTTCGGAGGAGGA 367
Db 336 ACTATTACTGTCTAGGTGTGGGATTTTCAGTAGTGATTATCTCTGTGGTATTTCGGCGGAGGA 395
QY 368 CCGGGTGACCGTCTTAGTTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTCCGGCCCT 427
Db 396 CCAAGCTGACCGTCTTAGTTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTCCGGCCCT 455
QY 428 CCTCTGAGGAGCTTCAAGCCCAACAAAGCCACACTGGTGTGCTCTCATAGTGACTTCTACC 487
Db 456 CCTCTGAGGAGCTTCAAGCCCAACAAAGCCACACTGGTGTGCTCTCATAGTGACTTCTACC 515
QY 488 CGGAGCCGTGACAGTGGCCTCGAAGGCAGATAGCAGCCCCCGTCAAGCGCGGAGTGGA 547
Db 516 CGGAGCCGTGACAGTGGCCTCGAAGGCAGATAGCAGCCCCCGTCAAGCGCGGAGTGGA 575
QY 548 CCACCACACCTCCAAACAAAGCAACAAAGTAGCGGCCAGCAGCTACTGAGCCTGA 607
Db 576 CCACCACACCTCCAAACAAAGCAACAAAGTAGCGGCCAGCAGCTATCTGAGCCTGA 635
QY 608 CGCTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCCAGGTCCAGCTGCGGAGGAGCA 667
Db 636 CGCTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCCAGGTCCAGCTGCGGAGGAGCA 695
QY 668 CCGTGGAAGAGACAGTGGCCCTTACAGAAATGTTTCAT 703
Db 696 CCGTGGAAGAGACAGTGGCCCTTACAGAAATGTTTCAT 731

RESULT 4
B0757730 796 bp mRNA linear EST 15-MAY-2001
LOCUS 602714835F1 NIH_MGC_48 Homo sapiens cdna clone IMAGE:4854921 5',
DEFINITION mRNA sequence.
ACCESSION B0757730
VERSION B0757730.1 GI:14068383
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 796)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1703 row: f column: 10
High quality sequence stop: 795.
Location/Qualifiers
1..796
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

/clone="IMAGE:4854921"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
BASE COUNT 177 a 244 c 231 g 143 t 1 others
ORIGIN

Query Match 78.3%; Score 552; DB 12; Length 796;
Best Local Similarity 89.2%; Pred. No. 2.5e-132;
Matches 618; Conservative 0; Mismatches 71; Indels 4; Gaps 2;

QY 11 CCCTCAGCTCCTGGGCTCCTGCTCTGGCTCCAGGTGCAGCATGTGCTATGAAC 70
DB 39 CCGTTCCTCTCGGCTCCTCTCTCACTG---CACAGGCTGTGACCTCCTATGTC 95
QY 71 TGACTCAGCCACCTCGGTGTCAAGTGTCCCGAGGACAGAGGAGGAGGAGGAGG 130
DB 96 TGACTCAGCCACCTCAGTGTCAAGTGTCCCGAGGAGGAGGAGGAGGAGGAGG 155
QY 131 GAGACACAGTAGAATATATGTCTCACTGTGTACAGAGAGGAGGAGGAGGAGG 190
DB 156 GAAATACATTTGAAGTAAACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 215
QY 191 TACTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
DB 216 TGTGTGCTATCAATATGATGATGATGATGATGATGATGATGATGATGATG 275
QY 251 CCAATCAGGGAACACCGCCACCTGACCATCAACCGGGTTCAGAGCGCGGGATG 310
DB 276 CCAATCTGGGAACACCGCCACCTGACCATCAACCGGGTTCAGAGCGCGGG 335
QY 311 ACTATTACTGTGAGGTGTGGGACAGGGCTAGTATCATCGGTCTTCGAGGAGG 370
DB 336 ACTATTACTGTGAGGTGTGGGATAGTATTAGCGATCATCGGGTGTTCGAGG 395
QY 371 GGTGACCGTCTTAGGTTCAGCCCAAGGCTGCCCGCTCGGTCACTGTTCGGG 430
DB 396 AGTGACCGTCTTAGGTTCAGCCCAAGGCTGCCCGCTCGGTCACTGTTCGGG 455
QY 431 CTGAGGAGCTTCAAGGCAACAGGCGCACACTGTGTGTCTCATAGTGAATCTT 490
DB 456 CTGAGGAGCTTCAAGGCAACAGGCGCACACTGTGTGTCTCATAGTGAATCTT 515
QY 491 GAGCGGTGACAGTGGCTGGAAGGAGATAGAGCCCGCTCAAGGCGGAGTGGAG 550
DB 516 GAGCGGTGACAGTGGCTGGAAGGAGATAGAGCCCGCTCAAGGCGGAGTGGAG 575
QY 551 CCACACCTCCAAACAAAGCAACAAAGTACCGGCGCAGCAGTACCTGAGCTG 610
DB 576 CCNACCTCCAAACAAAGCAACAAAGTACCGGCGCAGCAGTACCTGAGCTG 634
QY 611 CTGAGCAGTGGAGTCCCAAGAGCTTACAGTTCGCGAGGTTCAGCATGAAGG 670
DB 635 CTGAGCAGTGGAGTCCCAAGAGCTTACAGTTCGCGAGGTTCAGCATGAAGG 694
QY 671 TGGAGAGAGTGGGCGCTTACAGATGTTTCAT 703
DB 695 TGGAGAGAGTGGGCGCTTACAGATGTTTCAT 727

RESULT 5
BO707953
LOCUS BO707953 969 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_B353606 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279593

5', mRNA sequence.
BO707953
VERSION BO707953.1 GI:21846852
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2469 row: 9 column: 18
High quality sequence stop: 541.
FEATURES
Location/Qualifiers
1..969
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6279593"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."

BASE COUNT 226 a 309 c 251 g 174 t 9 others
ORIGIN
Query Match 78.3%; Score 552; DB 14; Length 969;
Best Local Similarity 89.1%; Pred. No. 2.6e-132;
Matches 620; Conservative 0; Mismatches 70; Indels 6; Gaps 2;
QY 11 CCGTCAAGCTCCTGGGCTCCTGCTGCTGCTGCCAGGTGCAGCATGTGCTATGAAC 70
DB 28 CCGTTCCTCTCGGCTCCTCTCTCACTG---CACAGGCTCTGTGACCTCTATGTC 84
QY 71 TGACTCAGCCACCTCGGTGTGAGTGTCCCGAGGACAGAGCGGCGGAGTACCTG 130
DB 85 TGACTCAGCCACCTCGGTGTGAGTGTCCCGAGGACAGAGCGGCGGAGTATTT 144
QY 131 GAGACACAGTAGAATATGATGTCCACTGTGTACAGCAGAGGAGGAGGAGGAGG 190
DB 145 GAAACACACCTGCAAGTAAAGTGTGACGTGTGTACAGCAGAGGAGGAGGAGG 204
QY 191 TACTGGTTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 250
DB 205 TGCTGGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 264
QY 251 CCAATCAGGGAACACCGCCACCTGACCATCAACCGGGTTCAGAGCGGAGGAG 310
DB 265 CCAATTCCTGGGAACACCGCCACCTGACCATCAACCGGGTTCAGAGCGGAGG 324
QY 311 ACTATTACTGTGAGGTGTGGGACAGGGCTAGTATGATC---ATCCGGTCTTCG 367
DB 325 ACTATTACTGTGAGGTGTGGGATGATGATGATGATGATGATGATGATGATG 384
QY 368 CCCGGGTGACCGTCTTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTC 427
DB 395 CCAAGCTGACCGTCTTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTC 444


```
/clone="IMAGE:6279636"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 216 a 281 c 246 g 176 t 1 others
ORIGIN
Query Match 77.8%; Score 548.8; DB 14; Length 920;
Best Local Similarity 88.8%; Pred. No. 1.8e-131;
Matches 618; Conservative 0; Mismatches 72; Indels 6; Gaps 2;
QY 11 CCGCTCAGCTCCTGGGCTCCTGCTCTGGCTCCAGGTGCACGATGTGCTATGAAC 70
DB 37 CCGTCTCTCTCTGGCTCCTCTCTCACTG---CACAGGCTGTGTACCTCTATGTGC 93
QY 71 TGACTCAGCCACCCTCGGTGTCTAGTGTCCAGGACAGACGCGCCAGGATCACCCTGTGGG 130
DB 94 TGACTCAGACACCCTCGGTGTCTAGTGTGGGCTCCTCTCTCACTG---CACAGGCTGTGTACCTCTATGTGC 153
QY 131 GAGACACAGTAGAATGATATGTCCACTGTGTACGAGCAGAGAGCCAGCGCGGCCCTTA 190
DB 154 GAAACAACTTGAAGAAAAGTGTCTACTGTGTACGAGCAGAGAGCCAGCGCCAGGCCCTC 213
QY 191 TACTGTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
DB 214 TGGTGTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 273
QY 251 CCAATCAGGGAACACCGCCACCTGTACATCAACAGGGGTGTAGGGCGGGGATGAGCTG 310
DB 274 CCAACTCTGGGAACACCGCCACCTGTACATCAACAGGGGTGTAGGGCGGGGATGAGGGCG 333
QY 311 ACTATTACTGTAGGTGTGGGACAGGCTAGTGTATCTATCC---GGTCTTCGAGGAGGGA 367
DB 334 ACTATTACTGTAGGTGTGGGATCTAGTGTGTATCTGTGTGTGTGTGTGTGTGTGTGT 393
QY 368 CCCGGGTGACCGTCTTAGGTGACGCCAAGGCTGCCCCCTCGGTCACTCTGTGTCCGCCCT 427
DB 394 CCAAGCTGACCGTCTTAGGTGACGCCAAGGCTGCCCCCTCGGTCACTCTGTGTCCGCCCT 453
QY 428 CCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCTATAAGTACTTCTACC 487
DB 454 CCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCTATAAGTACTTCTACC 513
QY 488 CGGAGCGGTGACAGTGTGGGAGGAGATAGCAGCCCGCTCAAGCGGGAGTGGAGA 547
DB 514 CGGAGCGGTGACAGTGTGGGAGGAGATAGCAGCCCGCTCAAGCGGGAGTGGAGA 573
QY 548 CCACACACCCCTCCAAACAAAGCAACAAAGTACAGCGGCCAGCAGTACTGAGCTGA 607
DB 574 CCACACACCCCTCCAAACAAAGCAACAAAGTACAGCGGCCAGCAGTACTGAGCTGA 633
QY 608 CGCTGAGCAGTGAAGTCCACAGAGCTACAGCTGCGAGGTGACGATGAAGGGAGCA 667
DB 634 CGCTGAGCAGTGAAGTCCACAGAGCTACAGCTGCGAGGTGACGATGAAGGGAGCA 693
QY 668 CCGTGGAGAACAGTGGCCCCCTACAGATGTTTAT 703
DB 694 CCGTGGAGAACAGTGGCCCCCTACAGATGTTTAT 729
RESULT 8
BO710672 BO710672 925 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_8484950 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301041
DEFINITION 5', mRNA sequence.
ACCESSION BO710672,
```

```
VERSION BQ710672.1 GI:21849571
SOURCE EST.
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 925)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2516 row: e column: 10
High quality sequence stop: 661.
FEATURES
source
1..925
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6301041"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 214 a 293 c 239 g 170 t 9 others
ORIGIN
Query Match 77.6%; Score 547.2; DB 14; Length 925;
Best Local Similarity 88.6%; Pred. No. 4.6e-131;
Matches 617; Conservative 0; Mismatches 73; Indels 6; Gaps 2;
QY 11 CCGCTCAGCTCCTGGGCTCCTGCTCTGGCTCCAGGTGCACGATGTGCTATGAAC 70
DB 38 CCGTCTCTCTCTGGGCTCCTCTCTCACTG---CACAGGCTGTGTACCTCTATGTGC 94
QY 71 TGACTCAGCCACCCTCGGTGTCTAGTGTCCCGAGCAGAGCGCCAGGATCACCTGTGGG 130
DB 95 TGACTCAGCCACCCTCGGTGTCTAGTGTGGGCCCGAGCAGACGCGCCAGGATTA 154
QY 131 GAGACAACTAGAAATGAATATGTCCACTGTGTACAGCAAGCCAGCGCGGCCCTTA 190
DB 155 GAAACAATATTGGAAGTAGAAGTGTGCACTGTGTACAGCAGACTTCAGGCCAGGCCCTG 214
QY 191 TACTGTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
DB 215 TGTGTGTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 274
QY 251 CCAATCAGGGAACACCGCCACCCTGTACCATCAACGGGGTGTAGCGCGGGGATGAGGCTG 310
DB 275 CCAACTCTGGGAACACCGCCACCCTGTATCATCAGCAGTGTGAAAGCGGGGATGAGGCG 334
QY 311 ACTATTACTGTGAGGTGTGGGACAGGCTAGTGTATCTATCCCG---TCTTTCGAGAGGGA 367
DB 335 CCTATTACTGTGAGGTGTGGCATAGTGTGTGTACTCATCTCTCTACTATTTCGGCGAGGGA 394
QY 368 CCCGGGTGACCGTCTTAGGTGACGCCAAGGCTGCCCCCTCGGTCACTCTGTTCGCCCT 427
DB 395 CCAAGCTGACCGTCTTAGGTGACGCCAAGGCTGCCCCCTCGGTCACTCTGTTCGCCCT 454
QY 428 CCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCTATAAGTACTTCTACC 487
```

```

Db 455 CCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGGTGTGTCTCATTAAGTGAATTTTACC 514
QY 488 CGGGAGCCGTGACAGTGGGCTCGAAGGCGAGATAGCAGAGCCCGCTCAAGCGCGGAGTGGAGA 547
Db 515 CGGGAGCCGTGACAGTGGGCTCGAAGGCGAGATAGCAGAGCCCGCTCAAGCGCGGAGTGGAGA 574
QY 548 CGACACACCCCTCCAAACAAAGCAACACAGTACCGCGCCGAGCAGCTACTGAGCCCTGA 607
Db 575 CCACACACCCCTCCAAACAAAGCAACACAGTACCGCGCCGAGCAGCTACTGAGCCCTGA 634
QY 608 CGCTGAGCAGTGAAGTCCCAAGAGCTACAGCTGCCAGGTCAACGATGAAGGAGCA 667
Db 635 CGCTGAGCAGTGAAGTCCCAAGAGCTACAGCTGCCAGGTCAACGATGAAGGAGCA 694
QY 668 CCCTGGAAGACAGTGGCCCTTACAGATGTTTAT 703
Db 695 CCCTGGAAGACAGTGGCCCTTACAGATGTTTAT 730

RESULT 9
BG746204/c 832 bp mRNA linear EST 15-MAY-2001
LOCUS 602723726T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4849878 3'
DEFINITION mRNA sequence.
ACCESSION BG746204
VERSION BG746204.1 GI:14056857
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 832)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1690 row: d column: 07
High quality sequence stop: 827.
Location/Qualifiers
1..832
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4849878"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
NOTE="Organ: spleen; Vector: pOT87; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 152 a 232 c 263 g 185 t
ORIGIN

Query Match 77.4%; Score 546; DB 12; Length 832;
Best Local Similarity 92.4%; Pred. No. 9.1e-131;
Matches 597; Conservative 0; Mismatches 45; Indels 4; Gaps 2;

QY 62 CCTATGAATCTGACTCAGCCACCCCTCGGTGTCTAGTCTCCCGAGGACAGAC-GGCCAGGATC 120
Db 739 CCAATGTGCTGACTCAGCCACCCCTCGGTGTCTAGTGTGGCCCGAGGACAGCGGGCCAGATT 680
QY 121 ACCTGTGGGGGAGACAAACAGTAGAATGATATGTCCTAGTACCGACAGCAAGCCAGCG 180

```

```

Db 679 ACCTGTGGGGTCCCAACATTGGAACCTTACAGTGTGCATTTACAGCAGAGTCAAGC 620
QY 181 CGGGCCCTATCTACTGTGTCTATGATGATAGTACCGCCCTCAGGGATCCCTGAGCGA 240
Db 619 CAGGCCCTGTGTGTGTCTATGATGATAGTACCGCCCTCAGGGATCCCTGAGCGA 560
QY 241 TTCTTGGCTCCAAATCAGGGAAACACCGCCACCTTGAACATCAACGGGGTCAAGCCGGG 300
Db 559 TTCTTGGCTCCAACTCTGGGAACACCGCCACCTTGAACATCAACGGGGTCAAGCCGGG 500
QY 301 GATGAGCTGACTATTACTGTGAGGTGTGGGACAGGCTAGTGTATCATCCCGT---CTTC 357
Db 499 GATGAGCCGACTATTACTGTGAGGTGTGGGACAGGCTAGTGTATCATCCCTGCAATT 440
QY 358 GGAGGAGGACCCCGGTGACCGTCTTAGGTACGCCAACAGGCTGCCCTCGGTCACTGTG 417
Db 439 GCGGAGGAGACCAAACTGACCGCTTCTAGGTACGCCAACAGGCTGCCCTCGGTCACT 380
QY 418 TTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGACCAACAGTGTGTCTCATAGT 477
Db 379 TTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGACCAACAGTGTGTCTCATAGT 320
QY 478 GACTTCTACCCCGGAGCCGTGACAGTGGCTTGAAGGAGGATAGCAGCCCGTCAAGGCG 537
Db 319 GACTTCTACCCCGGAGCCGTGACAGTGGCTTGAAGGAGGATAGCAGCCCGTCAAGGCG 260
QY 538 GGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGAGCTAC 597
Db 259 GGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGAGCTAT 200
QY 598 CTGAGCCTGACGCGCTGAGCAGTGGAGTCCCAAGAGTCCCAAGAGTACAGTGCAGGTCA 657
Db 199 CTGAGCCTGAGCGCTGAGCAGTGGAGTCCCAAGAGTCCCAAGAGTACAGTGCAGGT 140
QY 658 GAAGGAGGACCGTGGAGAGACAGTGGCGCCCTACAGATGTTTAT 703
Db 139 GAAGGAGGACCGTGGAGAGACAGTGGCGCCCTACAGATGTTTAT 94

RESULT 10
BO884067
LOCUS BO884067
DEFINITION BO884067
ACCESSION BO884067
VERSION BO884067.1 GI:22276075
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2519 row: p column: 24
High quality sequence stop: 687.
Location/Qualifiers
1..908
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6302471"
/clone_lib="NIH_MGC_113"

```



```

Db 515 GGAGCCGTGACAGTGGCCCTGGAAGACGATAGCAGCCCGCTCAAGGGGGAGTGGAGAC 574
QY 549 CACCAACCCCTCAAAACAAGCAACAAGTACGCGGCCAGCAGCTACTGAGCCTGAC 608
Db 575 CACCACACCCCTCAAAACAAGCAACAAGTACGCGGCCAGCAGCTACTGAGCCTGAC 634
QY 609 GCTGAGCAGTGGAGTCCCAAGAGCTACA-GCTGCCAGGTCAAGTGAAGGGAGCA 667
Db 635 GCTGAGCAGTGGAGTCCCAAGAGCTACAGGCTGCGAGGTCAAGTGAAGGGAGCA 694
QY 668 CCGTGAGAGAGCAGTGGCCCTCACAGAAATGTTTCAT 703
Db 695 CCGTGAGAGAGCAGTGGCCCTCACAGAAATGTTTCAT 730

RESULT 12
BG756256 6027113568F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853801 5',
LOCUS mRNA sequence.
DEFINITION BG756256 924 bp mRNA linear EST 15-MAY-2001
ACCESSION BG756256
VERSION BG756256.1 GI:14066909
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 924)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1700 row: g column: 18
High quality sequence stop: 786.
FEATURES
source
1..924
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4853801"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 226 a 272 c 257 g 169 t
ORIGIN

Query Match 77.3%; Score 545.2; DB 12; Length 924;
Best Local Similarity 92.7%; Pred. No. 1.5e-130;
Matches 595; Conservative 0; Mismatches 43; Indels 4; Gaps 2;

QY 62 CCTATGAACCTGACTCAGCCACCTCGGTGTCAGTGTCCCGAGCAGACACGCCAGGATCA 121
Db 14 CCTATGCTGACTCAGCCACCTCGGTGTCAGTGTCCCGAGCAGACACGCCAGGATTA 73
QY 122 CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCTGCTACCGACAGACAGCCAGCGC 191
Db 74 CCTGTGGGGGAAACAACATGGAGTAGTAAGTGTGCACTGTGCTATCAGCAGAGCGAGGCC 133

```

```

QY 182 GGCCCCCTATACTGCTCATCTATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGAT 241
Db 134 AGGCCCCCTGTGCTGGTGGTCTATGAAGATAGTACCGGCCCTCAGGGATCCCTGAGCGAT 193
QY 242 TCTGTGCTCTCAAAATCAGGGAAACACCGCCACCTGACACATCAACGGGGTTCGAGCCGGGG 301
Db 194 TCTGTGCTCTCAAACTCTGGGAAACACGGCCACCTGACCATCAGCAGGGTTCGAAGCCGGGG 253
QY 302 ATGAGGCTGACTATTAATCTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
Db 254 ATGAGGCCGACTATTACTGTGTCAGGTGTGGGATAGAAGTAGTG---ATGTAGTATTTCGGCG 310
QY 362 GAGGACCCCGGGTGCCTCTAGGTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 421
Db 311 GAGGACCAAGCTGACCGTGTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 370
QY 422 CGCCCTCTCTGAGGAGCTTCAAGCCAAACAAAGCCACACTGGTGTGTCTCATAAAGTGACT 481
Db 371 CGCCCTCTCTGAGGAGCTTCAAGCCAAACAAAGCCACACTGGTGTGTCTCATAAAGTGACT 430
QY 482 TCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGCAGCCCGCTCAAGCCGGAG 541
Db 431 TCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGCAGCCCGCTCAAGCCGGAG 490
QY 542 TGGAGACCAACACACCTCTCAAAACAAGCAACAAGTACGCGGCCAGCAGCTACTGA 601
Db 491 TGGAGACCAACACACCTCTCAAAACAAGCAACAAGTACGCGGCCAGCAGCTACTGA 550
QY 602 GCTGACGCTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCCAGGTCAAGCATGAAG 661
Db 551 GCCTGACGCTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCCAGGTCAAGCATGAAG 610
QY 662 GGAGCACCTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT 703
Db 611 GGAGCACCTGGAGAGACAGTGG-CCCTACAGAAATGTTTCAT 651

RESULT 13
BG924274 630576 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760519
LOCUS 5', mRNA sequence.
DEFINITION BG924274
ACCESSION BG924274
VERSION BG924274.1 GI:19374641
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1086)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12807 row: k column: 16
High quality sequence stop: 710.
FEATURES
source
1..1086
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5760519"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:

```

PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."

BASE COUNT 255 a 355 c 270 g 199 t 7 others

Query Match 77.3%; Score 545; DB 14; Length 1086;
Best Local Similarity 88.6%; Pred. No. 1.8e-130;
Matches 614; Conservative 0; Mismatches 75; Indels 4; Gaps 2;

QY 11 CCCTCAGCTCTCGGGCTCTCGCTGCTCTGGCTCCAGGTGCAGATGTGCCTATGAAC 70
DB 50 CCGTCTCTCTCGGCTCTCTCTCACTG---CACAGGCTCTCTGACCTCTATGTGC 106
QY 71 TGACTCAGCACCCTCGGTGTCAGTGTCCAGAGCAGACGCCAGGATCACTGTGGGG 130
DB 107 TGACTCAGCACCCTCGGTGTCAGTGTCCAGAGCAGACGCCAGGATCACTGTGG 165
QY 131 GAGACAACTAGTAAGTATATGCTGCTGCTCCAGGTGCAGATGTGCCTATGAAC 190
DB 166 GAACTACATTAAGATGTTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 225
QY 191 TACTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
DB 226 TATTGGCCGTCTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
QY 251 CCAATTCAGGAGACCGCCACCTGACCTCAACGAGGTGAGGCGGGGATGAGGCTG 310
DB 286 CCAAGTCTGAAACACGGCCATCTGACATCAGCAGGCTGAGGCGGGGATGAGGCG 345
QY 311 ACTATTACTGTGAGGTGGGACAGGCTGATGATCATCCGCTCTCGGAGGGAGGCC 370
DB 346 ACTATTACTGTGAGGTGGGACAGGCTGATGATCATCCGCTCTCGGAGGGAGGCC 405
QY 371 GGTGACCTCTCTAGTGCAGCCAGGCTGCGCCCTCGGTCACTGTGTCGCGCCCTCT 430
DB 406 AGCTGACCTCTCTAGTGCAGCCAGGCTGCGCCCTCGGTCACTGTGTCGCGCCCTCT 465
QY 431 CTGAGGAGCTTCAAGCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
DB 466 CTGAGGAGCTTCAAGCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 525
QY 491 GAGCGTGCAGTGGCTGGAGAGGAGATAGCAGCCCGCTCAAGCGGGAGTGAGACCA 550
DB 526 GAGCGTGCAGTGGCTGGAGAGGAGATAGCAGCCCGCTCAAGCGGGAGTGAGACCA 585
QY 551 CCACACCTTCAAAACAAGCAACAGTACGCGGCCAGCAGCTACTGAGCCTGACGC 610
DB 586 CCACACCTTCAAAACAAGCAACAGTACGCGGCCAGCAGCTACTGAGCCTGACGC 645
QY 611 CTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTCAGGTCAGGTCAGGTCAGGTC 670
DB 646 CTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTCAGGTCAGGTCAGGTCAGGTC 705
QY 671 TGGAGAGACAGTGGCCCTCAGAAATGTTCA 703
DB 706 TGGAGAGACAGTGGCCCTCAGAAATGTTCA 738

RESULT 14
LOCUS BQ711587
DEFINITION AGENCOURT_8475231 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301461
5', mRNA sequence.
ACCESSION BQ711587
VERSION BQ711587.1 GI:21850486

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 917)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2517 row: f column: 22
High quality sequence stop: 552.
Location/Qualifiers
1. 917
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:6301461"
/lab host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 223 a 286 c 242 g 166 t

Query Match 77.2%; Score 544.4; DB 14; Length 917;
Best Local Similarity 88.5%; Pred. No. 2.4e-130;
Matches 614; Conservative 0; Mismatches 76; Indels 4; Gaps 2;

QY 11 CCGCTCAGCTCTCGGGCTCTCTGCTCTGGCTCCAGGTGCAGATGTGCCTATGAAC 70
DB 38 CCGTCTCTCTCGGGCTCTCTCTCACTG---CACAGGCTGTGACCTCTATGTGT 94
QY 71 TGACTCAGCCACCTCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 130
DB 95 TGACTCAGCCACCTCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 154
QY 131 GAGACAACTAGTAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
DB 155 GGAACAACTAGTAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
QY 191 TACTGCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
DB 215 TCGTGTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 274
QY 251 CCAATTCAGGGAACACCGCCACCTGACCATCAACCGGGTTCGAGGCGGGGATGAGGCTG 310
DB 275 CCACCTTCTGGTGATACGGCCACCTGACCATCAGTGTGGTTCGAAGCGGGGATGAGGCG 334
QY 311 ACTATTACTGTGAGGTGGGACAGGCTAGTATCATCCGCTCTCGGAGGGAGGCC 370
DB 335 ACTATTACTGTGAGGTGGGACAGGCTAGTATCATCCGCTCTCGGAGGGAGGCC 394
QY 371 GGTGACCTCTCTAGGTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTCCCGCCCTCT 430
DB 395 GGTGACCTCTCGGGTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTCCCGCCCTCT 454
QY 431 CTGAGGAGCTTCAAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
DB 455 CTGAGGAGCTTCAAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 514

```

QY 491 GAGCCGTGACAGTGGCTTGAAGGACAGATAGCAGCCCCCGTCAAGCGGGAGTGGAGACCA 550
|
|
|
Db 515 GAGCCGTGACAGTGGCTTGAAGGACAGATAGCAGCCCCCGTCAAGCGGGAGTGGAGACCA 574
|
|
|
QY 551 CCACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACCTGAGCCTGAGCC 610
|
|
|
Db 575 CCACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACCTGAGCCTGAGCC 634
|
|
|
QY 611 CTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCGCAGGTCCAGCATGAAGGAGCA-CC 669
|
|
|
Db 635 CTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCGCAGGTCCAGCATGAAGGAGCA-CC 694
|
|
|
QY 670 GTGAGAGACAGTGGCCCTTACAGAATGTTTCAAT 703
|
|
|
Db 695 GTGAGAGACAGTGGCCCTTACAGAATGTTTCAAT 728
|
|
|

RESULT 15
BQ709509
LOCUS BQ709509
DEFINITION AGENCOURT_8418138 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281593
5', mRNA sequence.
ACCESSION BQ709509
VERSION BQ709509.1 GI:21848408
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 949)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLM2474 row: k column: 02
High quality sequence stop: 635.
Location/Qualifiers
1..949
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6281593"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
NIH_MGC Library"
BASE COUNT 221 a 301 c 247 g 179 t 1 others
ORIGIN
Query Match 76.9%; Score 542.4; DB 14; Length 949;
Best Local Similarity 88.2%; Pred. No. 8e-130;
Matches 614; Conservative 0; Mismatches 76; Indels 6; Gaps 2;

QY 11 CCGCTCAGCTCTCGGGCTCTCTGCTGCTGCCCTCCAGGTGACGATGTCCTATGAAC 70
|
|
|
Db 26 CCGTTCTCTCTCGGGCTCTCTGCTGCTGCCCTCCAGGTGACGATGTCCTATGTC 82
|
|
|
QY 71 TCAGCTCAGCCACCTCGGTGTCAGTGTCCCGAGGACAGCCGAGGATACCTGTGGG 130
|
|
|

```

Search completed: April 6, 2003, 06:20:13
Job time : 1346.86 secs

```

Db 83 TGACCACCCACCTCGGTGTCTCGTGGCCCCCAGGACAGACGGCCAGAATTTCCTGTGGAA 142
|
|
|
QY 131 GAGACACAGTAGAAATGAATATGTCCACTGGTACACGACGAGAGCCAGCGGGGCCCTTA 190
|
|
|
Db 143 GAAACCGAGTTGAAGTAGCAATATAAACTGGTACACGACGAGAACCCAGGCCAGGCCCTG 202
|
|
|
QY 191 TACTGGTCACTCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTTCTTGGCT 250
|
|
|
Db 203 TCCTGGTCTGTCTGTGATACCGACCGGCCCTCAGGGATCCCTGAGCGATTTCTTGGCT 262
|
|
|
QY 251 CCAATCAGGAAACACCGCCACCTGACCATCAACAGGGGTGAGGCCGGGATGAGGCTG 310
|
|
|
Db 263 CCAACTCTGGGAAACACCGCCACCTGACCATCAACAGGGGTGAGGCCGGGATGAGGCCG 322
|
|
|
QY 311 ACTATTACTGTCAAGTGTGGGACAGGGCTAGTGATATCC---GGTCTCGGAGGAGGA 367
|
|
|
Db 323 ACTATTATTGTCAAGTGTGGGATTAATAGTACTGACCACTGTGTGTTTCGGCGGAGGA 382
|
|
|
QY 368 CCGGGTGACCGTCTTAGGTGACGCCCAAGGCTGCCCTCGGTCACTCTGTTCCTCGGCCCT 427
|
|
|
Db 383 CCAAGCTGACCGTCTTAGGTGACGCCCAAGGCTGCCCTCGGTCACTCTGTTCCTCGGCCCT 442
|
|
|
QY 428 CCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCATTAAGTGACTTCTACC 487
|
|
|
Db 443 CCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCATTAAGTGACTTCTACC 502
|
|
|
QY 488 CGGAGCCGTGACAGTGGCTGGAAGGSCAGATAGCAGCCCCCGTCMAGGCCGGGAGTGAGA 547
|
|
|
Db 503 CGGAGCCGTGACAGTGGCTGGAAGGSCAGATAGCAGCCCCCGTCMAGGCCGGGAGTGAGA 562
|
|
|
QY 548 CCACCACACCTCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACTGAGCCCTGA 607
|
|
|
Db 563 CCACCACACCTCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACTGAGCCCTGA 622
|
|
|
QY 608 CGCTGAGCAGTGGAGTCCCAAGAGCTACAGTGTCCAGGTCAAGCATGAAGGGAGCA 667
|
|
|
Db 623 CGCTGAGCAGTGGAGTCCCAAGAGCTACAGTGTCCAGGTCAAGCATGAAGGGAGCA 682
|
|
|
QY 668 CCGTGGAGAGAGACAGTGGGCCCTTACAGAATGTTTCAT 703
|
|
|
Db 683 CCGTGGAGAGAGACAGTGGGCCCTTACAGAATGTTTCAT 718
|
|
|

```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 18:12:24 ; Search time 193.478 Seconds
(without alignments)
8205.894 Million cell updates/sec

Title: US-09-758-173-1

Perfect score: 705

Sequence: 1 ATGAGGTCCCGCTCAGCT.....CCCTACAGAAATGTTTCATGA 705

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	AA762509	Primates anti-hu
2	705	100.0	705	AAV35484	Macaque primatized
3	705	100.0	705	AA517242	DNA sequence of a
4	585.2	83.0	702	AA762867	Ant-CD4 monkey-hum
5	582.6	82.6	926	AA224427	Human bladder tumo
6	555.6	78.8	836	AA583482	DNA encoding novel
7	540.2	76.6	711	AAV35488	Macaque primatized
8	540.2	76.6	711	AA517246	DNA sequence of a
9	538.6	76.4	711	AA762512	Primates anti-hu

10	527.6	74.8	1027	24	ABQ54438	Human ovarian anti
11	524	74.3	841	23	AA583486	DNA encoding novel
12	520.8	73.9	904	24	ABK28671	Human cDNA encodin
13	520.4	73.8	869	22	AA522717	Human cDNA encodin
14	516	73.2	791	23	AA587271	DNA encoding novel
15	515	73.0	1825	22	AA522777	Human cDNA encodin
16	514.4	73.0	859	22	AA522481	Human cDNA encodin
17	512.8	72.7	960	21	AACT8188	Human cancer assoc
18	512	72.6	872	9	AA818555	VDJC regions of hu
19	511	72.5	654	22	AA513364	Human cDNA encodin
20	509.2	72.2	930	22	AA522541	Human cDNA encodin
21	506	71.8	793	23	AA583481	DNA encoding novel
22	504	71.5	807	23	AA583484	DNA encoding novel
23	495.2	70.2	863	24	ABK28650	Human cDNA encodin
24	480	68.1	849	22	AAH98186	Human EST-derived
25	474.2	67.3	884	11	AAQ03609	Sequence encoding
26	473.6	67.2	810	23	AA587270	DNA encoding novel
27	473	67.1	935	22	AA587270	Human immune syste
28	472	67.0	768	20	AA587270	Monoclonal antibod
29	472	67.0	768	20	AA587270	Monoclonal antibod
30	465.6	66.0	826	22	AA58109	Human polynucleoti
31	462.8	65.6	915	24	ABN97248	Gene #3746 used to
32	462.8	65.6	915	24	ABK64815	Human benign prost
33	462.8	65.6	915	24	ABL65478	Lung cancer relate
34	462.2	65.6	654	14	AAQ49835	Anti-HIV-1 recombi
35	462	65.5	762	22	AA584209	Plasmid Glambda-1B
36	462	65.5	5679	22	AA584207	Plasmid Glambda-1A
37	461.8	65.5	889	23	AA577073	DNA encoding novel
38	457	64.8	902	14	AAQ35100	Antibody D lambda
39	456	64.7	895	22	AA565530	Human immune syste
40	455.6	64.6	763	23	AA583480	DNA encoding novel
41	455.4	64.6	891	22	AA565528	Human immune syste
42	455.2	64.6	708	22	AAH47902	Human type anthum
43	453.6	64.3	783	23	AA583483	DNA encoding novel
44	452	64.1	876	23	AA583478	DNA encoding novel
45	451.6	64.1	651	19	AAV11293	Antibody HB4C5 lig

ALIGNMENTS

RESULT 1
AA762509
ID AA762509 standard; DNA; 705 BP.
XX
AC AA762509;
XX
DT 25-MAY-1997 (first entry)
XX
DE Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma; ss.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX

Db 1 ATGAGGGTCCCCGCTCAGCTCTCTGGGGTCTCTGTGTCTGTGGTCTCCAGGTGCACGATGT 60
 QY 61 GCCTATGAATGACTCAGCCACCTCTCGGTGTCTGTGTCTGTGGTCTCCAGGTGCACGATGT 120
 Db 61 GCCTATGAATGACTCAGCCACCTCTCGGTGTCTGTGTCTGTGGTCTCCAGGTGCACGATGT 120
 QY 121 ACCTGTGGGGAGACAAACAGTAGAATAATATGTCTCACTGTGTACAGAGAGAGCCAGCG 180
 Db 121 ACCTGTGGGGAGACAAACAGTAGAATAATATGTCTCACTGTGTACAGAGAGAGCCAGCG 180
 QY 181 CGGGCCCTTATCTGTCTCATCTATGATGATAGTAGTACCGGCTCAGGATCTCCGTGAGCGA 240
 Db 181 CGGGCCCTTATCTGTCTCATCTATGATGATAGTAGTACCGGCTCAGGATCTCCGTGAGCGA 240
 QY 241 TTCTCTGGCTCAAAATCAGGAAACACCGCCACCTCTGACATCAACGGGGTCGAGGCCGG 300
 Db 241 TTCTCTGGCTCAAAATCAGGAAACACCGCCACCTCTGACATCAACGGGGTCGAGGCCGG 300
 QY 301 GATGAGGCTGACTATTACTGTCTGAGTGTGGGACAGGGCTAGTGATCATCGGTCCTCGGA 360
 Db 301 GATGAGGCTGACTATTACTGTCTGAGTGTGGGACAGGGCTAGTGATCATCGGTCCTCGGA 360
 QY 361 GGAGGACCCGGGTGACCGTCTCTAGTTCAGCCCAAGGCTGCCCCCTCGGTCTCTGTTTC 420
 Db 361 GGAGGACCCGGGTGACCGTCTCTAGTTCAGCCCAAGGCTGCCCCCTCGGTCTCTGTTTC 420
 QY 421 CGCCCTCTCTGAGGAGCTTCAGGCAACAGCCACCTGACATCAACGGGGTCGAGGCCGG 480
 Db 421 CGCCCTCTCTGAGGAGCTTCAGGCAACAGCCACCTGACATCAACGGGGTCGAGGCCGG 480
 QY 481 TTCTACCGGGAGCCGTGACAGTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 Db 481 TTCTACCGGGAGCCGTGACAGTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 QY 541 GTGGAGACACACACCTCTCAAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 Db 541 GTGGAGACACACACCTCTCAAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 QY 601 AGCTTGAGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 Db 601 AGCTTGAGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 QY 661 GGGAGACCGTGGAGACAGAGTGGCCCTCAGAAATGTTTCATGA 705
 Db 661 GGGAGACCGTGGAGACAGAGTGGCCCTCAGAAATGTTTCATGA 705

RESULT 3

AASI17242

ID AASI17242 standard; DNA; 705 BP.

XX AC AASI17242;

XX DT 12-MAR-2002 (first entry)

XX DE DNA sequence of a primatised form of the light chain of 7C10 antibody.

XX KW Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;

XX KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;

XX KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;

XX KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;

XX KW graft-vs-host disease; immunosuppression; organ rejection;

XX KW interleukin-2; IL-2; mutant; ds.

XX OS Chimeric - Homo sapiens.

XX OS Chimeric - Macaca sp.

XX OS Synthetic.

XX FH Key

XX CDS Location/Qualifiers

XX 1..705

XX /tag= a

XX /product= "Light chain of 7C10 antibody"

XX PN WO200189567-A1.
 XX PD 29-NOV-2001.
 XX PF 22-MAY-2001; 2001WO-US16364.
 XX PR 22-MAY-2000; 2000US-0576424.
 XX PA (IDEC-) IDEC PHARM CORP.
 XX PI Anderson DR, Hanna N, Brans P;
 XX DR WPI; 2002-089895/12.
 XX DR P-PSDB; AAU11538.
 XX PT Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease such as
 PT allergy -
 XX

Example 8; Fig 3a; 89pp; English.

XX The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present nucleic
 CC acid sequence encodes the light chain of 7C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).

Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match 100.0%; Score 705; DB 24; Length 705;

Best Local Similarity 100.0%; Pred. No. 4e-167;

Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCCGCTCAGCTCTCTGGGGTCTCTGTGTCTGTGGTCTCCAGGTGCACGATGT 60

Db 1 ATGAGGGTCCCCGCTCAGCTCTCTGGGGTCTCTGTGTCTGTGGTCTCCAGGTGCACGATGT 60

QY 61 GCCTATGAATGACTCAGCCACCTCTCGGTGTCTGTGTCTGTGGTCTCCAGGTGCACGATGT 120

Db 61 GCCTATGAATGACTCAGCCACCTCTCGGTGTCTGTGTCTGTGGTCTCCAGGTGCACGATGT 120

QY 121 ACCTGTGGGGAGACAAACAGTAGAATAATATGTCTCACTGTGTACAGAGAGCCAGCG 180

Db 121 ACCTGTGGGGAGACAAACAGTAGAATAATATGTCTCACTGTGTACAGAGAGCCAGCG 180

QY 181 CGGGCCCTTATCTGTCTCATCTATGATGATAGTAGTACCGGCTCAGGATCTCCGTGAGCGA 240

Db 181 CGGGCCCTTATCTGTCTCATCTATGATGATAGTAGTACCGGCTCAGGATCTCCGTGAGCGA 240

QY 241 TTCTCTGGCTCAAAATCAGGAAACACCGCCACCTCTGACATCAACGGGGTCGAGGCCGG 300

Db 241 TTCTCTGGCTCAAAATCAGGAAACACCGCCACCTCTGACATCAACGGGGTCGAGGCCGG 300

QY 301 GATGAGGCTGACTATTACTGTCTGAGTGTGGGACAGGGCTAGTGATCATCGGTCCTTCGGA 360

Db 301 GATGAGGCTGACTATTACTGTCTGAGTGTGGGACAGGGCTAGTGATCATCGGTCCTTCGGA 360

treatment; gene therapy; EST; ss.
 XX Homo sapiens.
 XX DE19818619-A1.
 XX PD 28-OCT-1999.
 XX 21-APR-1998; 98DE-1018619.
 XX PR 21-APR-1998; 98DE-1018619.
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX WPI; 1999-612028/53.
 XX New nucleic acid sequences expressed in bladder tumor tissue, and
 XX derived polypeptides, for treatment of bladder tumor and identification
 XX of therapeutic agents -
 XX Claim 3; Page 90; 132pp; German.
 XX This invention describes novel polypeptide fragments (I) and the
 XX polynucleotides (II) that encode them that are highly expressed in a
 XX human bladder tumour and which have cytostatic activity. (II) are used
 XX for recombinant expression of (I) and to isolate complete genes. (I) are
 XX used to identify agents suitable for treatment of bladder cancer, to
 XX directly treat this form of cancer (including expression from gene
 XX therapy vectors) or are used in a preparation for cancer treatment. (I)
 XX is also used for the generation of specific antibodies. (II) are
 XX identified by assembling ESTs (expressed sequence tags) from a
 XX particular tissue type before comparison of expression patterns. This
 XX allows a significantly longer fragment of the gene to be revealed, and
 XX therefore reduces the number of failures associated with the fact that
 XX ESTs from different libraries may represent different parts of the same
 XX unknown gene, distorting the estimated frequency of occurrence in a
 XX particular tissue. AA243260-243309 represent expressed sequence tag (EST)
 XX fragments isolated from a human bladder tumour cDNA library which encode
 XX the proteins represented in AA243260-243309.
 XX Sequence 926 BP; 249 A; 275 C; 240 G; 162 T; 0 other;
 Query Match 82.6%; Score 582.6; DB 20; Length 926;
 Best Local Similarity 91.1%; Pred. No. 2e-136;
 Matches 631; Conservative 0; Mismatches 59; Indels 3; Gaps 1;
 QY 11 CCGCTCAGCTCCCTGGGCTCTCTGCTGCTCCAGGTGCGACGATGTCCTATGAAC 70
 DB 47 CCGTTCCTCTCTCGGCTCTCTCTCACTG---CACAGGCTCTGTGACCTCTATGTGC 103
 QY 71 TGACTCAGCCACCTCGGTGTCAGTGTCCCGAGGACAGCGCCAGGATCACCTGTGGG 130
 DB 104 TGACTCAGCCACCTCGGTGTCAGTGTGGGCGCCAGGACAGCGCCAGGATCACCTGTGGG 163
 QY 131 GAGACACAGTGAATATGTCCTGCTGCTCCAGGTGCGACGATGTCCTATGAAC 190
 DB 164 GAAACACATTTGAAGTAAAGTGTGCACTGTGTACAGGACAGGACGAGGCGGCTG 223
 QY 191 TACTGGTCACTATGATGATGATGACCGGCTCTCAGGATCCCTGAGCGATTCCTGTGGCT 250
 DB 224 TGCTGGTCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 283
 QY 251 CCAATCAGGAAACACCGCCACCTGACATCAACCGGGTTCGAGCGCGGGATGAGGCTG 310
 DB 284 CCAATCTGGAAACACCGCCACCTGACATCAGCAGGCTCGAAGCGGGGATGAGGCGG 343
 QY 311 ACTATTACTGTCAAGTGTGGGACAGGCTAGTATCATTCGGTCTCTCGAGGAGGACCC 370
 DB 344 ACTATTACTGTCAAGTGTGGGACAGGCTAGTATCATTCGGTCTCTCGAGGAGGACCA 403
 QY 371 GGGTGACCGCTCTAGTGTGACCGCAAGGCTGCGGCTCTGCTCTCTCTCTCTCTCTCTCTCT 430

Db 404 AGTGACCTCTAGGTGAGCCAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCT 463
 QY 431 CTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTGCTCTATAAGTGAATCTTACCCCG 490
 DB 464 CTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTGCTCTATAAGTGAATCTTACCCCG 523
 QY 491 GAGCCGTGACAGTGGCTGGAGGACGATAGCAGCCGCTCAAGGGGGGAGTGGAGACCA 550
 DB 524 GAGCCGTGACAGTGGCTGGAGGACGATAGCAGCCGCTCAAGGGGGGAGTGGAGACCA 583
 QY 551 CCACACCTCTCCAAACAAAGCAACAAAGTACGCGGCGCAGCAGCTACCTGAGCCTGACGC 610
 DB 584 CCACACCTCTCCAAACAAAGCAACAAAGTACGCGGCGCAGCAGCTACCTGAGCCTGACGC 643
 QY 611 CTGAGCAGTGGAGTCCACACAGAGCTACAGTCCAGGTCACGATGAGGAGGAGCACCG 670
 DB 644 CTGAGCAGTGGAGTCCACACAGAGCTACAGTCCAGGTCACGATGAGGAGGAGCACCG 703
 QY 671 TGAGGAAGACAGTGGCCCTCTACAGAAATGTTTCAT 703
 DB 704 TGGAGAAGACAGTGGCCCTCTACAGAAATGTTTCAT 736
 RESULT 6
 AAS83482
 ID AAS83482 standard; cDNA; 836 BP.
 XX AAS83482;
 XX 13-FEB-2002 (first entry)
 XX DNA encoding novel human diagnostic protein #19286.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.
 XX WO2001/75067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX P-PSDB; ABG19295.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity -
 XX Claim 1; SEQ ID No 19286; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 XX and gene mapping, and in recombinant production of (II). The
 XX polynucleotides are also used in diagnostics as expressed sequence tags
 XX for identifying expressed genes. (II) is useful in gene therapy techniques
 XX to restore normal activity of (II) or to treat disease states involving
 XX quantitating a polypeptide in tissue, as molecular weight markers and as
 XX a food supplement. (II) and its binding partners are useful in medical
 XX imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.
 The polypeptide and polynucleotide sequences have applications in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits to assess biodiversity
 and to produce other types of data and products dependent on DNA and
 amino acid sequences. AAS64197-AAS94564 represent novel human
 diagnostic coding sequences of the invention.
 Note: The sequence data for this patent did not appear in the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences.

Sequence 836 BP; 185 A; 262 C; 232 G; 157 T; 0 other;
 Query Match 78.8%; Score 555.6; DB 23; Length 836;
 Best Local Similarity 91.6%; Pred. No. 1.1e-129;
 Matches 588; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
 QY 62 CTTATGAAGTACTAGCCACCTCGGTGTCAGTGTCCCGAGGACAGCGCCAGGATCA 121
 DB 101 CTTTGTGCTGGCTCAGCCACCTCAGTGTGTCAGTGTCCCGAGGACAGCGCCAGGATTA 160
 QY 122 CTTGTGGGGGACACACAGTAGTAAGTAATGAATATGTCACCTGGTACCAGGACAGCGCCAGGCGC 181
 DB 161 CTTGTGGGGGACACACATTGGAGAGAGAGTGTCTCACTGTGTACCAACAGAGGCCAGGCC 220
 QY 182 GGGCCCTTACTGTCTATCATGATGATGATGACCGGCCCTCAGGGATCCCTGACCGAT 241
 DB 221 AGGCCCTTGTGTGTGTATCTATGATGATGACCGGCCCTCAGAAATCCCTCAGCGAT 280
 QY 242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACATCAACGGGGTCCAGGCCGGGG 301
 DB 281 TCTCTGGCTCCAACTCTGGGGACACCGCCACCTGACATCAACGGGGTCCAGGCCGGGG 340
 QY 302 ATGAGGCTGACTATTACTGTCAGGTGGGACAGGGCTAGTATCATCCGCTCTCGGAG 361
 DB 341 ATGAGGCGACTATTACTGTCAGGTGGGATGACGATATAGTCAATGTGTCTTCGGCG 400
 QY 362 GAGGACCGGGGTGACCTCTTAGGTGAGCCCAAGGCTGCCCCCTCGGTGACTCTGTTC 421
 DB 401 GAGGACCAAGCTGACCTCTCTGTGTGTCAGCCCAAGGCTGCCCCCTCGGTGACTCTGTTC 460
 QY 422 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGACACCTGGTGTCTTCATAAGTGACT 481
 DB 461 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGACACCTGGTGTCTTCATAAGTGACT 520
 QY 482 TCTACCGGGAGCCGTGACGTGGCTGGAGGAGATAGACGCCCTCGTCAAGGGGGAG 541
 DB 521 TCTACCGGGAGCCGTGACGTGGCTGGAGGAGATAGACGCCCTCGTCAAGGGGGAG 580
 QY 542 TGGAGACCAACACACCTCCCAAAACAAAGCAACAAAGTACGGGGCCAGCAGCTACCTGA 601
 DB 581 TGGAGACCAACACACCTCCCAAAACAAAGCAACAAAGTACGGGGCCAGCAGCTATCTGA 640
 QY 602 GCCTGACGCTGAGCAGTGGAGTCCCAACAGAGCTACCTCCAGGTCAGCGATGAAG 661
 DB 641 GCCTGACGCTGAGCAGTGGAGTCCCAACAGAGCTACCTCCAGGTCAGCGATGAAG 700
 QY 662 GGAGCACCCTGGAGAGACAGTGGCCCTCTACAGAAATGTTTCAAT 703
 DB 701 GGAGCACCCTGGAGAGACAGTGGCCCTCTACAGAAATGTTTCAAT 742

RESULT 7

AAV35488
 ID AAV35488 standard; DNA; 711 BP.
 XX
 AC AAV35488;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Macaque primatized 16C10 light chain DNA.
 XX
 KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;

KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation; ss.
 XX
 OS Macaca fascicularis.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..711
 FT /*tag= a
 FT /product= 16C10 light chain
 XX
 PN WO9819706-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 29-OCT-1997; 97WO-US19906.
 XX
 PR 08-NOV-1996; 96US-0746361.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Brams P, Hanna N;
 XX
 DR WPI: 1998-286601/25.
 DR P-PSDB; AAW63764.
 XX
 PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 PS Example 7; Fig 5a; 87pp; English.
 XX
 CC This sequence encodes a primatized form of the antibody 16C10 light chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 SQ Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match 76.6%; Score 540.2; DB 19; Length 711;
 Best Local Similarity 86.1%; Pred. No. 7.8e-126;
 Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;
 QY 1 ATGAGGGTCCCCGCTCAGCTCTCTGGGGCTCTGCTGTCTGGCTCCAGGTGACCATGT 60
 DB 1 ATGAGGGTCCCCGCTCAGCTCTCTGGGGCTCTGCTGTCTGGCTCCAGGTGACCATGT 60
 QY 61 GCCTATGAAGTACTAGCCACCTCGGTGTGTCAGTGTCCCGAGGACAGCGCCAGGATC 120
 DB 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTGTGGGGCCCCCAGGGCAGAGGTACCATTC 120
 QY 121 ACCTGTGGGGG-----AGACACAGTAGAATGAATATATCCACTGGTACAGCAGAAG 174
 DB 121 TCGTGCACTGGGAGCACCTCCAACTGGAGGTATGATCTCATTTGGTACCAAGCTC 180
 QY 175 CCAGCGGGGGCCCTTACTGTCATCTATGATGATAGTACCGGCCCTCAGGGATCCCT 234

quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct sequences.

SQ Sequence 841 BP; 191 A; 273 C; 224 G; 153 T; 0 other;
Query Match 74.3%; Score 524; DB 23; Length 841;
Best Local Similarity 89.7%; Pred. No. 9.3e-122;
Matches 576; Conservative 0; Mismatches 60; Indels 6; Gaps 1;

Qy	62	CTTATGAATCTGACTCAGCACA	CCCTTCGGTGTCTAGTGTCTCC	CAGGACAGACGGCCAGGATCA	121
Db	82	CCATAGAGCTGAATCAGCCAC	CCCTCTAGTGTCTCCAGGACAG	CACAGCAGCATCA	141
Qy	122	CCCTGTGGGGAGACAA	CAGTAGAAATATGCTCCACT	TGGTACCAGCAGAAAGCCAGCGC	181
Db	142	CCCTGCTCTGGAGATACAT	TGGGGGATATGCTTGTGTTAT	CAGCAGNAGCCAGGCC	201
Qy	182	GGGCCCCATATCTGGTCAAT	CTATGATGATAGTGA	CGGGCCCTCAGGGATCCCTGAGCGAT	241
Db	202	ACTCCCCGTCTGGTCAAT	CTTTCAAGATAGCAAGCGGCCCT	CAGGGATCCCTGAGCGAT	261
Qy	242	TCTCTGGCTCCAAATCAGGGAA	ACCGCCACCCCTGACCATCAA	CGGGGTCTAGGCCCGGGG	301
Db	262	TCTCTGGCTCCAACTCTCTGG	NACACAGCCACTCTGACCAT	CAGCGGACCCAGGCTATGG	321
Qy	302	ATGAGGCTGACTATTACTGT	CAGGTGTGGGACAGGGCT	TAGTGATCATCCGGTCTTGGAG	361
Db	322	ATGAGGCTGACTATTACTGT	CAGCGGTGGGACAGCAGCACTG	-----CGGTATTCGGCG	375
Qy	362	GAGGACCCGGGTGACCGTCT	TAGGTCAGCCCAAGGCTGCC	CCCTCGGTCACTCTGTTC	421
Db	376	GAGGACCAAGCTGACCGTCT	TAGGTCAGCCCAAGGCTGCC	CCCTCGGTCACTCTGTTC	435
Qy	422	CGCCCTCTCTTGAGAGCTTC	CAAGCCAAACAGGCCACACT	GGTGTGTCTCATAGTGACT	481
Db	436	CGCCCTCTCTTGAGAGCTTC	CAAGCCAAACAGGCCACACT	GGTGTGTCTCATAGTGACT	495
Qy	482	TCTACCCGGGACCGTGA	CAGTGGCTTGGAAAGCAGAT	GACGCCCCGTCAAGGCGGGAG	541
Db	496	TCTACCCGGGACCGTGA	CAGTGGCTTGGAAAGCAGAT	GACGCCCCGTCAAGGCGGGAG	555
Qy	542	TGGAGACCAACACACCTC	CAAAACAAAGCAACAAAGT	TACGCGGCCAGCAGTACTCGA	601
Db	556	TGGAGACCAACACACCTC	CAAAACAAAGCAACAAAGT	TACGCGGCCAGCAGTACTCGA	615
Qy	602	GCCTGACGCTGAGCATGT	GAAATCCCAACAGAGCTTA	CAGTTCGAGGTCAAGCATGAAG	661
Db	616	GCCTGACGCTGAGCATGT	GAAATCCCAACAGAGCTTA	CAGTTCGAGGTCAAGCATGAAG	675

Qy 662 GGAGCACCGTGGAGAGACAGCTGGGCCCTACAGATGTTTCAT 703
|||
Db 676 GGAGCACCGTGGAGAGACAGCTGGGCCCTACAGATGTTTCAT 717

RESULT 12
ABK28671
ID ABK28671 standard; cDNA; 904 bp.
XX
AC ABK28671;

XX
DT 09-APR-2002 (first entry)

DE XX KW KW KW KW KW KW KW KW KW XX OS XX PN XX PD XX PF XX PR PR PR PR PR PR PR XX PA XX PI PI PI PI XX DR DR XX PT PT PT PT XX PS XX CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC XX SQ

Human cDNA encoding secreted protein SECP38.

Human; ss; gene; SSCP; antiinflammatory; cytostatic; cardiac; immunosuppressive; antiviral; anti-HIV; antithrombotic; antitumor; muscular active general; aniconvulsant; antitropic; neuroprotective; antiallergic; myorelaxant; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; autoimmune disorder; inflammatory disorder; AIDS; acquired immunodeficiency syndrome; allergy; rheumatoid arthritis; cell proliferative disorder; cancer; developmental disorder; Duchenne muscular dystrophy; neurological disorder; epilepsy; Alzheimer's disease.

Homo sapiens.

WO200198353-A2

27-DEC-2001

20-TTY-2001.

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

23-JUN-2000; 2000US-213466P.

31-JUL-2000; 2000US-222372P;

08-SEP-2000; 2000US-231435P.
15-SEP-2000; 2000US-232889P.

/TNCRV-) TNCRVTE CENOMYCO TNC

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

Ramkumar J, Lal P, Xu Y,

Walia NK, Gandhi AR, Au-Yo

WPT: 2002-090431/12

P-PSDB; AAU82012.

Forty four human secreted pr

(e.g. atherosclerosis), auto

2
4
3
5
4
3
4
5
3
4
3
4
3
4
3
4
24
4
4
3
3

CLASS 3; PAGE 130; 193PP; EN

The invention relates to for

included are a host cell tra

antibody, use of the SECP pr

expression of the SECP nucle

polypeptides are useful in cardiovascular (e.g. atherosclerosis).

infarction), autoimmune/intel
syndrome (AIDS) allergies

(e.g. cancer), developmental

disorders. Numerous other ex-

[illegible]

TOP; 'V C27 '39 406 297145

Very Match

... 588; Conservative

4 AGGGTCCCGCTCAGCTCCTGGG

54 ATGGCCTGGACCCCTCTCCTGCT

64 TATGAACTGACTCAGCCACCCTC

114 TATGAGCTGACACAGCCACCTTC

100

PD 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US02623.
XX 25-JAN-2000; 2000US-0491404.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-451939/48.
XX P-PSDB; AAU14472.
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage -
XX Claim 1; Page 721-722; 894pp; English.
XX The invention relates to polynucleotides encoding novel human
XX proteins or their active domains. The polypeptides, polynucleotides and
XX antibodies raised against the polypeptides are used in a method of
XX treatment of a mammal and prevention of disorders caused by the aberrant
XX protein expression or activity. The polypeptides can be used as
XX molecular weight markers, food supplements, and in antibody production.
XX The polypeptides are used to identify compounds which bind to the
XX polypeptides. Polynucleotides of the invention are used as probes and
XX primers, for sequencing, for chromosome or gene mapping, in the
XX production of recombinant proteins, and in generating anti-sense DNA or
XX RNA and in gene therapy. Polypeptides of the invention can be used to
XX target drugs to a tumour, in assays to determine biological activity, to
XX raise antibodies/elicite an immune response, to determine quantitative
XX protein levels, as tissue markers, and to isolate receptors or ligands.
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,
XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
XX fungal infection or from autoimmunity, cancer, allergy, asthma,
XX graft-versus-host disease, eczema, haemophilia, thrombosis,
XX anti-inflammatory diseases, nervous system disorders, and infection.
XX The present sequence encodes a protein of the invention.
XX
SQ Sequence 1825 BP; 361 A; 509 C; 560 G; 395 T; 0 other;
Query Match 73.0%; Score 515; DB 22; Length 1825;
Best Local Similarity 87.4%; Pred. NO. 2e-119;
Matches 576; Conservative 0; Mismatches 80; Indels 3; Gaps 1;
QY 45 CCCAGGTGCGCAGTGTGCTATGAACTGACTCAGCCACCCCTCGGTGTGCTGCTCCCGAGG 104
DB 73 CACAGGGCCGTGGCTCTCTATGAGCTGATCTAGCCACCCCTCAGTGTGCTGCTCCCGAGG 132
QY 105 ACAGAGCCGCGAGGATCACTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTA 164
DB 133 ACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGATAAAATGCTTGTGCTGA 192
QY 165 CCAGCAGAGCCAGCGGGGCCCTATCTGCTCATCTATGATAGTAGTCCGGCCCTC 224
DB 193 TCAGCTGAAGCCAGCCAGTCCCTTTTGTGGTCAATCCATCAAGATACCAAGCGGCCCTC 252
QY 225 AGGGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAA 284
DB 253 AGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAG 312
QY 285 CCGGGTCCAGGCCCGGGATGAGGCTGACTTACTCTCAGGTGTGGGACAGGGCTAGTGA 344
DB 313 CCGGACCCAGGGCTATGGATGAGGCTGACTTATCTGTGAGCGGTGGGACAG---CAGCTC 369
QY 345 TCATCCGGTCTTCGGAGGAGGAGCCCGGGTGACCGCTCCTAGGTCAGCCCAAGGCTGCCCC 404
DB 370 TTATGTGGCGTTTCGGCGGAGGGAGCAAGCTGACCGTCTTAGGTTCAGCCCAAGGCTGCCCC 429

QY 405 CTCGGTCACTCTGTTCCTCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGT 464
DB 430 CTCGGTCACTCTGTTCCTCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGT 489
QY 465 GTGTCTCATTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAGGCGAGATAGCAG 524
DB 490 GTGTCTCATTAAGTGACTTCTACCCGGGAGTCTGTGACAGTGGCTGGAGGCGAGATAGCAG 549
QY 525 CCCGCTCAAGGCGGGAGTGGAGACCACACCCCTCCAAACAAAGCAACAAGTACGC 584
DB 550 CCCGCTCAAGGCGGGAGTGGAGACCACACCCCTCCAAACAAAGCAACAAGTACGC 609
QY 585 GGCACAGCAGCTACCTGAGCCTGAGCCTGAGCAGTGGAGTCCACAGAGCTACAGCTG 644
DB 610 GGTGAGCAGCTATCTGAGCCTGAGCCTGAGCAGTGGAGTCCACAGAGCTACAGCTG 669
QY 645 CCAGTCAACGATGAGGAGGAGCCGCTGGAGAGACAGTGGGCCCTTACAGAAATGTTTAT 703
DB 670 CCAGTCAACGATGAGGAGGAGCCGCTGGAGAGACAGTGGGCCCTTACAGAAATGTTTAT 728

Search completed: April 5, 2003, 20:19:14
Job time : 196.478 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:05 ; Search time 2212.18 seconds
(without alignments)
9274.790 Million cell updates/sec

Title: US-09-758-173-1

Perfect score: 705

Sequence: 1 ATGAGGGTCCCGCTACGCT.....CCCTACAGATGTTTCATGA 705

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sta:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pi:
26: em_ro:
27: em_sta:
28: em_un:
29: em_vi:
30: em_htg_hum:
31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pin:
35: em_htg_rtd:
36: em_htg_mam:
37: em_htg_vrt:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	100.0	705	705	6	AR108862 Sequence
2	83.0	585.2	702	6	AR135374 Sequence
3	81.5	574.4	820	9	AB064177 Homo sapi
4	81.0	571.2	901	9	BC028090 Homo sapi
5	80.8	569.8	803	9	HSIGVL022
6	79.7	561.8	747	9	HSIGVL031
7	77.0	542.8	648	9	HSAG09319
8	76.6	540.2	711	6	AR108866 Sequence
9	76.3	538	790	9	AB064230 Homo sapi
10	75.8	534.4	826	9	AB064174 Homo sapi
11	75.1	529.6	824	9	AB064176 Homo sapi
12	74.7	526.4	813	9	AB064167 Homo sapi
13	74.5	525.2	895	9	BC022823 Homo sapi
14	74.3	524	725	9	HSIGVL002
15	74.1	522.4	890	9	BC032452 Homo sapi
16	74.0	522	788	9	AB064168 Homo sapi
17	73.9	520.8	904	6	AX402510 Sequence
18	73.3	517	1154	9	BC007782 Homo sapi
19	73.3	516.8	821	9	AB064179 Homo sapi
20	73.2	516	791	9	HSIGVL028
21	73.0	514.4	839	9	HSIGVL026
22	72.6	512	798	9	AB064184 Homo sapi
23	72.6	512	872	6	E01593
24	72.6	512	872	9	HUMIGLAM2
25	72.5	511	654	6	AX232564 Sequence
26	72.4	510.4	789	9	AB064210 Homo sapi
27	72.4	510.4	795	9	AB064209 Homo sapi
28	72.2	508.8	737	9	HSIGVL023
29	72.2	508.8	795	9	AB064213 Homo sapi
30	71.9	507.2	794	9	AB064185 Homo sapi
31	71.9	507.2	794	9	AB064214 Homo sapi
32	71.9	507.2	807	9	AB064165 Homo sapi
33	71.8	506	780	9	HSIGVL011
34	71.5	504	806	9	HSIGVL005
35	71.1	501.2	811	9	AB064173 Homo sapi
36	70.8	499	788	9	AB064211 Homo sapi
37	70.6	497.6	796	9	AB064182 Homo sapi
38	70.4	496	790	9	AB064233 Homo sapi
39	70.3	495.8	801	9	AB064183 Homo sapi
40	70.2	495.2	863	6	AX402489 Sequence
41	69.7	491.2	791	9	AB064181 Homo sapi
42	69.5	490	886	6	AX400073 Sequence
43	69.2	488	793	9	AB064180 Homo sapi
44	69.0	486.4	788	9	AB064212 Homo sapi
45	68.3	481.6	790	9	AB064169 Homo sapi

ALIGNMENTS

RESULT 1
AR108862
LOCUS AR108862
DEFINITION Sequence 1 from patent US 6113898.
ACCESSION AR108862
VERSION AR108862.1 GI:12825138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 705)
AUTHORS Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
Patent: US 6113898-A 1 05-SEP-2000;
JOURNAL

Pred. No. is the number of results predicted by chance to have a

Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Unpublished
2 (bases 1 to 820)
Kurosawa, Y.
Direct Submission
Submitted (25-JUN-2001) Yoshihazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawafujita-hu.ac.jp, tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.

COMMENT

FEATURES
source

1. .820
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="L37"
/clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
1. .820
/gene="IGL"
1. .>820
/gene="IGL"
/codon_start=1
/product="immunoglobulin lambda light chain VLJ region"
/protein_id="BAC01805.1"
/db_xref="GI:21669561"
/translation="MKYLLPTAAAGLLLLAAQPMASVYLTQPPSVAPGKTARITC
GGNITGSKSVHWYQKQFQAPVLYVDSRPSGIPERFSGNSGNATLTISRVEAG
DEADYCYQWMDSSDHVFGGKTLVLGPKAAPSVTLPFSSSELOANKATLVCLLI
SDYPCATVAVKADSPVKAGVETTPSKSNKVAASSYLSLTPPEOMKSHRSYSCQ
VTHEGSTVEKTVATECSARQSTPFVCEYQGGSDLPQPPVAGGGSGGGGGS"
sig_peptide
1. .66
/gene="IGL"
/note="peb signal peptide"
BASE COUNT 183 a 240 c 238 g 159 t
ORIGIN

Query Match 81.5%; Score 574.4; DB 9; Length 820;
Best Local Similarity 93.6%; Pred. No. 2.9e-130;
Matches 599; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 62 CCTATGACTGACTGACGACCTCGGTGTCAGTGTCCCGAGGACAGCGCCGAGGATCA 121
DB 68 CCTATGCTGACTGACGACCTCGGTGTCAGTGTCCCGAGGACAGCGCCGAGGATTA 127
QY 122 CCTGTGGGGAGACACAGTGTAGTAATGATGTCCACTGTGTACGACAGGACAGCGCGC 181
DB 128 CCTGTGGGGAGACACATGTGAAGTAAAGTGTGCACTGTGTACGACAGGACAGCGCGC 187
QY 182 GGCGCCCTATCTGCTGATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 241
DB 188 AGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
QY 242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACCGGGTTCGAGCGCGGG 301
DB 248 TCTCTGGCTCCAACTCTGGGAACACCGCCACCTGACCATCAGCAGGTCGAGCGCGGG 307
QY 302 ATGAGGCTGACTTACTCTGAGGTGTGGACAGGGCTAGTGTATCTCCGGTCTTCGAG 361
DB 308 ATGAGGCGGACTTACTCTGAGGTGTGGGATAGTGTAGTGTATCTGAGTGTATTCGCG 367
QY 362 GAGGACCGCGGTGACCGCTCTAGGTTCAGCCCAAGGCTGCGCCCTCGGTCACTCTGTTC 421
DB 368 GAGGACCAAGCTGACCGTCTAGGTTCAGCCCAAGGCTGCGCCCTCGGTCACTCTGTTC 427
QY 422 GCGCCTCTCTGAGGAGCTTCAAGCAACAGGCGCACACTGGTGTGTCTCATTAAGTGACT 481
DB 428 CGCCCTCTCTGAGGAGCTTCAAGCAACAGGCGCACACTGGTGTGTCTCATTAAGTGACT 487

QY 482 TCTACCGGGAGCGCTGACAGTGGCTGGAGGAGCAGATAGCAGCCCGTCAAGCGGGAG 541
DB 488 TCTACCGGGAGCGCTGACAGTGGCTGGAGGAGCAGATAGCAGCCCGTCAAGCGGGAG 547
QY 542 TGGAGACCAACACACCTCCCAAAACAAAGCAACAAAGTACGGCGCCAGCAGTCTCTGA 601
DB 548 TGGAGACCAACACACCTCCCAAAACAAAGCAACAAAGTACGGCGCCAGCAGTCTCTGA 607
QY 602 GCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTCCAGGTCACGATGAG 661
DB 608 GCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTCCAGGTCACGATGAG 667
QY 662 GGAGCACCTGAGAGAGACAGTGGCGCCCTACAGATGTC 701
DB 668 GGAGCACCTGAGAGAGACAGTGGCGCCCTACAGATGTC 707

RESULT 4

BC028090
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BC028090
Homo sapiens, clone MGC:40381 IMAGE:4184029, mRNA, complete cds.
BC028090.1 GI:20380867
MGC.
Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Strausberg, R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karling, E., Laric, P., Legaapi, R., Maduro, Q.L.,
Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,
Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C.,
Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, D., Young, A.,
Zhang, L.-H. and Green, E.D.

REFERENCE

AUTHORS
TITLE
JOURNAL

REMARK

COMMENT

FEATURES
source

1. .901
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clones="MGC:40381 IMAGE:4184029"
/tissue="type=Brain, glioblastoma with EGFR amplification"
/clone_lib="NCI CGAP_Brn64"
/lab_hosts="DHL08"
/note="vector: pCMV-SPORT6"
40. .744
/codon_start=1

CDS

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 62 Row: k Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
Location/Qualifiers


```

QY 242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGCCGGGG 301
Db 248 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGCCGGGG 307
QY 302 ATGAGGCTGACTATTACTAGTGTGAGGTGGGACAGGCTAGTATCATCCGGTCTTCGGAG 361
Db 308 ATGAGGCTGACTATTACTAGTGTGAGGTGGGACAGGCTAGTATCATCCGGTCTTCGGAG 367
QY 362 GAGGACCCGGGTGACCGTCTTAGTGTGAGCCCAAGGCTGCCCCCTGGTCACTCTGTTC 421
Db 368 GAGGACCCAAAGCTGACCGTCTTAGTGTGAGCCCAAGGCTGCCCCCTGGTCACTCTGTTC 427
QY 422 CGCCCTCTCTGAGAGCTTCAAGCCCAAGGCTGAGGCTGAGTGTGTCTCATAGTACT 481
Db 428 CGCCCTCTCTGAGAGCTTCAAGCCCAAGGCTGAGGCTGAGTGTGTCTCATAGTACT 487
QY 482 TCTACCCGGGAGCGGTGACAGTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 541
Db 488 TCTACCCGGGAGCGGTGACAGTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 547
QY 542 TGGAGACCAACACCTCTCAAGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 601
Db 548 TGGAGACCAACACCTCTCAAGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 607
QY 602 GCCTGAGCGCTGAGAGTGGAGTCCACAGAGCTTACAGCTCCAGGTCACGCATGAAG 661
Db 608 GCCTGAGCGCTGAGAGTGGAGTCCACAGAGCTTACAGCTCCAGGTCACGCATGAAG 667
QY 662 GGAGCACCCTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703
Db 668 GGAGCACCCTGGAGAGACAGTGGCCCTACAGATGTTTCAT 709

RESULT 6
HSIGVL031
LOCUS Human rearranged immunoglobulin lambda light chain mRNA. PRI 04-NOV-1994
DEFINITION X57821
ACCESSION X57821
VERSION 1
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 747)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Klobeck, H.G.
Direct Submission
Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
2 (bases 340 to 386)
AUTHORS Combiato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
PUBMED 1904362
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.
FEATURES
Location/Qualifiers
1..747
/organism="Homo sapiens"
/isolate="individual ML"
/db_xref="taxon:9606"
/chromosome="22"
/clone="cML70"
/cell_type="B-cell"
/tissue_type="spleen"
/clone_lib="phase library cML"
1..747
/gene="immunoglobulin lambda light chain"
1..747
/gene="immunoglobulin lambda light chain"

```

```

CDS
/note="cDNA"
/evidence=experimental
6..704
/genes="immunoglobulin lambda light chain"
/codon_start=1
/protein_id="CAA40958.1"
/db_xref="GI:33742"
/translation="MAWTVLLGLLSHCTGVSVSYLTQPPSVSVAPKGTASITCGGN
NGSKSVHWYQKPGQAPLVVYDDSDRSPGIPERFSGNSGNTATLTISRVEAGDEA
DYQCQWDSDDVFGGKTLVLPKPAAPSVTLFPSPSELOAKATLVCLISDFY
PAWTVAMKADSPKAGVETTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHE
GSTVEKTVAPTECS"
6..62
sig_peptide
/genes="immunoglobulin lambda light chain"
63..384
misc_feature
/genes="immunoglobulin lambda light chain"
/notes="variable region; V(lambda)III"
347..384
misc_feature
/genes="immunoglobulin lambda light chain"
/notes="J-segment"
385..704
misc_feature
/genes="immunoglobulin lambda light chain"
/notes="constant region"
BASE COUNT 171 a 230 c 211 g 135 t
ORIGIN
Query Match 79.7%; Score 561.8; DB 9; Length 747;
Best Local Similarity 93.1%; Pred. No. 3.6e-127;
Matches 598; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
QY 62 CCTATGAACCTGACTCAGCCACCTCGGTGTCTAGTGTCTCCAGGACAGCGCCAGGATCA 121
Db 64 CCTATGTGTGCTGACTCAGCCACCTCGGTGTCTAGTGTCTCCAGGAAAGACGGCCATATTA 123
QY 122 CTTGTGGGGAGACAAACAGTAGAATATGTCTTCCACTGGTACCAGCAGAGCCAGCGC 181
Db 124 CTTGTGGGGAAATAACATTGGAAGTAAAGTGTGCATCTGGTACCAGCAGAGCCAGCGC 183
QY 182 GGGCCCTTACTTGTGTCTATGATGATGAGCGGCGCTCAGGGATCCCTGAGCGAT 241
Db 184 AGGCCCTTGTGTGTGTCTATGATGATGAGCGGCGCTCAGGGATCCCTGAGCGAT 243
QY 242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGG 301
Db 244 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGG 303
QY 302 ATGAGGCTGACTATTACTAGTGTGAGGTGGGACAGGCTAGTATCATCCGGTCTTCGGAG 361
Db 304 ATGAGGCTGACTATTACTAGTGTGAGGTGGGACAGGCTAGTATCATCCGGTCTTCGGAG 360
QY 362 GAGGACCCGGGTGACCGTCTTAGTGTGAGCCCAAGGCTGCCCCCTGGTCACTCTGTTC 421
Db 361 GAGGACCCAAAGCTGACCGTCTTAGTGTGAGCCCAAGGCTGCCCCCTGGTCACTCTGTTC 420
QY 422 CGCCCTCTCTGAGAGCTTCAAGCCCAAGGCTGAGGCTGAGTGTGTCTCATAGTACT 481
Db 421 CGCCCTCTCTGAGAGCTTCAAGCCCAAGGCTGAGGCTGAGTGTGTCTCATAGTACT 480
QY 482 TCTACCCGGGAGCGGTGACAGTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 541
Db 481 TCTACCCGGGAGCGGTGACAGTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 540
QY 542 TGGAGACCAACACCTCTCAAGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 601
Db 541 TGGAGACCAACACCTCTCAAGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 600
QY 602 GCCTGAGCGCTGAGAGTGGAGTCCACAGAGCTTACAGCTCCAGGTCACGCATGAAG 661
Db 601 GCCTGAGCGCTGAGAGTGGAGTCCACAGAGCTTACAGCTCCAGGTCACGCATGAAG 660
QY 662 GGAGCACCCTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703
Db 661 GGAGCACCCTGGAGAGACAGTGGCCCTACAGATGTTTCAT 702

```

RESULT 7
 HSA309319
 LOCUS HSA309319 648 bp mRNA linear PRI 16-NOV-2001
 DEFINITION Homo sapiens partial mRNA for anti-peptide/MHC complex
 ACCESSION AJ309319
 VERSION constant region; immunoglobulin light chain; monoclonal antibody;
 KEYWORDS variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Chames, P., Rojas, G., Dieckmann, D., Rem, L., Schuler, G. and
 Hoogenboom, H.R.
 TITLE TCR-like Human anti MHC-peptide antibodies: peptide
 fine-specificity is possible over a wide range of affinity
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 648)
 REFERENCE Chames, P.
 TITLE Direct Submission
 JOURNAL Submitted (14-MAY-2001) Chames P., Pathology, Azm, P. Debyealan 25,
 6202AZ Maastricht, NETHERLANDS
 FEATURES
 source
 1..648
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /rearranged
 <1..648
 /function="immune response"
 /codon_start=1
 /product="anti-peptide/MHC complex HLA-A1/WAGE-A1
 monoclonal antibody light chain"
 /protein_id="CAC85285.1"
 /db_xref="GI:16974104"
 /translations="AQSVLTPPSSVAPKTRITCGDNIYGRKSVHWYQORPQOAP
 LLLVDDGDRPSGIPDFSGNSAATLTISMVADPADYFCOVWMDSTTDWVFGG
 GTKLTVLGOPKAAPSVTLPPSSSEELQANKATLVCLISDFYPGAVTVAKKDSSPVKA
 GVETTRPSKSNKNKYAASSVLSLTPEQWKSYSQVTHEGSTVEKTVAPTECS"
 <1..327
 /product="immunoglobulin light chain variable region"
 328..648
 /product="immunoglobulin light chain constant region"
 BASE COUNT 152 a 199 c 182 g 115 t
 CDS
 V_region
 C_region
 BASE COUNT 152 a 199 c 182 g 115 t
 Query Match 77.0%; Score 542.8; DB 9; Length 648;
 Best Local Similarity 90.3%; Pred. No. 1.6e-122;
 Matches 580; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
 QY 64 TATGAACACTGACTCAGCCACCTCGGTGTCACTGTCCTCCAGGACAGAGCGCCAGGATCACC 123
 DB 7 TCTGTGCTGACTCAGCCACCTCGGTGTCACTGTCCTCCAGGACAGAGCGCCAGGATACC 66
 QY 124 TGTGGGGAGACACAGTAGAATAATATGTCACCTGGTACAGAGAGAGAGAGAGAGAGAGAG 183
 DB 67 TGTGGGGAGACACAGTAGAATAATGTCACCTGGTACAGAGAGAGAGAGAGAGAGAGAG 126
 QY 184 GCCCTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
 DB 127 GCCCTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 186
 QY 244 TGTGCTCAAAATCAGGAAACACCGACCCCTGACATCAACCGGGGTCGAGGCGGGGAT 303
 DB 187 TGTGCTCAAAATCAGGAGGCGGACCCCTGACATCAATGATGATGATGATGATGATGATG 246
 QY 304 GAGGCTGACTATTACTGTGAGGTGGGACAGGCTAGTGTATGATCATCGGTCTTCGGAGGA 363
 DB 247 GAGGCGGACTATTCTGTGAGGTGGGACAGGCTAGTGTATGATCATCGGTCTTCGGAGGA 306

QY 364 GGGACCCGGGTGACCGTCTTAGGTCAAGCCCAAGGCTGCCCCCTCGGTCACTCTGTGTCCCG 423
 DB 307 GGGACCAAGCTGACCGTCTCGGTCAAGCCCAAGGCTGCCCCCTCGGTCACTCTGTGTCCCA 366
 QY 424 CCTCTCTGAGGAGCTTCAAGCCCAAGGCTGCCCCCTCGGTCACTCTGTGTCTCATAGTACTTC 483
 DB 367 CCTCTCTGAGGAGCTTCAAGCCCAAGGCTGCCCCCTCGGTCACTCTGTGTCTCATAGTACTTC 426
 QY 484 TACCCGGGAGCCGTGACAGTGGCTGGAAGGAGAGATAGCAGGCCCCCTCAAGCGGGAGTG 543
 DB 427 TACCCGGGAGCCGTGACAGTGGCTGGAAGGAGAGATAGCAGGCCCCCTCAAGCGGGAGTG 486
 QY 544 GAGACACACACACCTTCAAGCCCAAGGCTGCCCCCTCGGTCAAGCGGGAGTACTTACCTGAGC 603
 DB 487 GAGACACACACACCTTCAAGCCCAAGGCTGCCCCCTCGGTCAAGCGGGAGTACTTACCTGAGC 546
 QY 604 CTGACGCTGAGCAGTGGAGTCCACAGAGTCCACAGAGTCCACAGTCCAGGTCACGCATGAAGG 663
 DB 547 CTGACGCTGAGCAGTGGAGTCCACAGAGTCCACAGAGTCCAGGTCACGCATGAAGG 606
 QY 664 AGCACCTGAGAGAGACAGTGGCCCCCTACAGATGTTTCATGA 705
 DB 607 AGCACCTGAGAGAGACAGTGGCCCCCTACAGATGTTTCATGA 648
 RESULT 8
 AR108866
 LOCUS AR108866 711 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 9 from patent US 6113899.
 ACCESSION AR108866
 VERSION AR108866.1 GI:12825142
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 711)
 AUTHORS Anderson, D.R., Brame, P., Hanna, N., Shestowsky, W.S. and Heard, C.
 TITLE Human B7.1-specific primatized antibodies and transfectomas
 expressing said antibodies
 JOURNAL Patent: US 6113899-A 9 05-SEP-2000;
 FEATURES Location/Qualifiers
 source
 1..711
 /organism="unknown"
 BASE COUNT 160 a 226 c 193 g 132 t
 ORIGIN
 Query Match 76.6%; Score 540.2; DB 6; Length 711;
 Best Local Similarity 86.1%; Pred. No. 7e-122;
 Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;
 QY 1 ATGAGGTCCCGCTCAGCTCCCTGGGGCTCTGCTGCTCTGCTGCTCCAGGTGACAGATGT 60
 DB 1 ATGAGGTCCCGCTCAGCTCCCTGGGGCTCTGCTGCTCTGCTGCTCCAGGTGACAGATGT 60
 QY 61 GCCTATCAACTGACTCAGCCACCTCGGTGTCACTGTCCTCCAGGACAGAGCGCCAGGATC 120
 DB 61 GAGTCTCTCTGACAGAGCGCCCTCAGTGTCTGGGGCCCCAGGCGAGAGGTCCACATC 120
 QY 121 ACCTGTGGGGG-----AGACAAACAGTAGAATAATGTCCACTGGTACCAGCAGAAG 174
 DB 121 TCGTGCACTGGGAGCACCTCCAAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
 QY 175 CCAGCGGGGCCCTTACTGTTTCATCTATGATGATGATGATGATGATGATGATGATGATGATG 234
 DB 181 CCAGGAACGGCCCCCAAACTCTCTATCTATGATGATGATGATGATGATGATGATGATGATG 240
 QY 235 GAGCGATTCTCTGGTCCAAATCAGGGAACACCGCCACCTGACCATCAACCGGGTCCAG 294
 DB 241 GACCGATTCTCTGGTCCAAATCAGGGAACACCGCCACCTGACCATCAACCGGGTCCAG 300
 QY 295 GCCGGGATCAGGCTGACTATTACTGTGAGGTGGGACAGGCTAGTGTATGATCATCGGTCT 354
 DB 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCCTGATGCTCAGGTA 360

```
QY 355 TTCGAGGAGGACCCGGGTGACCTCTAGTCTAGTCCAGCCAAAGGCTGCCCTCGGTCACT 414
Db 361 TTCGAGGAGGAGCCCGGTGACCTCTAGTCTAGTCCAGCCAAAGGCTGCCCTCGGTCACT 420
QY 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCACACAGGCCACACTGGTGTCTCATTA 474
Db 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCACACAGGCCACACTGGTGTCTCATTA 480
QY 475 AGTACTTTTACCCGGAGCCGTGACGTGGCTGGAAGGAGAGTAGCAGCCCGTCAAG 534
Db 481 AGTACTTTTACCCGGAGCCGTGACGTGGCTGGAAGGAGAGTAGCAGCCCGTCAAG 540
QY 535 GCGGAGTGGAGACACACACACCTTCCAAACAAAGCAACAAGTACGCGGCCAGCAGC 594
Db 541 GCGGAGTGGAGACACACACACCTTCCAAACAAAGCAACAAGTACGCGGCCAGCAGC 600
QY 595 TACCTGAGCTGACGCCCTGAGCAGTGGAGTCCCAACAGCAAGCTACAGTCCAGGTACG 654
Db 601 TACCTGAGCTGACGCCCTGAGCAGTGGAGTCCCAACAGCAAGCTACAGTCCAGGTACG 660
QY 655 CATGAAGGAGCACCCTGAGAGACAGTGGCCCTACAGAAATGTTATGA 705
Db 661 CATGAAGGAGCACCCTGAGAGACAGTGGCCCTACAGAAATGTTATGA 711

RESULT 9
AB064230 790 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGL mRNA for immunoglobulin lambda light chain VJLJ
DEFINITION region, partial cds, clone:L90.
ACCESSION AB064230
VERSION AB064230.1 GI:21669666
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Miura,K. and Kurosawa,Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 790)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyooka 470-1192, Japan
(S-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES
source
location/Qualifiers
1..790
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="L90"
/clone_lib="AIMS4"
/notes="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
1..790
/gene="IGL"
1..>790
/gene="IGL"
/codon_start=1
/product="immunoglobulin lambda light chain VJLJ region"
/protein_id="BAC01858.1"
/db xref="GI:21669667"
/tranlations="MKVLLPTAAAGLLLAQPMANFMLTQPLSVSVALGQATARITC
GGNIGSKNVHWYQQKPGQAPVLVYRDSNRFSGSGIPERFSGNSGNTATLTISRAQAG
```

```
DEADYYCQWDSSTVVFVGGTGLTVLGPKAAPSVTLPFPSSSEELQANKATLVCLISD
FYPGAVTVAMKADSPVAVKAGVETTTTPSKQNNKYAASVSLJLTPQWKSHRSYSQVVT
HSGSTVEKTVAPTECSARQSPFPVCEYQGSDDLQPPPVNAGGS"
sig_peptide 1..66
BASE COUNT 183 a 238 c 223 g 146 t
ORIGIN
Query Match 76.3%; Score 538; DB 9; Length 790;
Best Local Similarity 91.9%; Pred. No. 2.4e-121;
Matches 581; Conservative 0; Mismatches 45; Indels 6; Gaps 1;
QY 70 CTGACTCAGCCACCCCTCGGTGTGTCAGTGTCTCCAGGACAGACGCGCCAGGATCACCTCTGGG 129
Db 76 CTGACTCAGCCACTCTCAGTGTGTCAGTGGCCCTGGGACAGACGCGCCAGGATTAACCTGTGG 135
QY 130 GGAGACAACAGTAGAAATGAATATGTCTTCCACTGGTACCAGACAAGCCAGCGGGCCCT 189
Db 136 GGAAACAACATTTGGAAGTAAATAATGTCACTGGTACCAGACAAGCCAGCGGCCCT 195
QY 190 ATACTCGTCTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTCCTTGGC 249
Db 196 GTCTGTCTCATCTATAGGATAGCAACCGGCCCTCTGGGATCCCTGAGCGATTCCTTGGC 255
QY 250 TCCAAATCAGGGAAACACCGCCACCCCTGACCATCAACCGGGTTCAGGCCGGGATGAGGCT 309
Db 256 TCCAACTCGGGGAACACGCGCCACCCCTGACCATCAGCAGAGCCCAAGCCGGGATGAGGCT 315
QY 310 GACTATTACTGTCAAGTGTGGACAGGGCTAGTGATCATPCCGTCTTCGGAGGAGGAC 369
Db 316 GACTATTACTGTCAAGTGTGGACAGGGCTAGTGATCATPCCGTCTTCGGAGGAGGAC 369
QY 370 CGGTCACCGTCTTAGTTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGGCCCTCC 429
Db 370 AGCTCACCCTCTTAGTTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGGCCCTCC 429
QY 430 TCTGAGGAGCTTCAAGCCAAACAAAGGCCACACACCTGGTGTCTCATAGTGACTTCTACCCG 489
Db 430 TCTGAGGAGCTTCAAGCCAAACAAAGGCCACACACCTGGTGTCTCATAGTGACTTCTACCCG 489
QY 490 GGAGCCGTGACAGTGGCTTGGAAAGGAGAGATAGACCCCGTCAAGCGGGAGTGGAGACC 549
Db 490 GGAGCCGTGACAGTGGCTTGGAAAGGAGAGATAGACCCCGTCAAGCGGGAGTGGAGACC 549
QY 550 ACCACACCCCTCCAAACAAAGCAACAGTACGCGGCCAGCAGCTACCTGAGCCCTGAGC 609
Db 550 ACCACACCCCTCCAAACAAAGCAACAGTACGCGGCCAGCAGCTACCTGAGCCCTGAGC 609
QY 610 CCTGAGCAGTGGAAAGTCCCAAGAGCTACAGTCCAGGTCACGCATCAAGGGAGCACC 669
Db 610 CCTGAGCAGTGGAAAGTCCCAAGAGCTACAGTCCAGGTCACGCATCAAGGGAGCACC 669
QY 670 GTGGAGAGACAGTGGCCCTTACAGAAATGTTTC 701
Db 670 GTGGAGAGACAGTGGCCCTTACAGAAATGTTTC 701

RESULT 10
AB064174 826 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
DEFINITION region, partial cds, clone:L34.
ACCESSION AB064174
VERSION AB064174.1 GI:21669554
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
```


Query Match		75.1%; Score 529.6; DB 9; Length 824;
Best Local Similarity		89.2%; Pred. No. 2.7e-119;
Matches 571; Conservative		0; Mismatches 69; Indels 0; Gaps 0;
Qy	62	CCTATGAAGTACTGACGACACCTCGGTGTCAGTGTCCCGAGGACAGACGCGCAGGATCA 121
Db	68	CCTATGTGCTGACTCAGCACCTCGGTGTCGTCGCGTAAAGTTTACATGCTATCAGTGAAAGCAGGCC 127
Qy	122	CCTGTGGGGAGACAACTAGTAAATATGTCCATGCTGTACCGAGAGAGCCAGCGC 181
Db	128	CTTGTGGGGAGACAACTGTGCGGTAAAGTTTACATGCTATCAGTGAAAGCAGGCC 187
Qy	182	GGGCCCCCTACTGCTATCTATGATGATGATGACCGCCCTCAGGGATCCCTGAGCGAT 241
Db	188	AGGCCCCCTGCTCGGTGCTCTTTGATGACCGGACCGCCCTCAGGCATCCCTGACCGAT 247
Qy	242	TCTCGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGTGAGCGCGGG 301
Db	248	TCTCTGGAGCCAACTCTAGGACACCGCGCCCTCTGATCATCAGCAGGCTCAGGCCGGG 307
Qy	302	ATGAGGCTGACTATTAATCTCAGGTGTGGGACAGGCTAGTGATCATCCGCTCTTCGGAG 361
Db	308	ATGAGGCGGACTATTAATCTCAGGTGTGGGATGATATTTCTCGTCTGTGATTTTCGGCG 367
Qy	362	GAGGACCCGGGTGACCGTCTCTAGTCAAGCCAAAGGTGCCCCCTCGGTCACTCTGTTC 421
Db	368	GAGGACCCAGGTTGACCGTCTCTAGTCAAGCCAAAGGTGCCCCCTCGGTCACTCTGTTC 427
Qy	422	CGCCCTCTCTGAGGAGCTTCAAGCCAAAGGTGCCCCCTCGGTCACTCTGTTC 481
Db	428	CGCCCTCTCTGAGGAGCTTCAAGCCAAAGGTGCCCCCTCGGTCACTCTGTTC 487
Qy	482	TCTACCCGGGACCGTGTGACGTGCGCTGGAAGGAGATAGCAGCCCCCTCAAGCGGAG 541
Db	488	TCTACCCGGGACCGTGTGACGTGCGCTGGAAGGAGATAGCAGCCCCCTCAAGCGGAG 547
Qy	542	TGGAGACCAACACCTCCAAACAAAGCAACACAGTACCGCGCCAGCAGCTACCTGA 601
Db	548	TGGAGACCAACACCTCCAAACAAAGCAACACAGTACCGCGCCAGCAGCTACCTGA 607
Qy	602	GCCTGAGCCCTGAGCAGTGGGAAGTCCCAAGAGCTACAGTGCAGGTCCAGCATGAAG 661
Db	608	GCCTGAGCCCTGAGCAGTGGGAAGTCCCAAGAGCTACAGTGCAGGTCCAGCATGAAG 667
Qy	662	GGAGACCGTGGAGAGACAGTGGCCCTCAGAAATGTTT 701
Db	668	GGAGACCGTGGAGAGACAGTGGCCCTCAGAAATGTTT 707
RESULT 12		
AB064167		
LOCUS		
DEFINITION		Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
ACCESSION		AB064167
VERSION		AB064167.1 GI:21669540
KEYWORDS		
SOURCE		Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L27.
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		1 Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Miura,K. and Kurosawa,Y.
TITLE		Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL		Unpublished
REFERENCE		2 (bases 1 to 813)
AUTHORS		Kurosawa,Y.
TITLE		Direct Submission
JOURNAL		Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for

Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyosake 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.		
Location/Qualifiers		
1..813		
/organism="Homo sapiens"		
/db_xref="taxon:9606"		
/clone="L27"		
/clone_lib="AIMS4"		
/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"		
1..813		
/gene="IGL"		
1..>813		
/gene="IGL"		
/codon_start=1		
/product="immunoglobulin lambda light chain VLJ region"		
/protein_id="BAC01795.1"		
/db_xref="GI:21669541"		
/translation="MKYLLPAAAGLLLLAQPAMASVLTQPPSVSVSPGOTARITC SADALPKQYAYWQKPKQAPLVLYKDSERPSPGIPERPSGSSGTIVLLTISGVQAE DEADYQCSADSSGTIVVFGGKTLLVLGQPKAAPSVTLFPPSSEELQAKATLVCLI SDFPFGAVTVAWKADSSPKAGVETTPSKNNKYAASSVLSLTPEOMKSHRSVSCQ VTHEGSTVEKTVAPTECSARQSTPFVCEYQSSDLPQPPVYVAGGGSGGGG"		
1..66		
/sig_peptide		
/gene="IGL"		
/note="pelB signal peptide"		
BASE COUNT 187 a 242 c 227 g 157 t		
ORIGIN		
Query Match 74.7%; Score 526.4; DB 9; Length 813; Best Local Similarity 88.9%; Pred. No. 1.7e-118; Matches 569; Conservative 0; Mismatches 71; Indels 0; Gaps 0;		
Qy	62	CCTATGAACCTGACTCAGCACCTCGGTGTCAGTGTCCCGAGGACAGCGCCAGGATCA 121
Db	68	CCTATGTGCTGACTCAGCACCTCGGTGTCAGTGTCCCGAGGACAGCGCCAGGATCA 127
Qy	122	CCTGTGGGGAGACACAGTAGAATATGATATGTCCACTGTTACCAAGAGAGCCAGCGC 181
Db	128	CCTGTCTCTGAGATGCATTGCCAAAGCAATATGCTTTATTGGTACCAAGAGAGCCAGGCC 187
Qy	182	GGGCCCTTACTTGGTCACTATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGAT 241
Db	188	AGGCCCTTGTCTGGTGATATATAAGACAGTAGAGGCCCTCAGGGATCCCTGAGCGAT 247
Qy	242	TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGTGAGCGCGGG 301
Db	248	TCTCTGGCTCCAGCTCAGGGACAAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAG 307
Qy	302	ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGCTAGTGATCATCCGCTCTTCGGAG 361
Db	308	ACGAGGCTGACTATTACTGTCAATCAGACAGCAGTGGTACTTATGTGTGTTATTGGCG 367
Qy	362	GAGGGACCCGGGTGACCGTCTTAGTCAAGCCAAAGGTGCCCCCTCGGTCACTCTGTTC 421
Db	368	GAGGACCAAGCTGACCGTCTTAGTCAAGCCAAAGGTGCCCCCTCGGTCACTCTGTTC 427
Qy	422	CGCCCTCTCTGAGGAGCTTCAAGCCAAAGGTGCCCCCTCGGTCACTCTGTTCATAGTGACT 481
Db	428	CGCCCTCTCTGAGGAGCTTCAAGCCAAAGGTGCCCCCTCGGTCACTCTGTTCATAGTGACT 487
Qy	482	TCTACCCGGGACCGTGACGTGCGCTGGAAGGACATAGACGCCCGCTCAAGCGGGAG 541
Db	488	TCTACCCGGGACCGTGACGTGCGCTGGAAGGACATAGACGCCCGCTCAAGCGGGAG 547
Qy	542	TGGAGACCAACACCTCCAAACAAAGCAACAAAGTACCGCGCCAGCAGCTACCTGA 601
Db	548	TGGAGACCAACACCTCCAAACAAAGCAACAAAGTACCGCGCCAGCAGCTACCTGA 607
Qy	602	GCCTGAGCGCTGAGCAGTGGAAAGTCCCAAGAGCTACAGTGCAGGTCCAGCATGAAG 661

Db 608 GCGTACGCTGAGCAGTGAAGTCCACAGAGTACAGCTGCCAGGTACAGCATGAAG 667

QY 662 GGAGCACCGTGAGAGACAGTGGCCCTTACAGAATGTC 701

Db 668 GGAGCACCGTGAGAGACAGTGGCCCTTACAGAATGTC 707

RESULT 13

BC022823

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

source

CDS

BASE COUNT

ORIGIN

BC022823

Homo sapiens, clone MGC:39283 IMAGE:4856249, mRNA, complete cds.

BC022823

GI:18606083

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 895)

Direct Submission

Submitted (04-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs@mail.nih.gov

Tissue procurement: Louis Staudt

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Farvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 42 Row: g Column: 21

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.

Location/Qualifiers

1..895

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="MGC:39283 IMAGE:4856249"

/issue_type="Primary B-Cells from Tonsils"

/clone_lib="NIH_MGC_48"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

38..739

/codon_start=1

/product="Unknown (protein for MGC:39283)"

/protein_id="AAH22823.1"

/db_xref="GI:18606084"

/translation="MAWIFLLPLLTCTGTSBASVELTQPPSVSPQGARITCSGD ALPKQAYWYQKQGPVLVIYKDNERSGIPFSGSSGTTVLTISGVQAEDEA DYYCQASDSSGTWVFGGKTLTLQGPKAAPSVTLPSPSEELQAKATLVLIISDF YPGAVTVANKADSSPVKAGVEITTPSKQSNKNYAASSVLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECS"

230 a

275 c

225 g

165 t

Query Match

74.5%; Score 525.2; DB 9; Length 895;

Best Local Similarity 88.6%; Pred. No. 3.3e-118;

Mismatches 569; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 62 CCTATGAATGACTAGCCACCTCGGTGTCAAGTCCCGGACAGACAGCGGCAGATCA 121

Db 96 CCTATGAGCTGACACAGCCACCTCGGTGTCAAGTCCCGGACAGACAGCGGCAGATCA 155

QY 122 CCTGTGGGGAGACACAGTAGAATATGTCCTGCTGGTACAGCAGAGCCAGCC 181

Db 156 CCTGTGCTGTGAGATGCATTGCCAAAGCAATATGCTTATTTGGTACAGCAGAGCCAGGCC 215

QY 182 GGGCCCCCTATCTATGATGATAGTACCGGCCCTCAGGGATCCCTGTAGCGAT 241

Db 216 AGGCCCCCTGTGTTGGTGAATATATAAAGACAATGAGAGGCCCTCAGGGATCCCTGTAGCGAT 275

QY 242 TCTCTGGCTCCAAATCAGGGACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGG 301

Db 276 TCTCTGGCTCCAGTCAGGGACCAACAGTCACGTGTCACCATCAGTGGAGTCCAGGCAGAAAG 335

QY 302 ATGAGGCTGACTATTACTGTGAGGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361

Db 336 ACAGGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTACTTATTGGGTGTTGGCG 395

QY 362 GAGGAGCCCGGGTGACCGTCTCTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTC 421

Db 396 GAGGACCAAGCTGACCGTCTCTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTC 455

QY 422 CGCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCTCATAGTGACT 481

Db 456 CGCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCTCATAGTGACT 515

QY 482 TCTACCGGGAGCGGTGACAGTGGCTTGGAAAGCAGATAGCAGCCCCCGTCAAGCGCGGAG 541

Db 516 TCTACCGGGAGCGGTGACAGTGGCTTGGAAAGCAGATAGCAGCCCCCGTCAAGCGCGGAG 575

QY 542 TGGAGACCCACACACCTCCAAACAAAGCAACAAAGTACGGCGGCAGAGTACTACTGA 601

Db 576 TGGAGACCCACACACCTCCAAACAAAGCAACAAAGTACGGCGGCAGAGTACTACTGA 635

QY 602 GCCTGAGCCTGAGCAGTGGAGTCCACAGAGAGTACAGTCCAGGTCCAGCATGAAG 661

Db 636 GCCTGAGCCTGAGCAGTGGAGTCCACAGAGAGTACAGTCCAGGTCCAGCATGAAG 695

QY 662 GGAGCACCGTGAGAGACAGTGGCCCTTACAGAATGTCAT 703

Db 696 GGAGCACCGTGAGAGACAGTGGCCCTTACAGAATGTCAT 737

RESULT 14

HSIGVL002

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

HSIGVL002

Human rearranged immunoglobulin lambda light chain mRNA.

HSIGVL002

GI:33701

IG lambda light chain; immunoglobulin.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 725)

Direct Submission

Submitted (31-JAN-1991) H.G. Kloebeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

2 (bases 355 to 401)

Combrato, G. and Kloebeck, H.G.

V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism

Eur J Immunol. 21 (6), 1513-1522 (1991)

91257162

QY	482	TCTACCGGAGCCGCTGACAGTGGCTTGAAGGCAGATAGCAGCCCCCTCAAGGCGGAG	541
Db	496	TCTACCGGAGCCGCTGACAGTGGCTTGAAGGCAGATAGCAGCCCCCTCAAGGCGGAG	555
QY	542	TGGAGACCCACACACCTCCAAACAAAGCAACAAAGTACGGCGCCAGCAGCTACTCTGA	601
Db	556	TGGAGACCCACACACCTCCAAACAAAGCAACAAAGTACGGCGCCAGCAGCTACTCTGA	615
QY	602	GCCTGACGCTGAGCAGTGGAGTCCACAGAAGCTACAGTGCAGGTACGCGATGAAG	661
Db	616	GCCTGACGCTGAGCAGTGGAGTCCACAGAAGCTACAGTGCAGGTACGCGATGAAG	675
QY	662	GGAGCACCGTGGAGAACACAGTGGCCCTACAGATGTTTCAT	703
Db	676	GGAGCACCGTGGAGAACACAGTGGCCCTACAGATGTTTCAT	717

RESULT 15	BC032452	890 bp	mRNA	linear	PRI 26-JUN-2002
LOCUS	BC032452				
DEFINITION	Homo sapiens, clone MGC:40425 IMAGE:5177123, mRNA, complete cds.				
ACCESSION	BC032452				
VERSION	BC032452.1	GI:21595391			
KEYWORDS	MGC.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 890)				
TITLE	Strausberg R.				
JOURNAL	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgaps-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@hri.nih.gov Akhtar N., Ayale K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Hagnigni, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantirpop, S., Thomas, P.J., Touchman, J.W., Young, A., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H. and Green, E.D.				

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAC Plate: 64 Row: 1 Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.

FEATURES	Location/Qualifiers
source	1..890
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="MGC:40425 IMAGE:5177123"
	/tissue_type="Brain, lung, Testis, adult, pooled whole"
	/clone_lib="NIH_MGC_115"
	/lab_host="DH10B"
	/note="Vector: pCMV-SPORT6"
	26..727
	/codon_start=1

CDS	
-----	--

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 18:12:24 ; Search time 392.719 Seconds
(without alignments)
8205.894 Million cell updates/sec

Title: US-09-758-173-3

Perfect score: 1431

Sequence: 1 ATGAACACCTGCTGCTCTT.....CCCTGCTCCGGTAATGA 1431

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq 101002.*

1: /SID22/cgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID22/cgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID22/cgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID22/cgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID22/cgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID22/cgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID22/cgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID22/cgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID22/cgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID22/cgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SID22/cgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SID22/cgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SID22/cgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SID22/cgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SID22/cgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SID22/cgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SID22/cgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SID22/cgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID22/cgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID22/cgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID22/cgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID22/cgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID22/cgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/cgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %			ID	Description
		Match	Length	DB		
1	1431	100.0	1431	18	AA762510	Prima1ised anti-hu
2	1431	100.0	1431	19	AAV15485	Macaque primatized
3	1431	100.0	1431	24	AA517243	DNA sequence of a
4	1315.8	91.9	1431	18	AA762513	Prima1ised anti-hu
5	1315.8	91.9	1431	19	AAV62513	Macaque primatized
6	1315.8	91.9	1431	24	AA517247	DNA sequence of a
7	1246.4	87.1	1634	21	AA250012	Human immune syste
8	1237.2	86.5	1431	17	AA178059	Monoclonal antibod
9	1234.8	86.3	1567	22	AAC66522	Human immune syste

10	1231.6	85.4	1418	17	AAT626889	Anti-rhesus D reco
11	1171.4	81.9	1404	18	AAT62868	Human gamma-4 heav
12	1168.2	81.6	1404	18	AAT62870	Human gamma-4E hea
13	1166.6	81.5	1404	18	AAT62869	Human gamma-4E hea
14	1135	79.3	1428	22	AAT74680	Nucleotide sequenc
15	1125.2	78.6	1428	18	AAT61241	Human anti-RSV mon
16	1124.2	78.6	1507	21	AAA09695	Human immunoglobul
17	1122.8	78.5	1430	24	AAK98701	cDNA of the heavy
18	1117.2	78.1	1437	19	AAV35487	Macaque primatized
19	1117.2	78.1	1437	24	AAK17245	DNA sequence of a
20	1115.6	78.0	1437	18	AAT13847	Prima1ised anti-hu
21	1115.4	77.9	1442	22	AAC84208	Plasmid Glambda-1B
22	1113.4	77.8	1798	21	AAC98220	Human colon cancer
23	1113.2	77.8	1644	22	AAS22593	Human cDNA encodin
24	1112.8	77.8	19035	19	AAC61794	Traget plasmid Man
25	1112.2	77.7	6281	22	AAC84206	Plasmid Glambda-1A
26	1110.8	77.6	1428	18	AAT61279	Human anti-RSV mon
27	1103.6	77.1	1517	14	AAQ35099	Antibody D heavy c
28	1103	77.1	1467	13	AAQ23570	Reshaped CAMPATH-1
29	1102	77.0	1599	24	ABK64550	Human benign proet
30	1102	77.0	1599	24	ABL62673	Colon adenocarcino
31	1102	77.0	1599	24	ABL65479	Lung cancer relate
32	1102	77.0	1599	24	ABL66294	Lung cancer relate
33	1100.8	76.9	1427	19	AAV41429	Plasmid Hui9HCPcd
34	1100.8	76.9	1427	19	AAV41431	Plasmid Hui9HCPcd
35	1098.8	76.8	1449	20	AAK66931	Monoclonal antibod
36	1098.8	76.8	1449	20	AAK66932	Monoclonal antibod
37	1097.6	76.7	1427	19	AAV41432	Plasmid Hui9HCPcd
38	1096.6	76.6	1612	22	AAS22482	Human cDNA encodin
39	1096	76.6	7521	22	AAF30315	Bicistronic chimer
40	1094	76.5	1549	13	AAQ20056	Encodes heavy chai
41	1093.8	76.4	1458	13	AAQ23571	Reshaped CD4 antib
42	1093.8	76.4	1458	13	AAQ23581	Reshaped CD4 antib
43	1092.8	76.4	6284	19	AAV41427	Plasmid Hui9HCPcd
44	1092.6	76.4	6557	17	AAT15932	Anti-IgE VH expres
45	1092.2	76.3	1617	24	AAS62784	cDNA sequence #571

ALIGNMENTS

RESULT 1

AAT62510
ID AAT62510 standard; DNA; 1431 BP.

XX AC AAT62510;

XX AC AAT62510;

XX DT 25-MAY-1997 (first entry)

XX DE Prima1ised anti-human B7.1 antigen antibody 7C10 heavy chain DNA.

XX DE Monoclonal antibody; cynomolgus monkey; macaque; 7C10;

XX KW Prima1ised antibody; B7 antigen; CD28; immunosuppressive;

XX KW autoimmune disease; idiopathic thrombocytopaenia purpura;

XX KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;

XX KW type 1 diabetes mellitus; graft versus host disease;

XX KW hetero-hybridoma; transfectoma; ss.

XX OS Chimeric Macaca cynomolgus;

XX OS Chimeric Homo sapiens.

XX PN WO9640878-A1.

XX PD 19-DEC-1996.

XX PF 06-JUN-1996; 96WO-US10053.

XX PR 07-JUN-1995; 95US-0487550.

XX PA (IDEC-) IDEC PHARM CORP.

XX PI Anderson DR, Brans P, Hanna N, Shestowsky WS;

XX XX

WPI; 1997-108638/10.
P-PSDB: AAW01818.

P-PSDB: AAW01818.

Monkey monoclonal antibody binding human B7.1 or B7.2 antigen - useful for treating autoimmune disease or graft-versus-host disease

useful for treating autoimmune disease or graft-versus-host disease

Claim 7: Fig 8B: 81pp: English.

2 DNA sequences (AATG2509 and AATG2510) respectively code for primatised forms (AAW01817 and AAW01818) of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.

Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;

```
Query Match 100.0%; Score 1431; DB 18; Length 1431;
Best Local Similarity 100.0%; Pred. No. 1.1e-276;
Matches 1431; Conservative 0; Mismatches 0; Indels 0;
```

1	ATGAAACCTCTGTGGTTCTTCTCTCTCTGGTGCGCAGCTCCACAGATGGGTCCTGTGCCAG	60
1	ATGAAACCTCTGTGGTTCTTCTCTCTCTGGTGCGCAGCTCCACAGATGGGTCCTGTGCCAG	60
61	GTGAAGCTCAGCAGTGGGGCGAAGGACTTCTGCAGCCCTTCGGAGACCCCTGTCCCGCAC	120
61	GTGAAGCTCAGCAGTGGGGCGAAGGACTTCTGCAGCCCTTCGGAGACCCCTGTCCCGCAC	120
121	TGCGTTGTCTCTGTGGCTCCATCAGGGGTACTACTACTGACCTGGATCCGCGAGCC	180
121	TGCGTTGTCTCTGTGGCTCCATCAGGGGTACTACTACTGACCTGGATCCGCGAGCC	180
181	CCAGGAGGGGACTCGAGTGGATTTGGCCATPATTTATGTGTAATGTGGCGACCAACAATAC	240
181	CCAGGAGGGGACTCGAGTGGATTTGGCCATPATTTATGTGTAATGTGGCGACCAACAATAC	240
241	AATCCCTCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCTCAAGACCAAGTTCCTC	300
241	AATCCCTCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCTCAAGACCAAGTTCCTC	300
301	CTGAACCTGAATTCGTGACCGACCGCGACACCGCCGCTATTAATCTGTGCGAGAGCCCT	360
301	CTGAACCTGAATTCGTGACCGACCGCGACACCGCCGCTATTAATCTGTGCGAGAGCCCT	360
361	CGCCCTGATTGCAACAACATTTGTTATGCGCGCTGSGGTTCGATGCTCGGGGCCCGGAGAC	420
361	CGCCCTGATTGCAACAACATTTGTTATGCGCGCTGSGGTTCGATGCTCGGGGCCCGGAGAC	420
421	CTGGTCACCGTCTCTCAGCTAGCACCAAGGCCCATGGGCTTCCTCCCTGGCACCCCTCC	480
421	CTGGTCACCGTCTCTCAGCTAGCACCAAGGCCCATGGGCTTCCTCCCTGGCACCCCTCC	480
481	TCCAAGACACCTCTGGGGGACACAGCGCCCTGGGTCCTGGTCAAGGACTACTTCCCC	540
481	TCCAAGACACCTCTGGGGGACACAGCGCCCTGGGTCCTGGTCAAGGACTACTTCCCC	540
541	GAACCGGTGACGGTGTCTGTGAACTCAGGGCCCTTGACACAGCGCGGTGCACACTTCCCG	600
541	GAACCGGTGACGGTGTCTGTGAACTCAGGGCCCTTGACACAGCGCGGTGCACACTTCCCG	600
601	GCTGTCTTACGTCTCAGACTCTACTCTCCTCAGCAGCGGTGTGAACGCTGCCCTCCAGC	660
601	GCTGTCTTACGTCTCAGACTCTACTCTCCTCAGCAGCGGTGTGAACGCTGCCCTCCAGC	660
661	AGCTTGGGACCCAGACCTACTCTGCAACGTGGAATCAAGAGCCCGACACACCAAGGTTG	720
661	AGCTTGGGACCCAGACCTACTCTGCAACGTGGAATCAAGAGCCCGACACACCAAGGTTG	720

Qy	721	GACAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTACACATGCCCCACGGTGCCACGA	780
Db	721	GACAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTACACATGCCCCACGGTGCCACGA	780
Qy	781	CCTGAACCTCTGGGGGACCGTCAGCTTCTCTTCTTCCCCCAAAACCCCAAGGACACCCCTC	840
Db	781	CCTGAACCTCTGGGGGACCGTCAGCTTCTCTTCTTCCCCCAAAACCCCAAGGACACCCCTC	840
Qy	841	ATGATCTCCCGGACCCCTGAGGTGTCATGCGTGGTGGTGAGCGTGAGCCACAAAGACCT	900
Db	841	ATGATCTCCCGGACCCCTGAGGTGTCATGCGTGGTGGTGAGCGTGAGCCACAAAGACCT	900
Qy	901	GAGGTCAAGTTCACTGTGTAACGTGACGCGCGTGGAGTGCATTAATCCCAAGACAAAGCG	960
Db	901	GAGGTCAAGTTCACTGTGTAACGTGACGCGCGTGGAGTGCATTAATCCCAAGACAAAGCG	960
Qy	961	CGGAGGAGCAGTACACAGCAGCTACCGTGTGTGTGAGCGTCTCACCGTCTGTGACCCAG	1020
Db	961	CGGAGGAGCAGTACACAGCAGCTACCGTGTGTGTGAGCGTCTCACCGTCTGTGACCCAG	1020
Qy	1021	GACTGGCTGAATGCGAAGGAGTACAAGTGCAGAGTCTCCAAAGAGCCCTCCAGGCCCC	1080
Db	1021	GACTGGCTGAATGCGAAGGAGTACAAGTGCAGAGTCTCCAAAGAGCCCTCCAGGCCCC	1080
Qy	1081	ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACAGAGTGTCACCCCTG	1140
Db	1081	ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACAGAGTGTCACCCCTG	1140
Qy	1141	CCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCTGAGCTGACCTGCTGCTCAAGGC	1200
Db	1141	CCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCTGAGCTGACCTGCTGCTCAAGGC	1200
Qy	1201	TTCTATCCCAAGCAGCATCGCCGTGGAGTGGGAGAGCAATGGCGAGCCGGAGAACAACTAC	1260
Db	1201	TTCTATCCCAAGCAGCATCGCCGTGGAGTGGGAGAGCAATGGCGAGCCGGAGAACAACTAC	1260
Qy	1261	AAGACCGCGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTCTACAGCAAGCTCACC	1320
Db	1261	ANGACCAAGCTCCCGTGTGAGCTCCGAGCGGCTCTTCTTCTCTCTACAGCAAGCTCACC	1320
Qy	1321	GTGGACAAGAGCAGGTGGCAGCAGGGGAAAGCTCTTCTCATGTCTCCGTGTGATGATGAGCT	1380
Db	1321	GTGGACAAGAGCAGGTGGCAGCAGGGGAAAGCTCTTCTCATGTCTCCGTGTGATGATGAGCT	1380
Qy	1381	CTGCAACACCATACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1381	CTGCAACACCATACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA	1431

DEPT 5

RESULT 2

AAV35485

ID	AAV3
1	1
2	1
3	1
4	1
5	1
6	1
7	1
8	1
9	1
10	1
11	1
12	1
13	1
14	1
15	1
16	1
17	1
18	1
19	1
20	1
21	1
22	1
23	1
24	1
25	1
26	1
27	1
28	1
29	1
30	1
31	1
32	1
33	1
34	1
35	1
36	1
37	1
38	1
39	1
40	1
41	1
42	1
43	1
44	1
45	1
46	1
47	1
48	1
49	1
50	1
51	1
52	1
53	1
54	1
55	1
56	1
57	1
58	1
59	1
60	1
61	1
62	1
63	1
64	1
65	1
66	1
67	1
68	1
69	1
70	1
71	1
72	1
73	1
74	1
75	1
76	1
77	1
78	1
79	1
80	1
81	1
82	1
83	1
84	1
85	1
86	1
87	1
88	1
89	1
90	1
91	1
92	1
93	1
94	1
95	1
96	1
97	1
98	1
99	1
100	1

XX

AC AAV3

XX

DT 29-S

XX
XX

DE
MacDE
YY
MaccXY
YWKW
MONCKW
CD8E

KW T. CE

KW immu

KW T CE

XX

OS Maca

XX

Key

FT
CDS

51

15

13

Db	1081	ATCGAGAAACCATCTCCAAAGACCAAGAGGGCAGCCCCGAGAACCAACAGGTGTACACCGTG	1141
Qy	1141	CCCCCATCCCGGGATGAGTGCACCAAGAACCAAGGTCCAGCTGACCTGCTGGTCAAAGGC	1201
Db	1141	CCCCATCCCGGGATGAGTGCACCAAGAACCAAGGTCCAGCTGACCTGCTGGTCAAAGGC	1201
Qy	1201	TTCTATCCCAAGCAGATCCGCGTGGAGTGGGAGAGCAATAGGCGACCGGAGAACCACTAC	1261
Db	1201	TTCTATCCCAAGCAGATCCGCGTGGAGTGGGAGAGCAATAGGCGACCGGAGAACCACTAC	1261
Qy	1261	AAGACCAACGGCTCCCGCTGTGGACTCCGACGGCTCCCTCTTCTCTCTACAGCAAGCTACC	1321
Db	1261	AAGACCAACGGCTCCCGCTGTGGACTCCGACGGCTCCCTCTTCTCTCTACAGCAAGCTACC	1321
Qy	1321	GTGCAACAAGCAGAGTGGCAGCAGGAGGAAACGCTTCTTCATGCTCCGTGATGCATAGGCT	1381
Db	1321	GTGCAACAAGCAGAGTGGCAGCAGGAGGAAACGCTTCTTCATGCTCCGTGATGCATAGGCT	1381
Qy	1381	CTGCACAACCACTACACGAGAGAAGCGCTCTCCCTGTCTCCGGTGAATAATGA	1431
Db	1381	CTGCACAACCACTACACGAGAGAAGCGCTCTCCCTGTCTCCGGTGAATAATGA	1431
RESULT 4			
AAT62513			
ID	AAT62513 standard; DNA; 1431 BP.		
XX			
AC	AAT62513;		
XX			
DT	25-MAY-1997 (first entry)		
XX			
DE	Primaetised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.		
XX			
KW	Monoclonal antibody; cynomolgus monkey; macaque; 16C10;		
KW	primaetised antibody; B7 antigen; CD28; immunosuppressive;		
KW	autoimmune disease; idiopathic thrombocytopenia purpura;		
KW	systemic lupus erythematosus; rheumatoid arthritis; psoriasis;		
KW	type 1 diabetes mellitus; graft versus host disease;		
KW	hetero-hybridoma; transfectoma; ss.		
XX			
OS	Chimeric Macaca cynomolgus;		
OS	Chimeric Homo sapiens.		
XX			
PN	WO9640878-A1.		
PD	19-DEC-1996.		
XX			
PF	06-JUN-1996; 96WO-US10053.		
XX			
PPR	07-JUN-1995; 95US-0487550.		
XX			
PPA	(IDEC-) IDEC PHARM CORP.		
PI	Anderson DR, Brams P, Hanna N, Shestowsky WS;		
DR	WPI; 1997-108638/10.		
DR	P-PSDB; AAW01822.		
XX			
PPT	Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -		
XX	useful for treating autoimmune disease or graft-versus-host disease		
XX	Claim 11; Fig 10B; 81pp; English.		
PPS			
CCC	2 DNA sequences (AAT62512 and AAT62513) respectively code for		
CCC	primaetised forms (AAW01821 and AAW01822) of the light and heavy chains		
CCC	of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody		
CCC	16C10. Cloned 16C10 light and heavy variable genes are inserted		
CCC	into an expression vector (pref. NEOSPLA) which contains human light		
CCC	and heavy chain constant region genes to allow prodn. of primaetised		
CCC	antibody in e.g. CHO cells. Primaetised 7C10 and 7B6 anti-B7.1		
CCC	antibodies have also been produced (see also AAW01817-20). The		
CCC	primaetised antibodies inhibit the B7:CD28 pathway, making them		
CCC	useful immunosuppressants for the treatment of autoimmune disorders		


```

Db 78 ATGAACATCTGTGTTCTTCTCTGTGGGAGCTCCAGATGGTCTGTCCAG 137
Qy 61 GTGAAGCTGCAGCAGTGGGGGAAAGCACTTCTGACGCTTCGGAGACCTGTCCCGAC 120
Db 138 GTGACGCTGCAGGAGTCCGGCCAGCACTGGTGAAGCCTTCGGAGACCTGTCCCTCAC 197
Qy 121 TGGCTGTCTGTGGTCCATCAGCGTTACTACTGACTGGAACCTGGATCCGCCAGCC 180
Db 198 TGCACGTCTGTGGTCCATCAGGAGT---TACTACTGGAACCTGGATCCGGCTGCC 254
Qy 181 CCAGGAGGAGCTGACGTGGATTGGCCATATTTATGTAATGTGGACCACTAC 240
Db 255 CCAGGAAGGAGCTGGAATGGGTATATCTA---TACTAGTGGAGCACCACCTAC 311
Qy 241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACAGCTCCAAAGAACCACTTCTC 300
Db 312 AACCCCTCCCTCAAGAGTCGAGTCACCATGTCAGTAGACAGCTCCAGAACCACTTCTCC 371
Qy 301 CTGAACCTTGAATCTGTGACCGACCGGACAGCGCGCTCTATTACTGTGGAGAGGCCCT 360
Db 372 CTGAAGCTGAGCTGTGACCGCTGCGGACACGCGCGCTGTATTACTGTGGAGACCCCG 431
Qy 361 CCCCTGATTGCACACCATTTGTTATGGGGCTGGTTCGATGTCGGGCC- CGGGAGA 419
Db 432 CCCAAGCTACTACTA-----CGGTATGGACTTCTGGGGCCAAGGAGC 478
Qy 420 CCTGGTCAACGCTCTCTCAGTAGCACCAAGGCCCATCGGTCTTCCCTTGGCACCCCTC 479
Db 479 CCTGGTCAACGCTCTCTCAGCTCCACCAAGGCCCATCGGTCTTCCCTTGGCACCCCTC 538
Qy 480 CTCAAGAGCAGCTCTGGGGCACAGCGGCCCTGGGTCTGTGTCAGGACTACTTCCC 539
Db 539 CTCAAGAGCAGCTCTGGGGCACAGCGGCCCTGGGTCTGTGTCAGGACTACTTCCC 598
Qy 540 CGAACCGGTGACGGTGTGCGTGAACCTCAGCGCCCTCAGCAGCGGCTGCACACCTTCCC 599
Db 599 CGAACCGGTGACGGTGTGCGTGAACCTCAGCGGCCCTGACAGCGGCTGCACACCTTCCC 658
Qy 600 GGCTGTCTCAGTCTCAGGACTCTACTCCTCAGCAGCGTGGTACCGTGGCCCTCCAG 659
Db 659 GGCTGTCTCAGTCTCAGGACTCTACTCCTCAGCAGCGTGGTACCGTGGCCCTCCAG 718
Qy 660 CAGCTTGGGACCCAGACCTACATCTCGAAGTGAATCACAAGCCCAAGCAACCAAGGT 719
Db 719 CAGCTTGGGACCCAGACCTACATCTCGAAGTGAATCACAAGCCCAAGCAACCAAGGT 778
Qy 720 GGACAAGAAAGCAGAGCCCAAAATCTTGTGACAAATCTCACATGCCACCGTCCAGC 779
Db 779 GGACAAGAAAGTTCAGGCCCAATCTTGTGACAAATCTCACATGCCACCGTCCAGC 838
Qy 780 ACTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCCCT 839
Db 839 ACTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCCCT 898
Qy 840 CATGATCTCCCGGACCCCTGAGTCACTCGTGGTGGTGGAGCTGAGCCACCAAGACCC 899
Db 899 CATGATCTCCCGGACCCCTGAGTCACTCGTGGTGGTGGAGCTGAGCCACCAAGACCC 958
Qy 900 TGAGGTCAAGTTCAACTGGTACGTGGAGCGCTGGAGTGCATAATGCCAAGACCAAGCC 959
Db 959 TGAGGTCAAGTTCAACTGGTACGTGGAGCGCTGGAGTGCATAATGCCAAGACCAAGCC 1018
Qy 960 GCGGAGGAGCAGTACAAAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1019
Db 1019 GCGGAGGAGCAGTACAAAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1078
Qy 1020 GGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1079
Db 1079 GGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1138
Qy 1080 CATCGAGAAACCATCTCCAAAGCAAAAGGCGAGCCCGGAGACCAAGCTGTACACCT 1139

```

```

Db 1139 CATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCCT 1198
Qy 1140 GCCCCCATCCCGGATGAGCTGACCAAGAACACAGGTCAAGCTGACCTGCTGGTCAAAGG 1199
Db 1199 GCCCCCATCCCGGATGAGCTGACCAAGAACACAGGTCAAGCTGACCTGCTGGTCAAAGG 1258
Qy 1200 CTTCTATCCAGCAGCATCGCGTGGAGTGGGAGAGCAATGGGAGCCCGAGAACAACTA 1259
Db 1259 CTTCTATCCAGCAGCATCGCGTGGAGTGGGAGAGCAATGGGAGCCCGAGAACAACTA 1318
Qy 1260 CAAGACACGCTCCGCTGCTGGAATCCGACGGCTCTTCTTCTCTACAGCAAGCTCAC 1319
Db 1319 CAAGACACGCTCCGCTGCTGGAATCCGACGGCTCTTCTTCTCTACAGCAAGCTCAC 1378
Qy 1320 CGTGGACAAGAGCAGGTGGCAGCAGCGGGAACGCTTCTCATGCTCGGTGATCGATGAGG 1379
Db 1379 CGTGGACAAGAGCAGGTGGCAGCAGCGGGAACGCTTCTCATGCTCGGTGATCGATGAGG 1438
Qy 1380 TGTGCACAACTACACGACAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1431
Db 1439 TGTGCACAACTACACGACAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1490

```

RESULT 8

AAT18059

ID AAT18059 standard; DNA; 1431 BP.

XX AAT18059;

AC AAT18059;

DT 16-AUG-1996 (first entry)

XX

DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.

XX

KW Polymerase chain reaction; primer; amplify; PCR; light chain; MAB;

KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 1..1428

FT sig_peptide /*tag= a

FT mat_peptide /*tag= b

FT 3'UTR 58..1425

FT /*tag= c

FT /*tag= d

XX

PN JP08038178-A.

XX

PD 13-FEB-1996.

XX

PF 20-FEB-1995; 95JP-0030742.

XX

PR 18-FEB-1994; 94JP-0021628.

XX

PA (NISN) NISSHINO IND INC.

XX

PA (TANA) TANAKA H.

XX

DR WPI; 1996-154852/16.

XX

DR P-PSDB; AAR93553.

XX

PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -

PT produced by primer amplification, used in the diagnosis of hCMV

XX

XX infection

PS Claim 6; Page 16-18; 22pp; Japanese.

XX

CC The sequences given in AAT18059-60 encode the heavy and light chains

CC respectively of a monoclonal antibody against a 65 kD antigen of human

CC cytomegalovirus (hCMV). These sequences were amplified using the

CC sequences given in AAT18040-58. The monoclonal antibody may be used

CC in the diagnosis of hCMV.

- CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
- CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
- CC erythematosus, arteriosclerosis, cirrhosis and cancer.

Sequence 1567 BP; 346 A; 503 C; 428 G; 289 T; 1 other; XX

Query Match	86.3%	Score 1334.8;	DB 22;	Length 1567;
Best Local Similarity	92.9%	Pred. No. 1.6e-237;		
Matches 1332;	Conservative	0;	Mismatches 87;	Indels 15; Gaps 3;

Qy	1	ATGAAACACCTGTGGTCTTCTCTCTCTCTGTGGAGCTCCAGATGGGTCTGTGTCCAG	60
Db	78	ATGAAACACCTGTGGTCTTCTCTCTCTGTGGAGCTCCAGATGGGTCTGTGTCCAG	137
Qy	61	GTGAAGCTGCAGAGTGGGCGAAGACTTCTGCAGCCTTCGGAGACCCGTGTCCCGCACC	120
Db	138	GTGCAGCTGCAGAGTGGGCGCAGAGCTTGTGAAGCTTTCGGAGACCCGTGTCCCTCACC	197
Qy	121	TGCGTTGTCTCTGGTGGCTCCATC---AGCGGTTACTACTACTGGAACCTGGATCCGCCAG	177
Db	198	TGCGCTGTCTCTGGTGGCTCCATCACTAGTGGTGGTTACTACTGAGCTGGATCCGCCAG	257
Qy	178	ACCCAGGAGGGGACTGAGTGGATTGGCCATATTTATGTGTAATGTGGCGACACCAAC	237
Db	258	CCCCAGGGAAGGGGCTGGAGTGGATTGGGTACATCTA---TTACAGTGGGAGCACCTC	314
Qy	238	TACAATCCCTCCCTCAAGAGTCAGATGCACATTTTCAAAGACACGTCCAGAACCAAGTTC	297
Db	315	TACAACCCGTCCTCAAGAGTCGAGTTTCCATATCAGTAGACAGCTCCAGAACCAAGTTC	374
Qy	298	TTCTTGAACTTGAATTTCTGTGACCGACGGGACACGGCGCTCTATTACTGTGCGAGAGGC	357
Db	375	TTCTTGAAGCTGAGCTCTGTGACTGCGCGACACCGCGCTGTATTACTGTGCCAGAG--	432
Qy	358	CCTGCCCTGATTGCAACAACATTTGTTATGCGGGTGGGTGATGTCTGGGGGCCGGGA	417
Db	433	-----ATGACGCTAGGTTTAAAGGGGGGGAACTACGGTATGAGCGTCTGGGGCGAGGA	485
Qy	418	GACCTGTGACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCCCTGGCACCC	477
Db	486	ACCTGTGTACCGTCTCTCAGGCTTCCACAAGGGCCCATCGGTCTTCCCTCCCTGGCACCC	545
Qy	478	TTCTTCCAAGAGCACCTCTGGGGGACAGCGGGCCCTGGGCTGCTGGTCAAGGACTACTTTC	537
Db	546	TTCTTCCAAGAGCACCTCTGGGGGACAGCGGGCCCTGGGCTGCTGGTCAAGGACTACTTTC	605
Qy	538	CCGGAACCGGTGACGGTGTGCTGGAACTCAGAGGGCCCTGACACGAGGGGCGTGCAACCTTC	597
Db	606	CCGGAACCGGTGACGGTGTGCTGGAACTCAGAGGGCCCTGACACGAGGGGCGTGCAACCTTC	665
Qy	598	CCGGCTGTCTACAGTCTCAGAGCTCTACTCCCTCAGCAGGCTGGTACCGCTCCCTCC	657
Db	666	CCGGCTGTCTACAGTCTCAGAGCTCTACTCCCTCAGCAGGCTGGTACCGCTCCCTCC	725
Qy	658	AGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCAACGCCAGCAACACCAAG	717
Db	726	AGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCAACGCCAGCAACACCAAG	785
Qy	718	GTGACAGAAGAACGAGAGCCCAATCTTGTGACAAACCTCACATGTCGACCGTGGCCCA	777
Db	786	GTGACAGAAGAGAGTTGAGCCCAATCTTGTGACAAACCTCACATGTCGACCGTGGCCCA	845
Qy	778	GCACCTGAATCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAACCCAGGACACC	837
Db	846	GCACTGAATCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAACCCAGGACACC	905
Qy	838	CTCATGATCTCCCGGACCCCTGAGGTCACATGTGGTGGTGGAGCGTGAGCCAGCAAGAC	897
Db	906	CTCATGATCTCCCGGACCCCTGAGGTCACATGTGGTGGTGGAGCGTGAGCCAGCAAGAC	965
Qy	898	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAG	957
Db	966	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAG	1025

Qy	958	CCCGGGAGGAGGAGTACAAACAGCAGTACCGTGTGGTTCAGCGTCTCTGCAC	1017
Db	1026	CCCGGGAGGAGGAGTACAAACAGCAGTACCGTGTGGTTCAGCGTCTCTGCAC	1085
Qy	1018	CAGGACTGGCTGAATGGCAAGGATACAAGTCAAGTCTCCACAAGAGCCCTCCAGCC	1077
Db	1086	CAGGACTGGCTGAATGGCAAGGATACAAGTCAAGTCTCCACAAGAGCCCTCCAGCC	1145
Qy	1078	CCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCCCGAGAACCAACAGGTGTACAC	1137
Db	1146	CCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCCCGAGAACCAACAGGTGTACAC	1205
Qy	1138	CTGCCCCCATCCCGGATCAGCTGACCAAGAACAGGTCAGCTGACTGCTCGTGGTCAAA	1197
Db	1206	CTGCCCCCATCCCGGAGAGATGACCAAGAACAGGTCAGCTGACTGCTCGTGGTCAAA	1255
Qy	1198	GGCTTCTATCCACGACATCCCGCTGGAGTGGGAGACAATGGGCAGCCGGAGAACAC	1257
Db	1266	GGCTTCTATCCACGACATCCCGCTGGAGTGGGAGACAATGGGCAGCCGGAGAACAC	1325
Qy	1258	TACAGACACGGCTCCCGTGTGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTC	1317
Db	1326	TACAAGACACGGCTCCCGTGTGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTC	1395
Qy	1318	ACCGTGGACAAGAGCAGGTGGCAGAGGGGAACGTTCTCATGTCCGTGATGCATGAG	1377
Db	1386	ACCGTGGACAAGAGCAGGTGGCAGAGGGGAACGTTCTCATGTCCGTGATGCATGAG	1445
Qy	1378	GCTCTGCACAAACCACTACACGACAGAGGCTCTCCCTGTCTCTCGGGTAAATGA	1431
Db	1446	GCTCTGCACAAACCACTACACAGAGAGGCTCTCCCTGTCTCCCGGGTAAATGA	1499

RESULT 10

AAT26889
ID AAT26889 standard; cDNA; 1418 BP.

XX
AC AAT26889;XX
DT 30-OCT-19XX
DE Anti-rhesus D recombinant

Human monoclonal antibody: immunoglobulin isotype IgM: ag

KW rhesus positive; rhesus negative; haemolysis; heavy chain; gamma 1;
 KW variable region; insect host cell; baculovirus; recombinant production;
 KW ds.

XX Homo sapiens.

OS Synthetic.
xx

FH	Key	Location/Qualifiers
FM	1	57

```

ET      / *tag= a
ET      / *tag= a

```

mouse VH gene signal sequence"

FT / *tag:

```
FT
/processed_note/_construct f
/note= "constructed f
```

FT
FT
FT
FT

human gamma heavy chain constant region
and the variable region from anti-thetaus D
antibody D7C2"

XX
PN
FR2724182-A1.

XX PD 08-MAR-1996

XX
PF 02-SEP-1994: 94ER-0010566.

XX
DP 02-SEP-1994: 94EP-0010566

XX

PA (INSP) INST PASTEUR.
PA (PROT-) PROTEINE PERFORMANCE.
XX
PI Chaabihi H, Edelman L, Kaczorek M, Margaritte C;
XX
DR WPI: 1996-162018/17.
DR P-PSDB; AAR93166.
XX
PT Recombinant anti-rhesus D monoclonal antibody - expressed by
PT baculovirus-transformed insect cells and useful for preventing
PT haemolysis in new-born babies
XX
PS Claim 1; Page 35-37; 46pp; French.

XX The human monoclonal antibody D7C2, of isotype IgM, recognises a
CC 30-32 kD polypeptide on the membrane of rhesus positive red blood
CC cells. The antibody agglutinates rhesus positive cells but not
CC rhesus negative cells and is useful diagnostically and also for
CC preventing haemolysis in new-born rhesus positive babies.
CC Recombinant IGM-D7C2 can be produced by insect cells which have
CC been transformed by a baculoviral vector comprising a D7C2
CC expression cassette. The present sequence encodes a recombinant
CC IGM-D7C2 heavy chain fused to a mouse VH signal peptide.

XX Sequence 1418 BP; 333 A; 458 C; 378 G; 249 T; 0 other;

Query Match 85.4%; Score 1221.6; DB 17; Length 1418;
Best Local Similarity 92.9%; Pred. No. 7e-235;
Matches 1317; Conservative 0; Mismatches 89; Indels 12; Gaps 3;

QY 13 TGGTCTTCTCTCTGTGTCAGCTCCAGATGGTCTGTCTCCAGGTGAAGTGGAG 72
DB |||||
QY 73 CAGTGGGGGAAGGACTCTCGAGCTTCGGAGACCTGTCCCGACCTGGTGTCTCT 132
DB |||||
QY 73 CAGTGGGGGCGAGGACTGTGAAGCTTCGGAGACCTGTCTCCCTCAGCTGCTAT 132
QY 133 GTTGGCTCCATCAGCGGTTACTACTGTGACTCGGCTGGATCCGCGAGACCCAGGAGGGGA 192
DB |||||
QY 193 CTGGAGTGATTTGGCCATATTTATGGTAATGTGGCGACCAACCACTAATCCCTCCCTC 252
DB |||||
QY 190 CTGGAGTGATTTGGGGAATCAA--TCAATAGTGAAGACCACTAACAACCCGCTCCCTC 246
QY 253 AAGAGTCGAGTCACCATTTCAAAGACACGTCCTAAGAACCAAGTCTTCTCTGAATTTGAAT 312
DB |||||
QY 247 AAGAGTCGAGTCACCATATCAGTAGACAGCTCCAAGAACCAAGTCTTCTCTGAAGTGAAC 306
QY 313 TCTGTGACCGACCGGACACGGCCGCTTATTACTGTGCGAGAGGCCCTTCGCCCTGATTGC 372
DB |||||
QY 307 TCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGCGAGGG-----CCCCAGAGTAT 360
QY 373 ACAACCATTTGTTATGGCGGCTGGGTGATGTCTGGGGCCCGGGAGACCTGGTCAACGTC 432
DB |||||
QY 361 AAATGGAAGTATCATTTGGGAGCTGGTTCGACCCCTGGGGCCCAAGGTATACCACTGTCAACGTC 420
QY 433 TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCGGACACCTCTCCAAGAGCAC 492
DB |||||
QY 421 TCCTCAGCTCACCACAGGGCCCATCGGTCTTCCCTCGGACACCTCTCCAAGAGCAC 480
QY 493 TCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGGACTACTTCCCGAACCGGTGACG 552
DB |||||
QY 481 TCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGGACTACTTCCCGAACCGGTGACG 540
QY 553 GGTGCTGGAACCTCAGGCGCCCTGACCGAGCGGTGACACCTTCCCGGCTGCTCAG 612
DB |||||
QY 541 GTGTGTAACCTCAGGCGCCCTGACCAAGCGGCTGACACCTTCCCGGCTGCTCAG 600
QY 613 TCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGCTTGGGCACC 672
DB |||||
QY 601 TCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGCTTGGGCACC 660

QY 673 CAGACCTACATCTGCAACGTAATCAAGCCCGAGCAACCAAGGTGGACAAAGCA 732
DB |||||
QY 661 CAGACCTACATCTGCAACGTAATCAAGCCCGAGCAACCAAGGTGGACAAAGCA 720
QY 733 GAGCCCAATCTTTGTGACAAATCAACATGCCCCACCGTGCCCGACGACTGAATCTCTG 792
DB |||||
QY 721 GAGCCCAATCTTTGTGACAAATCAACATGCCCCACCGTGCCCGACGACTGAATCTCTG 780
QY 793 GGGGACCGCTCAGTCTTCTTCTTCCCCCAAAACCAAGGACACCTCATGATCTCTCCCG 852
DB |||||
QY 781 GGGGACCGCTCAGTCTTCTTCTTCCCCCAAAACCAAGGACACCTCATGATCTCTCCCG 840
QY 853 ACCCTGAGGTACATGCGTGTGTGAGCGTGCAGCCAGCAAGACCCCTGAGGTCAAGTTTC 912
DB |||||
QY 841 ACCCTGAGGTACATGCGTGTGTGAGCGTGCAGCCAGAGACCCCTGAGGTCAAGTTTC 900
QY 913 AACTGTGACGTCGACCGGCTGAGGTGCATTAATGCAAGCAAAAGCCGCGGAGGAGCAG 972
DB |||||
QY 901 AACTGTGACGTCGACCGGCTGAGGTGCATTAATGCAAGCAAAAGCCGCGGAGGAGCAG 960
QY 973 TACAACAGCAGCTACCGTGTGTGTCAGCGTCTCACCGTCTTCCACCGAGCTGGCTGAAT 1032
DB |||||
QY 961 TACAACAGCAGCTACCGGCTGTGTCAGCGTCTTCAAAGTCTTGCACCGAGCTGGCTGAAT 1020
QY 1033 GGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACC 1092
DB |||||
QY 1021 GGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACC 1080
QY 1093 ATCTCAAAGCCAAAGGCGAGCCCGAGAAACACAGGTGTACACCTGCCCCCATCCCCG 1152
DB |||||
QY 1081 ATCTCAAAGCCAAAGGCGAGCCCGAGAAACACAGGTGTACACCTGCCCCCATCCCCG 1140
QY 1153 GATGAGTGCACCAAGAACAGGTGACGCTGCTGCTGCTCAAAGGCTTCTATCCAGC 1212
DB |||||
QY 1141 GATGAGTGCACCAAGAACAGGTGACGCTGCTGCTGCTCAAAGGCTTCTATCCAGC 1200
QY 1213 GACATCCCGTGGAGTGGAGAGCAATGGGCGAGCCGGAGAACAACTACAAGACCAAGCT 1272
DB |||||
QY 1201 GACATCCCGTGGAGTGGAGAGCAATGGGCGAGCCGGAGAACAACTACAAGACCAAGCT 1260
QY 1273 CCGTCTGTCGACTCCGACGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1332
DB |||||
QY 1261 CCGTCTGTCGACTCCGACGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
QY 1333 AGGTGCGAGCAGGGGAAACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1392
DB |||||
QY 1321 AGGTGCGAGCAGGGGAAACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
QY 1393 TACACGCAAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1430
DB |||||
QY 1381 TACACGCAAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1418

RESULT 11
AAT62868
ID AAT62868 standard; DNA; 1404 BP.
XX
AC AAT62868;
XX
DT 18-OCT-1997 (first entry)
XX
DE Human gamma-4 heavy chain DNA.
XX
KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukaemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma 4; ss.
OS Homo sapiens.
XX
PN WO9709351-A1.
XX

Qy	1141	CCCCATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTGCCTGGTCAAAAGC	1200
Db	1138	CCCCATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTGCCTGGTCAAAAGC	1197
Qy	1201	TTCTATCCCAAGCACATCGCCGTGGAGTGGGAGAGCAATGGCGAGCCGGAGAACCACTAC	1260
Db	1198	TTCTATCCCAAGCACATCGCCGTGGAGTGGGAGAGCAATGGCGAGCCGGAGAACCACTAC	1257
Qy	1261	AAGACACGCTCCCGTGTGGATCCGACGCTCCTTCTTCTCTACAGCAAGCTCACC	1320
Db	1258	AAGACACGCTCCCGTGTGGATCCGACGCTCCTTCTTCTCTACAGCAAGCTCACC	1317
Qy	1321	GTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCATGCTCCGTGATGCATGAGGCT	1380
Db	1318	GTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCATGCTCCGTGATGCATGAGGCT	1377
Qy	1381	CTGCACAACCACTACACGCAGAGAGCCCTCCCTGTCTCCGGGTAAATGA	1431
Db	1378	CTGCACAACCACTACACGCAGAGAGCCCTCCCTGTCTCCGGGTAAATGA	1428

RESULT 15	
AAT61241	
ID	AAT61241 standard; DNA; 1428 BP.
XX	XX
AC	AAT61241;
XX	XX
DT	13-MAY-1997 (first entry)
XX	XX
DE	Human anti-RSV monoclonal antibody RF-1 heavy chain DNA.
XX	XX
KW	Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus;
KW	RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;
KW	Epstein Barr virus; immortalisation; recombinant antibody; ss.
XX	XX
OS	Homo sapiens.

Key	Location/Qualifiers
sig_peptide	1..57
mat_peptide	/*tag= a 58..1425 /*tag= b
WO640252-Al.	
19-DEC-1996.	
06-JUN-1996;	96WO-US10070.
07-JUN-1995;	95US-0488376.
(IDEC-) IDEC PHARM CORP.	
Brams P, Chamat SS, Heard CU, Newman RA, Pan L; Walsh EE;	
WPI; 1997-099892/09.	
P-PSDB; AAW11639.	
Human monoclonal antibody specific for respiratory syncytial virus fusion protein - used for the prevention and treatment of RSV infection	
Claim 9; Fig 9b-c; 85pp; English.	
A DNA sequence (AAT61241) codes for a polypeptide (AAW11639) comprising a leader sequence, RF1 heavy chain variable region (see also AAW11637), and human gamma 1/constant region. RF1 is a human monoclonal antibody (hMAb) specific for the fusion protein of respiratory syncytial virus (RSV). The DNA sequence, in vector NEOSP4, can be used to produce the light chain construct in transfected eukaryotic (e.g. CHO) cells. RF-1 and RF-2 heavy and light chain constructs (see also AAT61240, AAT61242, AAT61279)	

CC	similarly used. The transfected host cells provide a constant,
CC	stable supply of anti-RSV F-protein mAbs for use in the treatment
CC	or prevention of RSV infection.
XX	
SQ	Sequence 1428 BP; 326 A; 465 C; 372 G; 265 T; 0 other;
	Query Match 78.6%; Score 1125.2; DB 18; Length 1428;
	Best Local Similarity 88.6%; Pred. No. 1.2e-215;
	Matches 1256; Conservative
	Mismatches 153; Indels 9; Gaps
QY	17 TCCTTCCTCCTGGTGAGCACTCCAGATGGGTCTGTCACAGGTGAAGCTGCACAGT 76
DB	17 TCTTGCTCTTCCTTGCTGCTGTGCTACGGGTGCTGTCCTCCAGGTGCAGTTGCAGAGT 76
QY	77 GGGCGAAGCACTTCTGCAGCCTTCGGAGACCCTGTGCCGACCTCGTGTGTCTCTGGTG 136
DB	77 CTGGTCTCTGGTGGTGAACCCACAGAGACCCCTCACGCTGACCTGCACCGTCTCTGGGT 136
QY	137 GCTC---CATCAGGGTTACTACTGAGACCTGGATCGCCAGACCCCAGGAGGGGAC 193
DB	137 TCTCACTCAGCAACCCCTAGAATGGGTGTGACCTGTGATCGCTAGCCCCCGGAAGGCC 196
QY	194 TGGAGTGGATTGGCCATATTTATGTGTAATGTTGCGGACCACTAACTACAATCCCTCTCA 253
DB	197 TAGAATGGCTTGGAAACATTTTTTCAGATGACGAGAAGTC---CTTCAGTCTCTCTGA 253
QY	254 AGAGTCGAGTCACCATTTCAAAGACACGTCCAAGAACCAAGTTCTTCTCGAACTGGAAT 313
DB	254 AGACAGACTCACACCTCCAGGACACCTCCAGAAAGCCAGGTGGTCTTAAGCTTGACCA 313
QY	314 CTGTGACCGACGGGACACGGCCGTCTATTACTGTGCGAGAGGCCCTCGCCCTGATTGCA 373
DB	314 ACGTGGACCTGTGTGACACAGCCACATATTACTGTGTC---ACGGGTAGGACTGTATGACA 370
QY	374 CAACCATTTGTTATGGCGGTGGGTGATGCTGTGGGCGCGGAGACCTGCTCACCGTCT 433
DB	371 TCAATGCTTATTACCTATACTACTGTGATTTTGGGGGAGGGAACCTTGTCAACGTCT 430
QY	434 CCTCAGCTAGCACCAAGGGGCCATCTCGTCTTCCCTCTGGCACCTCTCTCCAAGAGCACCT 493
DB	431 CCTCAGCTAGCACCAAGGGGCCATCGTCTTCCCTCTGGCACCTCTCTCCAAGAGCACCT 490
QY	494 CTGGGGGACAGGGCCCTGGGTGCTGTGTAAGGACTACTTCCCGCAACCGGTGACGG 553
DB	491 CTGGGGGACAGGGCCCTGGGTGCTGTGTAAGGACTACTTCCCGCAACCGGTGACGG 550
QY	554 TGTCGTGGAACTCAGGCGCCTGACAGCGCGCTGACACCTTCCCGGTGCTCTACAGT 613
DB	551 TGTCTGGAACTCAGGCGCCTGACAGCGCGCTGACACCTTCCCGGTGCTCTACAGT 610
QY	614 CCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCC 673
DB	611 CCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCC 670
QY	674 AGACTCATCTGCAACGTGAATCAGAAGCCCAAGCAACCAAGGTGGACAAGAAAGCAG 733
DB	671 AGACTCATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGGACAAGAAAGCAG 730
QY	734 AGCCCAATCTTGTGCAAAACTCACATGTGCCACCGTCCCGACCACTGAACTCCTGG 793
DB	731 AGCCCAATCTTGTGCAAAACTCACATGTGCCACCGTCCCGACCACTGAACTCCTGG 790
QY	794 GGGGACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCTCATGATCTCCCGGA 853
DB	791 GGGGACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCTCATGATCTCCCGGA 850
QY	854 CCCCTGAGGTCAATGCGTGGTGGAGTGAAGCCACGAAGACCTTGAGGTCAAGTTCA 913
DB	851 CCCCTGAGGTCAATGCGTGGTGGAGTGAAGCCACGAAGACCTTGAGGTCAAGTTCA 910
QY	914 ACTGTCAGTGGACGGGTGGAGTGCATTAATGCCAAGACAAAGCCCGGAGGACAGT 973
DB	911 ACTGTCAGTGGACGGGTGGAGTGCATTAATGCCAAGACAAAGCCCGGAGGACAGT 970

```
QY 974 ACAACAGCAGTACCGTGTGGTCAGCGTCTCACCCTCTGCAACGAGGACTGGCTGAATG 1033
Db 971 ACAACAGCAGTACCGTGTGGTCAGCGTCTCACCCTCTGCAACGAGGACTGGCTGAATG 1030
QY 1034 GCNAGAGTACNAGTCCNAGGTTCCNAAANAGCCCTCCAGCCCCCATCGAGAAAACCA 1093
Db 1031 GCAAGAGTACNAGTCCNAGGTTCCNAAANAGCCCTCCAGCCCCCATCGAGAAAACCA 1090
QY 1094 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCCCTGCCCCCATCCCGGG 1153
Db 1091 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCCCTGCCCCCATCCCGGG 1150
QY 1154 ATGAGCTGACCAAGAACCAAGTTCAGCTTGACCTGGTCAAGGGCTTCTATCCAGCG 1213
Db 1151 ATGAGCTGACCAAGAACCAAGTTCAGCTTGACCTGGTCAAGGGCTTCTATCCAGCG 1210
QY 1214 ACATCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAAGCCTC 1273
Db 1211 ACATCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAAGCCTC 1270
QY 1274 CCGTGTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAAGACA 1333
Db 1271 CCGTGTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAAGACA 1330
QY 1334 GGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATGATGAGGCTCTGCACAAACCACT 1393
Db 1331 GGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATGATGAGGCTCTGCACAAACCACT 1390
QY 1394 ACACGAGAAAGCCCTCTCCCTGTCTCCGGGTAATGA 1431
Db 1391 ACACGAGAAAGCCCTCTCCCTGTCTCCGGGTAATGA 1428
```

Search completed: April 5, 2003, 20:19:18
Job time : 396.719 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:54 ; Search time 2723.68 Seconds
(without alignments)
8508.978 Million cell updates/sec

Title: US-09-758-173-3

Perfect score: 1431

Sequence: 1 ATGAACACCTGTGCTTCTT.....CCCTGTCTCCGGTAATGA 1431

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estcom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_othr:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	902	63.0	1020	14	BQ062878
2	864	60.4	947	14	BQ0709771
3	850.4	59.4	958	14	BQ0706140
4	842.4	58.9	926	12	BG755166
5	831.2	58.1	901	13	BM007892
6	830.4	58.0	988	14	BQ0708857

7	824.4	57.6	1029	14	BQ0631185
8	822.8	57.5	887	14	BQ711255
9	822.2	57.5	918	14	BQ708022
10	815.2	57.0	995	14	BM914540
11	808.8	56.5	881	14	BQ711291
12	800.2	55.9	1031	14	BQ064886
13	797.4	55.7	936	14	BQ711727
14	796	55.6	940	14	BQ705928
15	787.4	55.0	977	14	BQ710532
16	786.4	55.0	980	14	BM914504
17	785.2	54.9	843	13	BM007897
18	778.8	54.4	991	14	BQ708936
19	777.2	54.3	973	14	BQ706204
20	772.6	54.0	930	13	BM007597
21	770.6	53.9	981	14	BM914528
22	764.6	53.4	926	14	BQ710304
23	764.2	53.4	917	14	BQ708169
24	759.4	53.1	961	14	BQ710233
25	756.6	52.9	945	14	BQ712403
26	752.4	52.6	1012	14	BM914556
27	750.4	52.4	783	13	BM007838
28	750.2	52.4	895	14	BQ708303
29	748	52.3	1026	14	BM914288
30	741.4	51.8	914	14	BQ712363
31	738	51.6	913	14	BQ707472
32	733.8	51.3	944	14	BQ712397
33	733.6	51.3	919	14	BQ709339
34	732.8	51.2	936	14	BQ707530
35	732.6	51.2	906	14	BQ711709
36	731.8	51.1	1014	14	BM914505
37	730.4	51.0	973	14	BQ708902
38	729.6	51.0	888	12	BG757604
39	728.8	50.9	941	14	BQ712021
40	728.6	50.9	925	14	BQ709853
41	728.4	50.9	991	14	BQ707621
42	727.6	50.8	855	13	BM007689
43	726.8	50.8	870	12	BG757815
44	726.2	50.7	925	14	BQ709152
45	725.8	50.7	923	14	BQ881523

ALIGNMENTS

RESULT 1
BQ062878
LOCUS
DEFINITION BQ062878 1020 bp mRNA linear EST 02-APR-2002
AGENCY AGENCOURT 6826949 NIH_MGC_99 Homo sapiens cdna clone IMAGE:5924420
5' mRNA sequence.
ACCESSION BQ062878
VERSION BQ062878.1 GI:19890085
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1020)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2094 row: h column: 21
High quality sequence start: 21
High quality sequence stop: 681.
Location/Qualifiers

```

source
1. 1020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5924420"
/clone_lib="NIH MGC 99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 239 a 344 c 269 g 166 t 2 others
ORIGIN
Query Match 63.0%; Score 902; DB 14; Length 1020;
Best Local Similarity 98.0%; Pred. No. 1.1e-204;
Matches 923; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

QY 489 CACCTCTGGGGGACAGCGGCTGGGCTGCTGCTCAAGGACTACTTCCCGGAACCGGT 548
DB 36 CACCTCTGGGGGACAGCGGCTGGGCTGCTGCTCAAGGACTACTTCCCGGAACCGGT 95
QY 549 GACGCTGTGTGGAACTCAGCGGCTGTGACAGCGGCTGTGACACCTTCCCGGCTGTCT 608
DB 96 GACGCTGTGTGGAACTCAGCGGCTGTGACAGCGGCTGTGACACCTTCCCGGCTGTCT 155
QY 609 ACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGTGTGACCGTGGCTTCCAGCAGCTTGGG 668
DB 156 ACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGTGTGACCGTGGCTTCCAGCAGCTTGGG 215
QY 669 CACCCAGACCTTACATCTGTGAACGTGAATCAAGCCAGCAGCAACCAAGGTGGACAAGAA 728
DB 216 CACCCAGACCTTACATCTGTGAACGTGAATCAAGCCAGCAGCAACCAAGGTGGACAAGAA 275
QY 729 AGCAGAGCCCAAAATCTTGTGACAAAATCTACACATGCTGCGTGGCCAGCAGCTGAATCT 788
DB 276 AGTTGAGCCCAAAATCTTGTGACAAAATCTACACATGCTGCGTGGCCAGCAGCTGAATCT 335
QY 789 CTGGGGGACCGTCAGTCTTCTTCTTCCCGGCAAAACCCAGGACACCTCATGATCTC 848
DB 336 CTGGGGGACCGTCAGTCTTCTTCTTCCCGGCAAAACCCAGGACACCTCATGATCTC 395
QY 849 CCGGACCCCTGAGGTCAATGCGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 908
DB 396 CCGGACCCCTGAGGTCAATGCGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 455
QY 909 GTTCAACTGTGTACGTGACCGGTGGAGGTGCTATATGCAAGACAAAGCCCGGGAGGA 968
DB 456 GTTCAACTGTGTACGTGACCGGTGGAGGTGCTATATGCAAGACAAAGCCCGGGAGGA 515
QY 969 GCAGTCAACAGCAGTACCGTGTGTGTGTCAGCGTCTTCCCGTCTGACACAGGACTGGCT 1028
DB 516 GCAGTCAACAGCAGTACCGTGTGTGTGTCAGCGTCTTCCCGTCTGACACAGGACTGGCT 575
QY 1029 GAATGGCAAGGAGTACAGGTGCAAGTCTTCCACAAAGCCCTCCAGCCCGCCATCGA 1088
DB 576 GAATGGCAAGGAGTACAGGTGCAAGTCTTCCACAAAGCCCTCCAGCCCGCCATCGA 635
QY 1089 AACCATCTTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTATACCTCTCCCGCCATC 1148
DB 635 AACCATCTTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTATACCTCTCCCGCCATC 695
QY 1149 CCGGATGAGCTGACCAAGAACAGGTGACGCTGCTGCTGGTCAAGGCTTCTATCC 1208
DB 696 CCGGATGAGCTGACCAAGAACAGGTGACGCTGCTGCTGGTCAAGGCTTCTATCC 755
QY 1209 CAGCGACATCCCGCTGGAGTGGGAGGCAATGGGCGAGCCGGA--GAACAACTACAAGACC 1266

```

```

DB 756 CAGCGACATCGCGCTGGAGTGGGAGAGCAATGGGACGCGGAGAACTACTACTAGACC 815
QY 1267 AGCCTCTCCGCTCGGACTCCGACGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1326
DB 816 AGCCTCTCCGCTCGGACTCCGACGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 875
QY 1327 AAGAGCAGGTGGCAGCAGCGGAAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1386
DB 876 CAGAGCAGGTGGCAGCAGCGGAAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 935
QY 1387 AACCACTACACGACGAGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1428
DB 936 AACCACTACACGACGAGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 977

RESULT 2
BO709771 BO709771 947 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
DEFINITION 5', mRNA sequence.
ACCESSION BO709771
VERSION BO709771.1 GI:21848670
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 947)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2466 row: m column: 16
High quality sequence start: 3
High quality sequence stop: 675.
Location/Qualifiers
1. 947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6278583"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 225 a 320 c 252 g 150 t
ORIGIN
Query Match 60.4%; Score 864; DB 14; Length 947;
Best Local Similarity 99.4%; Pred. No. 1.2e-195;
Matches 867; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 560 GGAATCTAGCGCCCTGACAGCGGCTGACACCTTCCCGGCTGTCTTACAGTCTCTCAG 619
DB 9 GGAATCTAGCGCCCTGACAGCGGCTGACACCTTCCCGGCTGTCTTACAGTCTCTCAG 68
QY 620 GACTCTACTCTTCTAGCAGCGTGTGACCGTGGCTTCCAGCAGCTTGGGACCCAGACCT 679
DB 69 GACTCTACTCTTCTAGCAGCGTGTGACCGTGGCTTCCAGCAGCTTGGGACCCAGACCT 128

```

QY 680 ACATCTGCAACGCTGAATCACAAAGCCAGCAACACCAAGGTGGACAGAAAGAGAGCCCA 739
 |||||
 Db 129 ACATCTGCAACGCTGAATCACAAAGCCAGCAACACCAAGGTGGACAGAAAGGTGGACCA 188
 |||||
 QY 740 AATCTTTGTGACAAAACCTCACACATGCCCCCAGCGTCCAGCACCTGAACTCTCTGGGGGAC 799
 |||||
 Db 189 AATCTTTGTGACAAAACCTCACACATGCCCCCAGCGTCCAGCACCTGAACTCTCTGGGGGAC 248
 |||||
 QY 800 CGTGAGTCTTCTCTTCTCCCGCAAAACCAAGAGACACCTCATGATCTCCCGGACCCCTG 859
 |||||
 Db 249 CGTGAGTCTTCTCTTCTCCCGCAAAACCAAGAGACACCTCATGATCTCCCGGACCCCTG 308
 |||||
 QY 860 AGGTCAATGCTGCTGCTGAGCTGAGCACAGAGACCTTGAGGTCAAGTTCAACTGCT 919
 |||||
 Db 309 AGGTCAATGCTGCTGCTGAGCTGAGCACAGAGACCTTGAGGTCAAGTTCAACTGCT 368
 |||||
 QY 920 AGTGGACGGCTGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAA 979
 |||||
 Db 369 AGTGGACGGCTGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAA 428
 |||||
 QY 980 GCACGTACCGTGTGCTGAGCTCTCACCGTCTGACACAGGACTGCTGAATGGCAAG 1039
 |||||
 Db 429 GCACGTACCGTGTGCTGAGCTCTCACCGTCTGACACAGGACTGCTGAATGGCAAG 488
 |||||
 QY 1040 AGTCAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCCGCCATCGAGAAACCATCTCCA 1099
 |||||
 Db 489 AGTCAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCCGCCATCGAGAAACCATCTCCA 548
 |||||
 QY 1100 AAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGC 1159
 |||||
 Db 549 AAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGC 608
 |||||
 QY 1160 TGACCAAGAACACAGGTGACCTGCTGCTGCTCAAGAGCTTCTATCCAGCGACATCG 1219
 |||||
 Db 609 TGACCAAGAACACAGGTGACCTGCTGCTGCTCAAGAGCTTCTATCCAGCGACATCG 668
 |||||
 QY 1220 CCGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACAACTACAAGACAGCTCCCGTGC 1279
 |||||
 Db 669 CCGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACAACTACAAGACAGCTCCCGTGC 728
 |||||
 QY 1280 TGGACTCCGAGCGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGAGAGTGC 1339
 |||||
 Db 729 TGGACTCCGAGCGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGAGAGAGAGAGTGC 788
 |||||
 QY 1340 AGCAGGGAAAGCTTCTTCATGCTCCGTGATGATGAGGTCTTGCAACACCACTACAGC 1399
 |||||
 Db 789 AGCAGGGAAAGCTTCTTCATGCTCCGTGATGATGAGGTCTTGCAACCACTACAGC 848
 |||||
 QY 1400 AGAAGAGCTCTCCCTGCTCTCCGGTAAATGA 1431
 |||||
 Db 849 AGAAGAGCTCTCCCTGCTCTCCGGTAAATGA 880
 |||||

RESULT 3
 BQ706140
 LOCUS BQ706140 958 bp mRNA linear EST 16-JUL-2002
 DEFINITION AGENCOURT 8352177 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277512
 5' mRNA sequence.

ACCESSION BQ706140
 VERSION BQ706140.1 GI:21845039
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 958)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbe-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLC2464 row: a column: 01
 High quality sequence stop: 705.

FEATURES

source
 1..958
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6277512"
 /clone_lib="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

BASE COUNT 229 a 319 c 256 g 150 t 4 others
 ORIGIN

Query Match 59.4%; Score 850.4; DB 14; Length 958;
 Best Local Similarity 99.2%; Pred. No. 2.2e-192;

Matches 865; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 558 GTGGAATCAGCGCGCTGACAGCGGCTGCACACCTTCCCGCTGCTCTACAGTCTC 617
 |||||

Db 11 GTGGAATCAGCGCGCTGACAGCGGCTGCACACCTTCCCGCTGCTCTACAGTCTC 70
 |||||

QY 618 AGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGCACCAGAC 677
 |||||

Db 71 AGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGCACCAGAC 130
 |||||

QY 678 CTATCTCTCAACGCTGAATCAAGCCAGCAACCAAGGTGGACAAAGAGCAGAGCC 737
 |||||

Db 131 CTATCTCTCAACGCTGAATCAAGCCAGCAACCAAGGTGGACAAAGAGTGGAGCC 190
 |||||

QY 738 CAAATCTGTGACAAAACCTCACATGCCACCGTCCAGCAGCTTCTCTGGGGG 797
 |||||

Db 191 CAAATCTGTGACAAAACCTCACATGCCACCGTCCAGCAGCTTCTCTGGGGG 250
 |||||

QY 798 ACCGTGAGTCTTCTCTTCTCCCGCCAAAGACACCTCATGATCTCCCGGACCCC 857
 |||||

Db 251 ACCGTGAGTCTTCTCTTCTCCCGCCAAAGACACCTCATGATCTCCCGGACCCC 310
 |||||

QY 858 TGAGGTCAATCGTGTGTGGAGTGGAGCCAGAGACCCCTGAGGTCAAGTTCAACTG 917
 |||||

Db 311 TGAGGTCAATCGTGTGTGGAGTGGAGCCAGAGACCCCTGAGGTCAAGTTCAACTG 370
 |||||

QY 918 GTACGTGAGCGCTGGAGGTGCATAATGCCAAGACCAAGCCCGGAGGAGCAGTACAA 977
 |||||

Db 371 GTACGTGAGCGCTGGAGGTGCATAATGCCAAGACCAAGCCCGGAGGAGCAGTACAA 430
 |||||

QY 978 CAGCAGTACCGTGTGGTCAAGCTCTCACCGTCTGCACAGGACTGGGTGAATGGCAA 1037
 |||||

Db 431 CAGCAGTACCGTGTGGTCAAGCTCTCACCGTCTGCACAGGACTGGGTGAATGGCAA 490
 |||||

QY 1038 GGAGTACAGTGCAGAGGTCTCCACAGCCCTCCAGCCCGCCATCGAGAAACCATCTC 1097
 |||||

Db 491 GGAGTACAGTGCAGAGGTCTCCACAGCCCTCCAGCCCGCCATCGAGAAACCATCTC 550
 |||||

QY 1098 CAAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTTCCCGGATGTA 1157
 |||||

Db 551 CAAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTTCCCGGATGTA 610
 |||||

QY 1158 GCTGACCAAGACAGGTGACCTGCTGGTCAAGAGGTCTTATCCAGGACAT 1217
 |||||

Db 611 GCTGACCAAGACAGGTGACCTGCTGGTCAAGAGGTCTTATCCAGGACAT 670
 |||||

QY 1218 CGCGTGGAGTGGAGCAATGGGAGCGGAGAACAACTACAGAACACCGCTCCCGT 1277
 |||||
 Db 671 CGCGTGGAGTGGAGCAATGGGAGCGGAGAACAACTACAGAACACCGCTCCCGT 730
 |||||
 QY 1278 GCTGGACTCGAGCGGTCTCTTCTTCTACAGAGCTCACCCTGGAGCAAGAGAGTG 1337
 |||||
 Db 731 GCTGGACTCGAGCGGTCTCTTCTTCTACAGAGCTCACCCTGGAGCAAGAGAGTG 790
 |||||
 QY 1338 GCAGAGGGGAAAGCTCTTCTCATGCTCCGTGATGATGAGGCTTCGCAACCACTACAC 1397
 |||||
 Db 791 GCAGAGGGGAAAGCTCTTCTCATGCTCCGTGATGATGAGGCTTCGCAACCACTACAC 850
 |||||
 QY 1398 GCAG-AGAGCCTCTCCCTGTCTCCGGGTAAA 1428
 |||||
 Db 851 ACAGAAAGAGCCTCTCCCTGTCTCCCGGTAA 882
 |||||

RESULT 4
 BG755166 926 bp mRNA linear EST 15-MAY-2001
 LOCUS 602711488F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852076 5',
 DEFINITION mRNA sequence.
 ACCESSION BG755166
 VERSION BG755166
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 926)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgapps-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCMI695 row: o column: 21
 High quality sequence stop: 888.
 Location/Qualifiers
 1..926
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4852076"
 /clone_lib="NIH_MGC_48"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 225 a 309 c 244 g 148 t
 ORIGIN

Query Match 58.9%; Score 842.4; DB 12; Length 926;
 Best Local Similarity 98.2%; Pred. No. 1.8e-190;
 Matches 852; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 564 CTACAGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTGTCCTACAGTCTCTCAGGACT 623
 |||||
 Db 2 CTACAGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTGTCCTACAGTCTCTCAGGACT 61
 |||||
 QY 624 CTACTCCCTCAGCAGCGGTGGTGCACCGTGCCTCCAGCAGCTTGGGCGACCCAGACCTACAT 693
 |||||

Db 62 CTACTCCCTCAGCAGCGGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACTCCAGCTACAT 121
 |||||
 QY 684 CTGCAACTGTGAATCACAAGCCCAAGCAACCAAGTGGAGCAAGAAAGCAGAGCCCAATC 743
 |||||
 Db 122 CTGCAACTGTGAATCACAAGCCCAAGCAACCAAGTGGAGCAAGAAAGTGTAGGCCCAATC 181
 |||||
 QY 744 TTGTGACAAAACTCACACATGCCACCGTGCACGACCTTCAATCTCTGGGGGAGCCGTC 803
 |||||
 Db 182 TTGTGACAAAACTCACACATGCCACCGTGCACGACCTTCAATCTCTGGGGGAGCCGTC 241
 |||||
 QY 804 AGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCGGACCTCTGAGT 863
 |||||
 Db 242 AGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCGGACCTCTGAGT 301
 |||||
 QY 864 CACATGCGTGTGGTGGAGCTGAGCCACGAGACCTTCAAGTTCAACTTGGTACGCT 923
 |||||
 Db 302 CACATGCGTGTGGTGGAGCTGAGCCACGAGACCTTCAAGTTCAACTTGGTACGCT 361
 |||||
 QY 924 GGACGCGTGGAGTGCATATGCAAGAACCAAGCCCGGGAGGAGCAGTACAAAGCAC 983
 |||||
 Db 362 GGACGCGTGGAGTGCATATGCAAGAACCAAGCCCGGGAGGAGCAGTACAAAGCAC 421
 |||||
 QY 984 GTACCGTGTGGTTCAGCGTCTCACCCTCTCTGACCAAGGACTGGCTGAATGGCAAGGAT 1043
 |||||
 Db 422 GTACCGTGTGGTTCAGCGTCTCACCCTCTCTGACCAAGGACTGGCTGAATGGCAAGGAT 481
 |||||
 QY 1044 CAAAGTGAAGTGTCCAAAGACCTTCCAGACCTTCCAGACCTTCCAGACCTTCCAAAGC 1103
 |||||
 Db 482 CAAAGTGAAGTGTCTCCAAAGACCTTCCAGACCTTCCAGACCTTCCAAAGC 541
 |||||
 QY 1104 CAAAGGCGAGCCCGGAGAACCAAGGTTACACCTCTCCCGGATGAGTGCAC 1163
 |||||
 Db 542 CAAAGGCGAGCCCGGAGAACCAAGGTTACACCTCTCCCGGATGAGTGCAC 601
 |||||
 QY 1164 CAAAGAACGCTGACGCTGACCTGCTCCCTGCTCAAAGGCTTCTATCCAGCAGCATCCCGCT 1223
 |||||
 Db 602 CAAAGAACGCTGACGCTGACCTGCTCCCTGCTCAAAGGCTTCTATCCAGCAGCATCCCGCT 661
 |||||
 QY 1224 GGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAAGACCAAGCTTCCCTGCTGGA 1283
 |||||
 Db 662 GGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAAGACCAAGCTTCCCTGCTGGA 721
 |||||
 QY 1284 CTCGACCGCTCTCTTCTCTTCTCTACAGAGCTCACCGTGGAGCAAGAGTGGGAGCA 1343
 |||||
 Db 722 CTCGACCGCTCTCTTCTCTTCTCTACAGAGCTCACCGTGGAGCAAGAGTGGGAGCA 781
 |||||
 QY 1344 GGGGAAACGCTTCTCTCATGCTCCGCTGATGATGAGGCTCTGCACACCACTACACGAGAA 1403
 |||||
 Db 782 GGGGAAACGCTTCTCTCATGCTCCGCTGATGATGAGGCTCTGCACACCACTTACACGAGAA 841
 |||||
 QY 1404 GAGCCTCTCTCTGCTCTCCGGGTAAATGA 1431
 |||||
 Db 842 AAAGCCTCTCTCTCTCCGGGTAAATGA 869
 |||||

RESULT 5
 BM007892 901 bp mRNA linear EST 30-OCT-2001
 LOCUS 603617577F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450611 5',
 DEFINITION mRNA sequence.
 ACCESSION BM007892
 VERSION BM007892
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 901)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: j column: 20
High quality sequence stop: 834.
Location/Qualifiers

FEATURES

source
1. 901
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5450611"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 209 a 315 c 234 g 143 t
ORIGIN

Query Match 58.1%; Score 831.2; DB 13; Length 901;
Best Local Similarity 97.7%; Pred. No. 8.3e-188;
Matches 864; Conservative 0; Mismatches 18; Indels 2; Gaps 2;
QY 408 GGGCCCGGAGACTGTGTCACCGTCTCTCAGCTAGCAGCAAGGCGCCATCGGTCTTCCC 467
Db 19 GGGCCGAGAACCTGTGTACCGTCTCTCAGCTCTCCACCAAGGCGCCATCGGTCTTCCC 78
QY 468 CTTGSCACCTCTCCAGAGACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGTGTCAA 527
Db 79 CTTGSCACCTCTCTCAAGAGACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGTGTCAA 138
QY 528 GGACTACTTCCCGAACCGGTGAGCGTCTCTGGAACCTCAGCGCCCTGACGAGCGCGT 587
Db 139 GGACTACTTCCCGAACCGGTGAGCGTCTCTGGAACCTCAGCGCCCTGACGAGCGCGT 198
QY 588 GCACACTTCCCGGTGTCCTACAGTCTCTCAGACTCTACTCTCTCAGCAGCGGTGTGAC 647
Db 199 GCACACTTCCCGGTGTCCTACAGTCTCTCAGACTCTACTCTCTCAGCAGCGGTGTGAC 258
QY 648 GTGCGCTTCCAGAGCTTGGCACCAGCTTACCTGCAACCTGATCACAAGCCAG 707
Db 259 GTGCGCTTCCAGAGCTTGGGACCCAGACCTACCTGCAACCTGATCACAAGCCAG 318
QY 708 CAACACCAAGGTGGACAAGAACGAGAGCCCAAAATCTTGTGACAAAACCTCACACATGCC 767
Db 319 CAACACCAAGGTGGACAAGAACGAGAGCCCAAAATCTTGTGACAAAACCTCACACATGCC 378
QY 768 ACCGTGCCAGACCTGAACTCTTGGGGGACCGTCACTCTTCTTCTTCCCGCAAAAC 827
Db 379 ACCGTGCCAGACCTGAACTCTTGGGGGACCGTCACTCTTCTTCTTCCCGCAAAAC 438
QY 828 CAAGGACACCTCATGATCTCCCGGACCCCTGAGTCCACATCGTGTGTGTGACGTGAG 887
Db 439 CAAGGACACCTCATGATCTCCCGGACCCCTGAGTCCACATCGTGTGTGTGACGTGAG 498
QY 888 CCACGAAGACCTTGAGGTCAAGTTCAACTGTGACGTGGAGCGGTGGAGTGCATATGC 947
Db 499 CCACGAAGACCTTGAGGTCAAGTTCAACTGTGACGTGGAGCGGTGGAGTGCATATGC 558
QY 948 CAAGCAAGCCGCGGGAGGAGAGTCAACAGCACCTGACCGTGTGTGTGACGTCTCAC 1007
Db 559 CAAGCAAGCCGCGGGAGGAGAGTCAACAGCACCTGACCGTGTGTGTGACGTCTCAC 618
QY 1008 CGTCTGCACCAAGGACTGGCTGAATGGCAGGAGTCAAGTGCAGAGTCTTCCAAAGAGC 1067

Db 619 CGTCTGCACCAAGGACTGGCTGAATGGCAGGAGTACAAGTCAAGGTCTTCCAAAGC 678
QY 1068 CTTCCAGCCCGCCCATCGAGAAAACCATCTCCAAAGCAAGGCGCAGCCCGGAGAACACA 1127
Db 679 CTTCCAGCCCGCCCATCGAGAAAACCATCTCCAAAGCC-AAGGGCAGCCCGGAGAACACA 737
QY 1128 GGTGTACACCTGCTCCCGGATCCCGGATGAGTGCACCAAGAACCAAGTCTGACCTG 1187
Db 738 GGTGTACACCTGCTCCCGGATCCCGGATGAGTGCACCAAGAACCAAGTCTGACCTG 797
QY 1188 CTTGTCAAAGGCTTCTATCCAGCGACATCG-CCGTGGAGTGGGAGACAATGGGCGC 1246
Db 798 CTTGTCAAAGGCTTCTATCCAGCGACATCGCCCGTGGAGTGGGAGACATCCCGGCGC 857
QY 1247 CGGAGAACCACTACAGAGCACCGCTCCCGTGTGACTCCGAC 1290
Db 858 CGGAGAACCACTACAGAGCACCGCTCCCGTGTGACTCCGAC 901
RESULT 6
LOCUS B0708857
DEFINITION B0708857 988 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8352194 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277561
5', mRNA sequence.
ACCESSION B0708857
VERSION B0708857.1 GI:21847756
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 988)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: c column: 02
High quality sequence stop: 716.
Location/Qualifiers
1. 988
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277561"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 230 a 338 c 258 g 162 t
ORIGIN
Query Match 58.0%; Score 830.4; DB 14; Length 988;
Best Local Similarity 94.6%; Pred. No. 1.3e-187;
Matches 904; Conservative 0; Mismatches 46; Indels 6; Gaps 4;
QY 393 CTGGGTTCGATGTCGGGCGCGGAGACCTGTCAACCGTCTCTCAGCTAGCACCAGG 452
Db 5 CTACTTTGACTCTGGGCGGAGAACCTGTGTCAACCGTCTCTCTCGGCTTCCACCAAGG 64

```
QY 453 CCCATCGGTCTTCCCTGCGACCTCTCCCAAGAGACACTCTGCGGGGCACAGCGGCCCT 512
Db 65 CCCATCGGTCTTCCCTGCGACCTCTCTCAAGAGACACTCTGCGGGGCACAGCGGCCCT 124
QY 513 GGCTCGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGGTGTGTGAACTCAGGCGC 572
Db 125 GGCTCGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGGTGTGTGAACTCAGGCGC 184
QY 573 CTTGACAGCGGGGTGACACCTTCCGGGTGTCCTACAGTCTCAGGACTCTACTCCCT 632
Db 185 CTTGACAGCGGGGTGACACCTTCCGGGTGTCCTACAGTCTCAGGACTCTACTCCCT 244
QY 633 CAGCAGCGTGGTCAAGCGCTCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGT 692
Db 245 CAGCAGCGTGGTCAAGCGCTCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGT 304
QY 693 GAATCAACAGCCAGCAACACCAAGGTGGAAGAAAGAGAGACCCCAATCTGTGACAA 752
Db 305 GAATCAACAGCCAGCAACACCAAGGTGGAAGAAAGTGTGAGCCCAATCTGTGACAA 364
QY 753 AACTCACAGATGCCACCGCTGCCAGCAGCTGAATCTCTGGGGGACCGTCACTCTTCT 812
Db 365 AACTCACAGATGCCACCGCTGCCAGCAGCTGAATCTCTGGGGGACCGTCACTCTTCT 424
QY 813 CTTCCCCCAAAACCCCAAGGACACCTCTCATGATCTCCCGACCCCTGAGGTCAACATGCT 872
Db 425 CTTCCCCCAAAACCCCAAGGACACCTCTCATGATCTCCCGACCCCTGAGGTCAACATGCT 484
QY 873 GGTGGTGGAGCGTGAGCACAAGAACCCCTGAGGTCAAGTTCATCTGGTACGTGGACGGCT 932
Db 485 GGTGGTGGAGCGTGAGCACAAGAACCCCTGAGGTCAAGTTCATCTGGTACGTGGACGGCT 544
QY 933 GGAGGTGCATTAATGCCAAGAACCGCGGGAGGAGCAGTCAACAGCAGCTGACCGTGT 992
Db 545 GGAGGTGCATTAATGCCAAGAACCGCGGGAGGAGCAGTCAACAGCAGCTGACCGTGT 604
QY 993 GGTGAGCGTCTCTCACCCTCTCCAGCAGGACTGGCTGAATGGCAAGGAGTACAAAGTGC 1052
Db 605 GGTGAGCGTCTCTCACCCTCTCCAGCAGGACTGGCTGAATGGCAAGGAGTACAAAGTGC 664
QY 1053 GGTCTCAAAACAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCA 1112
Db 665 GGTCTCAAAACAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCA 724
QY 1113 GCCCGGAGAACACAGGTGTACACCTGCCCTCCATCCGGGATGAGTCAACAGAAACCA 1172
Db 725 GCCCGGAGAACACAGGTGTACACCTGCCCTCCATCCGGGATGAGTCAACAGAAACCA 783
QY 1173 GGTGAGCGTCACTGCTGCTCAAGGCTTTCTATCCAGCGACATCGCCGTGAGTGGGA 1232
Db 784 GGTGAGCGTCACTGCTGCTCAAGGCTTTCTATCCAGCGACATCGCCGTGAGTGGGA 843
QY 1233 GAGCAATGGGAG-CGGAGAAACAACTCAAGACCAACCGCTCCCGTG-CTGAGTCCG 1288
Db 844 GAGCAATGGGAGCCGGAGAAACAACTCAAGACCAACCGCTCCCGTGCTGGAATCCG 903
QY 1289 ACGGC-TCCTTTCTTCTTACAGCAAGCTACCGTGACAAAGAGCAGGTGGCAGCA 1343
Db 904 ACGGTTCTTCTTCTTCTTACAGAAAGCTCCCGGGGGAACAAAGCAGGTGGCA 959
```

```
RESULT 7
B0063185
LOCUS B0063185
DEFINITION AGENCOURT_6876667 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924769
5', mRNA sequence.
ACCESSION B0063185
VERSION B0063185.1 GI:19890681
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1029)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2095 row: g column: 10
High quality sequence stop: 723.

FEATURES

source

1..1029
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5924769"
/clone_lib="NIH MGC 99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 237 a 350 c 276 g 165 t 1 others
ORIGIN

Query Match 57.68; Score 824.4; DB 14; Length 1029;

Best Local Similarity 99.08; Pred. No. 3; 7e-186;

Matches 861; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

```
QY 483 CAAGAGACCTCTGCGGGGCACAGCGGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCCGA 542
Db 4 CCAGAGACCTCTGCGGGGCACAGCGGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCCGA 63
QY 543 ACCGGTGAAGTGTGTGGAACTCAGCGGCCCTGACAGCGGGGTGACACCTTCCCGGC 602
Db 64 ACCGGTGAAGTGTGTGGAACTCAGCGGCCCTGACAGCGGGGTGACACCTTCCCGGC 123
QY 603 TGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAG 662
Db 124 TGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAG 183
QY 663 CTTGGGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGGA 722
Db 184 CTTGGGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGGA 243
QY 723 CAAGAAAGCAGAGCCCAAACTCTGTGACAAAACCTACACATGCCCGCCCGTCCAGCACC 782
Db 244 CAAGAAAGTGAAGCCCAAACTCTGTGACAAAACCTACACATGCCCGCCCGTCCAGCACC 303
QY 783 TGAATCTCTGGGGGACCGTCACTCTTCTTCCCCCAAAACCCCAAGGACACCTCAT 842
Db 304 TGAATCTCTGGGGGACCGTCACTCTTCTTCCCCCAAAACCCCAAGGACACCTCAT 363
QY 843 GATCTCCCGGACCCCTGAGGTCACTGCGTGGTGGAGCGTGAAGCCACGAAGACCTTGA 902
Db 364 GATCTCCCGGACCCCTGAGGTCACTGCGTGGTGGAGCGTGAAGCCACGAAGACCTTGA 423
QY 903 GGTCAAGTTCAACTGTTAGTGGAGCGGTGGAGTGCATTAATGCCAAGCAAAAGCCCGC 962
Db 424 GGTCAAGTTCAACTGTTAGTGGAGCGGTGGAGTGCATTAATGCCAAGCAAAAGCCCGC 483
QY 963 GGAGGAGCAGTACAAACAGCAGCAGTACCGTGTGTGCTGAGCGTCTCAGCGTCTGCAACGGA 1022
```


ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 918)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2469 row: i column: 20
 High quality sequence stop: 667.
 Location/Qualifiers
 1. 918
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6279643"
 /clone_lib="NIH MGC 113"
 /lab_hosts="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC Library."
 BASE COUNT 208 a _316 c 245 g 147 t 2 others
 ORIGIN
 Query Match 57.5%; Score 822.2; DB 14; Length 918;
 Best Local Similarity 95.4%; Pred. No. 1.2e-185;
 Matches 867; Conservative 0; Mismatches 40; Indels 2; Gaps 2;
 QY 398 TCGATGTCGGGGCCGGGAGACCTGGTCCACCGTCTCTCAGCTAGCACCAAGGGCCCAT 457
 Db 1 TTGACCGTGGGGCAGGAGACGTGGTCCACCGTCTCTCAGCTCCACCAAGGGCCCAT 60
 QY 458 CGGTCTTCCCTTGCACCTCTCCAGAGACCTCTGGGGGACAGCGCCCTGGGGCT 517
 Db 61 CGGTCTTCCCTTGCACCTCTCCAGAGACCTCTGGGGGACAGCGCCCTGGGGCT 120
 QY 518 GCCTGGTCAAGGACTACTTCCCGAAGCGGTGACGGTGTCTGGAACTCAGGCGCCCTGA 577
 Db 121 GCCTGGTCAAGGACTACTTCCCGAAGCGGTGACGGTGTCTGGAACTCAGGCGCCCTGA 180
 QY 578 CCAGGGCGGTGCACACTTCCGGGTGTCTACAGTCTCAGACTCTACTCTCCAGCA 637
 Db 181 CCAGGGCGGTGCACACTTCCGGGTGTCTACAGTCTCAGACTCTACTCTCCAGCA 240
 QY 638 GCGTGGTCAAGGACTACTTCCCGAAGCGGTGACGGTGTCTGGAACTCAGGCGCCCTGA 697
 Db 241 GCGTGGTCAAGGACTACTTCCCGAAGCGGTGACGGTGTCTGGAACTCAGGCGCCCTGA 300
 QY 698 ACAAGCCAGCAGCAGCAGGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 757
 Db 301 ACAAGCCAGCAGCAGCAGGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 758 ACACATGCCCGTCCCGAGCAGCAGTGAATCTCTGGGGGACCGGTGAGTCTTCTCTCC 817
 Db 361 ACACATGCCCGTCCCGAGCAGCAGTGAATCTCTGGGGGACCGGTGAGTCTTCTCTCC 420
 QY 818 CCCAAAACCCAGGACACCTCATGATCTCCGGACCCCTGAGTGCATGCGGTGG 877
 Db 421 CCCAAAACCCAGGACACCTCATGATCTCCGGACCCCTGAGTGCATGCGGTGG 480
 QY 878 TGGACGTAGCCAGGAGACCCCTGAGGTCAAGTTCACTGGTACGTGGAGCGGTGGAGG 937

Db 481 TGACGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTGGAGCGGTGGAGG 540
 QY 938 TGCATATCCCAAGACAAAGCCGGGAGGAGCAGTACAAACAGCACGTCACGTGTGTGTC 997
 Db 541 TGCATATCCCAAGACAAAGCCGGGAGGAGCAGTACAAACAGCACGTCACGTGTGTGTC 600
 QY 998 GGTCTCTACCTCTCTGACACAGGACCTGGCTGAATGCGAGGAGTCAAGTGAAGGTCT 1057
 Db 601 GGTCTCTACCTCTCTGACACAGGACCTGGCTGAATGCGAGGAGTCAAGTGAAGGTCT 660
 QY 1058 CCAACAAAGCCCTCCAGCCCTCCATCGAGAAACATCTCCAAAGCCAAAGGGCAGCCCC 1117
 Db 661 CCAACAAAGCCCTCCAGCCCTCCATCGAGAAACATCTCCAAAGCCAAAGGGCAGCCCC 720
 QY 1118 GAGAACACAGGTGTACACCTCCGCCCCATCCGGGATGAGCTGACCAAGAACCCAGGTCA 1177
 Db 721 GAGAACACAGGTGTACACCTCCGCCCCATCCGGGATGAGCTGACCAAGAACCCAGGTCA 780
 QY 1178 GCTGACCTGCTGTCAAAAGCTTCTATCCAGCGACATCGCCGT-GGAGTGGGAGAGC 1236
 Db 781 GCTGACCTGCTGTCAAAAGCTTCTATCCAGCGACATCNCNGNGGAGTGGGAGAGC 840
 QY 1237 AATGGGACG-CCGGAGAACAACTACAAGACCAACGCTCCCGTGTGACTCCGACGGCTC 1295
 Db 841 AATGGGACG-CCGGAGAACAACTACAAGACCAACGCTCCCGTGTGACTCCGACGGCTC 900
 QY 1296 TTCTTTCT 1304
 Db 901 GTCTTTCT 909
 RESULT 10
 LOCUS BM914540 995 bp mRNA linear EST 12-MAR-2002
 DEFINITION AGENCOURT_6615506 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480223
 5', mRNA sequence.
 ACCESSION BM914540
 VERSION BM914540.1 GI:19364919
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 995)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2002 row: 1 column: 16
 High quality sequence stop: 718.
 Location/Qualifiers
 1. 995
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5480223"
 /clone_lib="NIH MGC 113"
 /lab_hosts="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a

FEATURES
 source

BASE COUNT 241 a 330 c 259 g 165 t
ORIGIN

Query Match 57.0%; Score 815.2; DB 14; Length 995;
Best Local Similarity 96.1%; Pred. No. 5.7e-184;
Matches 857; Conservative 0; Mismatches 33; Indels 2; Gaps 2;

QY 393 CTGGGTGATGTCCTGGGGCCGGAGACTGGTCAACGCTCTCTCAGCTAGCACCAAGG 452
Db 6 CTACTTTGAGATTGGGGCCAGGAACGCTGGTCAACGCTCTCTCAGCTCTCAACGAGG 65

QY 453 CCCATCGGTCTTCCCTCGGACCTCTCCAAAGAGACCTCTGGGGGACACGGGCCCT 512
Db 66 CCATCGGTCTTCCCTCGGACCTCTCTCCAGAGACCTCTGGGGGACACGGGCCCT 125

QY 513 GGCTGCTGTTGATGAGACTACTTCCCGAAACCGGTGACGGTGTCTGGAACTCAGGCGC 572
Db 126 GGGCTGCTGTTGATGAGACTACTTCCCGAAACCGGTGACGGTGTCTGGAACTCAGGCGC 185

QY 573 CTGTACACGCGGTGACACCTTCCCGGCTGTCTCAGTCTCTCAGGACTCTACTCCCT 632
Db 186 CTGTACACGCGGTGACACCTTCCCGGCTGTCTCAGTCTCTCAGGACTCTACTCCCT 245

QY 633 CAGCAGCGGTGACGCTGCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGT 692
Db 246 CAGCAGCGGTGACGCTGCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGT 305

QY 693 GAATCACAGCCAGCACACCAAGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 752
Db 306 GAATCACAGCCAGCACACCAAGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 365

QY 753 AACTCACATGCCACCGTGGCCAGCAGCTGAACTCTCTGGGGGACCGTCACTCTTCT 812
Db 366 AACTCACATGCCACCGTGGCCAGCAGCTGAACTCTCTGGGGGACCGTCACTCTTCT 425

QY 813 CTTTCCCCCAGAACCCAGGACACCTTATCTCTCCGGACCCCTGAGTCACTGCT 872
Db 426 CTTTCCCCCAGAACCCAGGACACCTTATCTCTCCGGACCCCTGAGTCACTGCT 485

QY 873 GGTGTGGACGTGAGCCAGCAGACCTCTGAGGTCAAGTTCAACTGGTACCTGGACGGCT 932
Db 486 GGTGTGGACGTGAGCCAGCAGACCTCTGAGGTCAAGTTCAACTGGTACCTGGACGGCT 545

QY 933 GGAGGTGATATGCAAGACCAAGCCCGGAGGAGGAGTACAAAGCAGCTACCGTGT 992
Db 546 GGAGGTGATATGCAAGACCAAGCCCGGAGGAGGAGTACAAAGCAGCTACCGTGT 605

QY 993 GGTGACGCTCTCACCGCTCTGACACGAGTGGCTGAATGGCAAGGATACAAAGTGCAA 1052
Db 606 GGTGACGCTCTCACCGCTCTGACACGAGTGGCTGAATGGCAAGGATACAAAGTGCAA 665

QY 1053 GGTCTCAACAAAGCCCTCCAGCCCTCATGAGAAACCATCTCCAAAGCCAAAGGCA 1112
Db 666 GGTCTCAACAAAGCCCTCCAGCCCTCATGAGAAACCATCTCCAAAGCCAAAGGCA 725

QY 1113 GCCCGGAGAACCAAGGTGTACACCTCTCCCGGATGAGTGAACCAAGAACCA 1172
Db 726 GCCCGGAGAACCAAGGTGTACACCTCTCCCGGATGAGTGAACCAAGAACCA 785

QY 1173 GGTGACCTGACCTGCTGTTCAAGGGTTCTATCCAGGAGACATGCCGTGAGTGGG- 1231
Db 786 GGTGACCTGACCTGCTGTTCAAGGGTTCTATCCAGGAGACTTTCCTCCCGGAGTGGGA 845

QY 1232 AGAGCAATGGGAGCGGAGAACCACTACAGA-CCACGCTCTCCGTGCTGG 1282
Db 846 AAAGCAATGGGAGCGGAGAACCACTACAGA-CCACGCTCTCCGTGCTGG 897

RESULT 11
BQ711291
LOCUS
DEFINITION AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096
EST 16-JUL-2002

5', mRNA sequence.
BQ711291
BQ711291.1 GI:21850190
EST.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2468 row: c column: 01
High quality sequence stop: 721.

FEATURES

source
1..881
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6279096"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOT97; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GSCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 220 a 285 c 237 g 139 t
ORIGIN

Query Match 56.5%; Score 808.8; DB 14; Length 881;
Best Local Similarity 99.8%; Pred. No. 1.8e-182;
Matches 810; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 612 GTCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCAC 671
Db 1 GTCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCAC 60

QY 672 CCAGACTACATCTCAAGTGAATCAGCCAGCCAGCAACACCAAGGTGACAGAAAGC 731
Db 61 CCAGACTACATCTCAAGTGAATCAGCCAGCCAGCAACACCAAGGTGACAGAAAGT 120

QY 732 AGAGCCCAATCTTGTGACAAACTCACACATGCCCGTCCCGCAGCAGCTTCAACTCTCT 791
Db 121 TGAGCCCAATCTTGTGACAAACTCACACATGCCCGTCCCGCAGCAGCTTCAACTCTCT 180

QY 792 GGGGGACCGTCACTCTCTTCTCCCGGACCCAGGACACCTCATGATCTCCCG 851
Db 181 GGGGGACCGTCACTCTCTTCTCCCGGACCCAGGACACCTCATGATCTCCCG 240

QY 852 GACCCCTGAGGTACATGCTGTGTGTGAGTGTGAGCCAGGACACCTGAGGTCAAGTT 911
Db 241 GACCCCTGAGGTACATGCTGTGTGTGAGTGTGAGCCAGGACACCTGAGGTCAAGTT 300

QY 912 CAATGTTGAGTGTGAGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 971
Db 301 CAATGTTGAGTGTGAGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360

QY 972 GTACAAACAGCAGTACCGT 1031
Db 361 GTACAAACAGCAGTACCGT 420

Qy 1032 TGGCAAGAGTACAAGTGAAGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAAC 1091
 Db 421 TGGCAAGAGTACAAGTGAAGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAAC 480
 Qy 1092 CATCTCAAGAGCMAAGGGAGCGCCGAGAACACAGAGTGTATACCTGCGCCCATCCCG 1151
 Db 481 CATCTCAAGAGCMAAGGGAGCGCCGAGAACACAGAGTGTATACCTGCGCCCATCCCG 540
 Qy 1152 GGATGAGCTGACCAAGAACACAGGTCAGCTGACCTGCTCCCTGGTCAAAAGGCTTCTATCCAG 1211
 Db 541 GGATGAGCTGACCAAGAACACAGGTCAGCTGACCTGCTCCCTGGTCAAAAGGCTTCTATCCAG 600
 Qy 1212 CGACATCGCGTGGAGTGGAGAGCAATGGGACGCGAGAGCAATACAGACCAACGCC 1271
 Db 601 CGACATCGCGTGGAGTGGAGAGCAATGGGACGCGAGAGCAATACAGACCAACGCC 660
 Qy 1272 TCCCGTGTGAGTCTCCAGCGGCTCTTCTCTCTCTACAGCAAGCTCACCGTGGACAAGAG 1331
 Db 661 TCCCGTGTGAGTCTCCAGCGGCTCTTCTCTCTCTACAGCAAGCTCACCGTGGACAAGAG 720
 Qy 1332 CAGTGGAGAGGAGAACTCTTCTCATGCTCCGCTGATGATGAGGCTGTGACAACCA 1391
 Db 721 CAGTGGAGAGGAGAACTCTTCTCATGCTCCGCTGATGATGAGGCTGTGACAACCA 780
 Qy 1392 CTACACGAGAGAGGCTCTCCCTGTCTCCG 1423
 Db 781 CTACACGAGAGGCTCTCCCTGTCTCCG 812

RESULT 12
 BQ064886
 LOCUS
 DEFINITION AGENCOURT 6887080 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929343
 5', mRNA sequence.

ACCESSION BQ064886
 VERSION BQ064886.1 GI:19899392
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1031)
 NIH-MGC <http://mgs.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2107 row: e column: 24
 High quality sequence stop: 573.
 Location/Qualifiers
 1..1031
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5929343"
 /clone_lib="NIH MGC 99"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph. Vector: pOTB7. Site 1: XhoI; Site 2:
 EcoRI. cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 248 a 349 c 271 g 162 t 1 others
 ORIGIN
 Query Match 55.9%; Score 800.2; DB 14; Length 1031;
 Best Local Similarity 94.4%; Pred. No. 2.2e-180;
 Matches 840; Conservative 0; Mismatches 49; Indels 1; Gaps 1;
 Qy 491 CCTCTGGGGGACACGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGGAACCGGTGA 550
 Db 11 CCTCTGGGGGACACGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGGAACCGGTGA 70
 Qy 551 CGGTGCTGAGAACTCAGCGCCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTCTAC 610
 Db 71 CGGTGCTGAGAACTCAGCGCCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTCTAC 130
 Qy 611 AGTCTCTCAGGACTCTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCA 670
 Db 131 AGTCTCTCAGGACTCTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCA 190
 Qy 671 CCAGACCTACATCTGCAACCGTGAATCAAGCCACGAAACACCAAGGTGGACAAGAAAG 730
 Db 191 CCAGACCTACATCTGCAACCGTGAATCAAGCCACGAAACACCAAGGTGGACAAGAAAG 250
 Qy 731 CAGAGCCCAAAATCTTGTGACAAAACTCACACATGCCACCGTGCACAGCACTGAACTCC 790
 Db 251 TTGAGCCCAAAATCTTGTGACAAAACTCACACATGCCACCGTGCACAGCACTGAACTCC 310
 Qy 791 TGGGGGACCGTCACTCTTCTTCCCGCCAAACCAAGGACCCCTCATGATCTCCC 850
 Db 311 TGGGGGACCGTCACTCTTCTTCCCGCCAAACCAAGGACCCCTCATGATCTCCC 370
 Qy 851 GGACCCCTGAGGTACATGCTGCTGCTGAGCGTGCAGCAAGAGCCCTGAGGTCAAGT 910
 Db 371 GGACCCCTGAGGTACATGCTGCTGCTGAGCGTGCAGCAAGAGCCCTGAGGTCAAGT 430
 Qy 911 TCACTGTGTACGTGACCGCGTGTGAGTGCATATGCAAGAACCCCGGAGGAGGC 970
 Db 431 TCACTGTGTACGTGACCGCGTGTGAGTGCATATGCAAGAACCCCGGAGGAGGC 490
 Qy 971 AGTACAAACAGCAGCTACCGTGTGCTGAGCGTCTTCCAGCGTCTTCCAGCAGGACTGGCTGA 1030
 Db 491 AGTACAAACAGCAGCTACCGTGTGCTGAGCGTCTTCCAGCGTCTTCCAGCAGGACTGGCTGA 550
 Qy 1031 ATGGCAAGAGTACAAGTGCAGAGTCTTCCAAAGAGCCCTCCAGCCCCCATCGAGAAA 1090
 Db 551 ATGGCAAGAGTACAAGTGCAGAGTCTTCCAAAGAGCCCTCCAGCCCCCATCGAGAAA 610
 Qy 1091 CCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAACAGGCTACACCTGCCCCCATCCC 1150
 Db 611 CCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAACAGGCTACACCTGCCCCCATCCC 670
 Qy 1151 GGGATGAGTGAACCAAGAACCAAGTCAAGCTGAGCTGCTGCTGCTCAAGGCTTCTATCCCA 1210
 Db 671 GGGATGAGTGAACCAAGAACCAAGTCAAGCTGAGCTGCTGCTGCTCAAGGCTTCTATCCCA 730
 Qy 1211 GCGACATCGCCCT -GGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAAGACCAGC 1269
 Db 731 GCGACATCGCCCTGGAGTGGGAACCAATGGGAGCGGAGAACCACTACAAGACCAGC 790
 Qy 1270 CTTCCCGTGTGAGATCCGACGGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAAG 1329
 Db 791 CTTCCCGTGTGAGATCCGACGGCTCTTCTTCTCTACAGCAAGCTACCGTGGGACA 850
 Qy 1330 AGCAGGTGGACAGGGGAAAGCTTCTTCTCATGCTCCGCTGATGATGAGGC 1379
 Db 851 AAAGCAGGGGGGCAACCGGGGGGAAAGCTTCTTCTCAATGCTCCGTGATGC 900

RESULT 13
 BQ711727
 LOCUS
 DEFINITION AGENCOURT 8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961
 5', mRNA sequence.


```
Query Match      55.6%; Score 796; DB 14; Length 940;
Best Local Similarity 99.3%; Pred. No. 2.1e-179;
Matches 810; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 617 CAGGACTCTACTCCCTOAGCAGCGTGTGACCTGCTCCCTCCAGCAGCTTGGGACCCAGA 676
Db 1 CAGGACTCTACTCCCTCAGCAGCGTGTGACCTGCTCCCTCCAGCAGCTTGGGACCCAGA 60
QY 677 CCTACATCTGCAAGTGAATCAAGCCAGCAACCCAGGTTGGACAGAAAGCAGAC 736
Db 61 CCTACATCTGCAAGTGAATCAAGCCAGCAACCCAGGTTGGACAGAAAGTGGAC 120
QY 737 CCAATCTTGTGACAAATCAACATGCCACCGTGCCTCCAGCAGCCTGAACTCTCTGGGG 796
Db 121 CCAATCTTGTGACAAATCAACATGCCACCGTGCCTCCAGCAGCCTGAACTCTCTGGGG 180
QY 797 GACCGTCAGTCTTCTCTCTCCCTCCCAAAACCCAGAGCAGCCCTCATGATCTCCCGGACCC 856
Db 181 GACCGTCAGTCTTCTCTCTCCCTCCCAAAACCCAGAGCAGCCCTCATGATCTCCCGGACCC 240
QY 857 CTGAGTCAATGCTGCTGCTGAGCGTGGACGACGACGACGACGACGACGACGACGACGAC 916
Db 241 CTGAGTCAATGCTGCTGCTGAGCGTGGACGACGACGACGACGACGACGACGACGACGAC 300
QY 917 GGTACGTGGACGCGTGGAGTGCATTAATGCCAAGCAAAAGCCGCGGAGGACGATACA 976
Db 301 GGTACGTGGACGCGTGGAGTGCATTAATGCCAAGCAAAAGCCGCGGAGGACGATACA 360
QY 977 ACAGCAGTACCGTGTGGTGCAGCGTCTCAACGCTCTGACACGAGGACTGCTGAATGGCA 1036
Db 361 ACAGCAGTACCGTGTGGTGCAGCGTCTCAACGCTCTGACACGAGGACTGCTGAATGGCA 420
QY 1037 AGGAGTCAAGTGCAGGCTCTCAACAAAGCCCTCCAGCAGCCCTCCAGAGAAACCATCT 1096
Db 421 AGGAGTCAAGTGCAGGCTCTCAACAAAGCCCTCCAGCAGCCCTCCAGAGAAACCATCT 480
QY 1097 CCAAGCCAAAGGCGAGCCGCGAGAACCAAGGTGTACACCTGCCCCCAATCCCGGATG 1156
Db 481 CCAAGCCAAAGGCGAGCCGCGAGAACCAAGGTGTACACCTGCCCCCAATCCCGGATG 540
QY 1157 AGCTGACCAAGAACCAAGTGCAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCGACA 1216
Db 541 AGCTGACCAAGAACCAAGTGCAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCGACA 600
QY 1217 TCGCGTGGAGTGGAGAGCAATGGGAGCGGAGAGAACCACTAAGACCAACGCTCCCG 1276
Db 601 TCGCGTGGAGTGGAGAGCAATGGGAGCGGAGAGAACCACTAAGACCAACGCTCCCG 660
QY 1277 TGCTGGACTCCGACGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGACAAAGCAGGT 1336
Db 661 TGCTGGACTCCGACGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGACAAAGCAGGT 720
QY 1337 GGCAGCAGGGGAAAGCTTCTCTCATGCTCCGATGATGATGAGGCTCTGCACAAACCTACA 1396
Db 721 GGCAGCAGGGGAAAGCTTCTCTCATGCTCCGATGATGATGAGGCTCTGCACAAACCTACA 780
QY 1397 GCG-AGAGAGCCTCTCCCTGCTCTCCGGTAAATGA 1431
Db 781 GCGAAAAAGAGCCTCTCCCTGCTCTCCGGTAAATGA 816

RESULT 15
LOCUS B0710532
DEFINITION AGENCOURT_8352211 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277538
5', mRNA sequence.
ACCESSION B0710532
VERSION B0710532.1 GI:21849431
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
```

```
1 (bases 1 to 977)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM2464 row: b column: 03
High quality sequence stop: 749.
FEATURES
source
1..977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277538"
/lab_host="NIH MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming, directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 227 a 331 c 264 g 154 t 1 others
ORIGIN
Query Match 55.0%; Score 787.4; DB 14; Length 977;
Best Local Similarity 92.5%; Pred. No. 2.4e-177;
Matches 886; Conservative 0; Mismatches 57; Indels 15; Gaps 5;
QY 475 CCCTCTCTCAAGAGCAGCTCTTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGACTAC 534
Db 11 CCCTCTCTCAAGAGCAGCTCTTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGACTAC 70
QY 535 TTCCCGAACCGGTGACCGTGTCTGGAACTCAGCGGCCCTGACAGCGGCTGCACACC 594
Db 71 TTCCCGAACCGGTGACCGTGTCTGGAACTCAGCGGCCCTGACAGCGGCTGCACACC 130
QY 595 TTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCC 654
Db 131 TTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCC 190
QY 655 TCCAGAGCTTGGGACCCAGACCTTACATCTGCAACGTTGATCAAGCCAGCAGCACC 714
Db 191 TCCAGCACTTCCGACCCAGACCTTACATCTGCAACGTTGATCAAGCCAGCAGCACC 250
QY 715 AAGGTGGACAAAGAGCAGAGCCAAATCTTGTGACAAAACCTCAGACATGCCCGCTGC 774
Db 251 AAGGTGGACAAAGAGTGTGAGCGCAAAATGTTGTGCGA-----GTGCCCGCTGC 301
QY 775 CCAGCAGCTGAACTCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAACCCAGGAC 834
Db 302 CCAGCAGC---ACCTGTGGCAGGACCGTCAAGTCTTCTTCTTCCCCCAAAACCCAGGAC 358
QY 835 ACCCTCATGATCTCCCGACCCCTGAGTGCATCGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 894
Db 359 ACCCTCATGATCTCCCGACCCCTGAGGTGACGTGGTGGTGGTGGTGGTGGTGGTGGTGG 418
QY 895 GACCTCTGAGTCAAGTTCAACTGGTACGTTGACGCGGCTGGAGGTGCATAATGCCAAGACA 954
Db 419 GACCCGAGGTCCAGTTCAACTGGTACGTTGACGCGGCTGGAGGTGCATAATGCCAAGACA 478
QY 955 AAGCCCGGGAGGAGCAGTACAAAGCAGCTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1014
Db 479 AAGCCACGGGAGGAGCAGTTCAAAGCAGCTTCCGTTGGTGGTGGTGGTGGTGGTGGTGG 538
```



```
Qy 1015 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC AAGGTCTCCAAACAAAGCCCTCCCA 1074
Db 539 CACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGC AAGGTCTCCAAACAAAGCCCTCCCA 598
Qy 1075 GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCCGAGAACACACAGGTGTAC 1134
Db 599 GCCCCCATCGAGAAACCATCTCCAAACAAAGGGCAGCCCCCGAGAACACACAGGTGTAC 658
Qy 1135 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACACAGGTACGCTGACCTGGCTGGTC 1194
Db 659 ACCCTGCCCCCATCCCGGGAGAGATGACCAAGAACACAGGTACGCTGACCTGGCTGGTC 718
Qy 1195 AAAGGCTTCTATCCAGCGACATC-GCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAA 1253
Db 719 AAAGGCTTCTACCCAGCGACATCTCCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAA 778
Qy 1254 CAACTACAAGACCAAGCCTCCCGTGGCTGGACTCCGACGGCTCTTCTCTCTACAGCAA 1313
Db 779 CAACTANACAGACCAACACTCCCATGCTGGACTCCGACGGGCTCTTCTCTCTACAGC-A 837
Qy 1314 GCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAAAGTCTTCTCATGCTCCGTGATGCA 1373
Db 838 GCTCACCGTGGACAGAGCAAGTGGCAGCAGGGGAAAGTCTTCTCATGCTCCGTGATGCA 897
Qy 1374 TGAGGCTCTGCACACCACTACACGACAGAGAGCCTTCTCCCTGTCTCCGGGTAAATGA 1431
Db 898 TGAGGCTCTGGCCCAACCCCTACACACA-AAGAGCCTCTCCCTGGTCTCGGGTAAATGA 954
```

Search completed: April 6, 2003, 06:20:24
Job time : 2734.68 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:05 ; Search time 4490.25 Seconds
(without alignments)
9274.790 Million cell updates/sec

Title: US-09-758-173-3

Perfect score: 1431

Sequence: 1 ATGAAACACTGGTCTT.....CCTGTCTCCGGTAAATGA 1431

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sta.*

28: em_un.*

29: em_vi.*

30: em_hg_hum.*

31: em_hg_inv.*

32: em_hg_other.*

33: em_hg_mus.*

34: em_hg_pln.*

35: em_hg_rod.*

36: em_hg_nam.*

37: em_hg_vrt.*

38: em_sv.*

39: em_hgo_hum.*

40: em_hgo_mus.*

41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1431	100.0	1431	6	AR108863	AR108863 Sequence
2	1315.8	91.9	1431	6	AR108867	AR108867 Sequence
3	1237.2	86.5	1431	6	E10697	E10697 cDNA encodi
4	1234.8	86.3	1567	6	AR135359	AR135359 Sequence
5	1227.6	85.8	1596	9	AK098516	AK098516 Homo sapi
6	1221.6	85.4	1418	6	A49389	A49389 Sequence 7
7	1215.2	84.9	1594	9	AK057754	AK057754 Homo sapi
8	1210.4	84.6	1418	6	AR176296	AR176296 Sequence
9	1209.6	84.5	1589	9	AK057775	AK057775 Homo sapi
10	1171.4	81.9	1404	6	AR135375	AR135375 Sequence
11	1170	81.8	1566	9	AK097365	AK097365 Homo sapi
12	1168.2	81.6	1404	6	AR135377	AR135377 Sequence
13	1166.6	81.5	1404	6	AR135376	AR135376 Sequence
14	1125.8	78.7	1633	9	AK097859	AK097859 Homo sapi
15	1124.2	78.6	1507	6	BD000501	BD000501 Process f
16	1123.6	78.5	1428	6	AR031184	AR031184 Sequence
17	1123.6	78.5	1428	6	AR042589	AR042589 Sequence
18	1123.6	78.5	1428	6	AR059282	AR059282 Sequence
19	1123.6	78.5	1428	6	AR076260	AR076260 Sequence
20	1122.8	78.5	1430	6	AX419496	AX419496 Sequence
21	1117.4	78.1	1679	9	BC018747	BC018747 Homo sapi
22	1117.2	78.1	1437	6	AR108865	AR108865 Sequence
23	1116.2	78.0	1624	9	HSIGG1KH	Y14735 Homo sapien
24	1115.4	77.9	1630	9	BC024289	BC024289 Homo sapi
25	1113.2	77.8	1673	9	HSIGG1LH	Y14737 Homo sapien
26	1113.2	77.8	1438	6	BC019046	BC019046 Homo sapi
27	1112.4	77.7	1428	6	AR031186	AR031186 Sequence
28	1112.4	77.7	1428	6	AR042591	AR042591 Sequence
29	1112.4	77.7	1428	6	AR059284	AR059284 Sequence
30	1112.4	77.7	1428	6	AR076262	AR076262 Sequence
31	1112.4	77.7	1990	9	AK098817	AK098817 Homo sapi
32	1109.2	77.5	1631	9	AK097010	AK097010 Homo sapi
33	1104.6	77.2	1465	10	S79307	S79307 Ig gamma =1
34	1103.6	77.1	1617	6	A29585	A29585 H.sapiens c
35	1102	77.0	1599	6	AX330501	AX330501 Sequence
36	1102	77.0	1599	6	AX333307	AX333307 Sequence
37	1102	77.0	1599	6	AX334122	AX334122 Sequence
38	1102	77.0	1599	9	HUMIGEPAH	MB7789 Human (hybr
39	1096.4	76.6	1633	9	AK097367	AK097367 Homo sapi
40	1096	76.6	7521	6	AX080951	AX080951 Sequence
41	1095.6	76.6	1549	6	A21385	A21385 Plasmid DNA
42	1092.6	76.4	6557	6	I26929	I26929 Sequence 3
43	1092.4	76.3	1666	9	BC006402	BC006402 Homo sapi
44	1091.8	76.3	1341	6	A07562	A07562 DNA sequenc
45	1091.4	76.3	1639	9	AK097950	AK097950 Homo sapi

ALIGNMENTS

RESULT 1
AR108863
LOCUS AR108863
DEFINITION Sequence 3 from patent US 6113898.
ACCESSION AR108863
VERSION AR108863.1 GI:12825139
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1431)
AUTHORS Anderson,D.R., Brans,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
JOURNAL Patent: US 6113898-A 3 05-SEP-2000;

Qy	1	ATGAAACACCTGTGGTTCCTCTCTCTGTGGCAGCTCCAGATGGTCTCTGCCAG	60
Db	1	ATGAAACACCTGTGGTTCCTCTCTCTGTGGCAGCTCCAGATGGTCTCTGCCAG	60
Qy	61	GTGAAGCTGCAGCAGTGGGGCGAAGACTTCTGCAGCCCTCCGAGACCTCTCCCGCACC	120
Db	61	GTGCAGCTGCAGGAGTCGGGCCCGAGCTGTGTGAAGCCCTCGGAGACCTGTCTCCCTCACC	120
Qy	121	TGGGTTCTCTGTGGCTCCATCAGCGGTACTACTACTCGACCTCGATCCGCGACACC	180
Db	121	TGGCGTGTCTCTGTGTGGCTCCATCAGCGGTGTATGGCTGGGCTGGATCCGGCAGGCC	180
Qy	181	CCAGGAGGGGACCTGGAGTGGATTGGCCATATTTATGGTAAATGGTGGCAGCCACCAACTAC	240

Db	433	 -----ATGACGTAGGTTTAAGGGGGGGGAACCTACGGTATGACACGTCTGGGGCCAGGGA	485
Qy	418	GACCTGGTCACCGTCTCCTCAGCTAGCACCAAGAGGCCCATCGGTCTTCCCTCGGCACCC	477
Db	486	ACCCTGGTCACCGTCTCCTCAGCCTCCACAAAGAGGCCATCGGTCTTCCCTCGGCACCC	545
Qy	478	TCCTCAAGAGCACCTCTGGGGGSCACAGCGGCCCTGGGCTGCTGGTCAAGGACCTACTTC	537
Db	546	TCCTCCAAGAGCACCTCTGGGGGSCACAGCGGCCCTGGGCTGCTGGTCAAGGACCTACTTC	605
Qy	538	CCGGAACCGGTGACGCTGTCTGCGAACTCAGCGGCCCTGACAGCGCGGTGCAACCTTC	597
Db	606	CCGGAACCGGTGACGCTGTCTGCGAACTCAGCGGCCCTGACAGCGCGGTGCAACCTTC	665
Qy	598	CCGGCTGTCTTACAGTCTCCTCAGGACCTACTCTCCTCAGCAGCGTGGTGACCGTGCCCTCC	657
Db	666	CCGGCTGTCTTACAGTCTCCTCAGGACCTACTCTCCTCAGCAGCGTGGTGACCGTGCCCTCC	725
Qy	658	AGCAGCTTGGCCACCCAGACCTACATCTGCAACGTGAATCACAAAGCCCAAGCAACACCAAG	717
Db	726	AGCAGCTTGGCCACCCAGACCTACATCTGCAACGTGAATCACAAAGCCCAAGCAACACCAAG	785
Qy	718	GTGGCAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCAACCGTGCCCA	777
Db	786	GTGGCAAGAGAGTGTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCAACCGTGCCCA	845
Qy	778	GCACCTGAACCTCTGGGGGAGCCGTGAGTCTTCCTCTTCCGCCCAAAACCCGAAGGACAC	837
Db	846	GCACCTGAACCTCTGGGGGAGCCGTGAGTCTTCCTCTTCCGCCCAAAACCCGAAGGACAC	905
Qy	838	CTCATGATCTCCCGGACCCCTGAGGTCTCATGCGTGGTGGAGCGTGAGGCCACGAAGAC	897
Db	906	CTCATGATCTCCCGGACCCCTGAGGTCTCATGCGTGGTGGAGCGTGAGGCCACGAAGAC	965
Qy	898	CTGAGGTCAAGTTCAACTGTTAGTGGAGCGCGCTGGAGGTGCATTAATGCCAAGACAAG	957
Db	966	CTGAGGTCAAGTTCAACTGTTAGTGGAGCGCGCTGGAGGTGCATTAATGCCAAGACAAG	1025
Qy	958	CCGCGGAGGAGCAGTACAACAGCAGCTTACCGTGTGTCAGCGTCTCACCGTCTCGAC	1017
Db	1026	CCGCGGAGGAGCAGTACAACAGCAGCTTACCGTGTGTCAGCGTCTCACCGTCTCGAC	1085
Qy	1018	CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTTCAACAAAGCCCTCCCGAC	1077
Db	1086	CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTTCAACAAAGCCCTCCCGAC	1145
Qy	1078	CCCATCGAAGAACCATCTCCAAAGCCAAAGGCGCGCCGAGAACCAAGGTGTACAC	1137
Db	1146	CCCATCGAAGAACCACTCTCCAAAGCCAAAGGCGCGCCGAGAACCAAGGTGTGTACAC	1205
Qy	1138	CTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTCTGAGCTGACCTGCTGGTCAAA	1197
Db	1206	CTGCCCCCATCCCGGAGGAGATGACCAAGAACAGGTCTGAGCTGACCTGCTGGTCAAA	1265
Qy	1198	GGCTTCTATCCCGAGCACAATCCCGTGGAGTGGGAGAGCAATGGCGAGCCGAGAACAC	1257
Db	1266	GGCTTCTATCCCGAGCACAATCCCGTGGAGTGGGAGAGCAATGGCGAGCCGAGAACAC	1325
Qy	1258	TACAAGACCAAGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTCTCTACAGCAAGCTC	1317
Db	1326	TACAAGACCAAGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTCTCTACAGCAAGCTC	1385
Qy	1318	ACCGTGGACAAGACAGGTGGGACGAGGGGAACGTCTTCTCATGTCTCGTGATGCATGAG	1377
Db	1386	ACCGTGGACAAGACAGGTGGGACGAGGGGAACGTCTTCTCATGTCTCGTGATGCATGAG	1445
Qy	1378	GCTCTGCAACAACCTACACGCAAGAGCCTCTCCCTGTCTCCGGTAAATGA	1431
Db	1446	GCTCTGCAACAACCTACACGCAAGAGCCTCTCCCTGTCTCCGGTAAATGA	1499

RESULT 5

AKO98516		1596 bp	mRNA	linear	PRI 15-JUL-2002
LOCUS					
DEFINITION	Homo sapiens cDNA FLJ25650 fis, clone SYN01104, highly similar to Ig gamma =immunoglobulin heavy chain.				
ACCESSION	AKO98516.1 GI:21758543				
VERSION	AKO98516				
KEYWORDS	oligo capping; fis (full insert sequence).				
SOURCE	Homo sapiens synovial membrane (knee) cDNA to mRNA, clone_lib:SYN clone:SYN01104.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 Ishibaashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Hiraoaka,S., Murakawa,K., Takiguchi,S., Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Suzuki,I., Hata,H., Nakagawa,K., Mizuno,S., Morikawa,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.				
TITLE	NEDO human cDNA sequencing project				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1596)				
AUTHORS	Sugano,S. and Suzuki,Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shitokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:c dna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)				
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; Clone selection for full insert sequencing: RAB and Helix Research Institute.				
FEATURES	Location/Qualifiers				
source	1..1596 <code>/organism="Homo sapiens"</code> <code>/db_xref="taxon.9606"</code> <code>/clone="SYN01104"</code> <code>/cfeature_type="synovial membrane (knee)"</code> <code>/clone_lib="SYN"</code> <code>/note="cloning vector: pME18SFL3"</code>				
BASE COUNT	342 a	540 c	426 g	288 t	
ORIGIN					
Query Match	85.8%	Score 1227.6;	DB 9;	Length 1596;	
Best Local Similarity	92.5%;	Pred. No. 86-239;			
Matches 126;	Conservative 0;	Mismatches 99;	Indels 9;	Gaps 3;	
Qy 1	ATGAACAACCTGTGGTCTTCCTCCTCGTGAGCCAGCTCCAGATGGGTCGTGCCAG	60			
Dd 36	ATGAACAACCTGTGGTCTTCCTCCTCGTGAGCCAGCTCCAGATGGGTCGTGCCAG	95			
Qy 61	GTGAAGCTGCAGACTGGGGCGAAGGACTTCTCGACCTTCGGAGACCCTGTCGGCAC	120			
Dd 96	GTGCACCTGCAGGAGTCCGGCTCAGGACTGGTAGGCCCTTCAAGCTCTGTCCCTCAC	155			
Qy 121	TGGGTGTCTCTGGTGGCTCCAT---CAGCGGTACTACTATGGAAGTTGATCCGCCAG	177			
Dd 156	TGCGCTGTCTCTGGTGAATCATCACCAGTGGTGTCTCACTCTCGTAGGTGATCCGCCAG	215			
Qy 178	ACCCAGGAGGAGGAACTGGAGTGGATTGGGCATATTATTGTTAATGTTGCACACCAAC	237			
Dd 216	CCACGAGGAGGGCCCTGGAGTGGATTGGCTACGTCTATCTCA---GTGGGAGCACTCT	272			
Qy 238	TACATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAGACACGTCCAAGAACCAAGTTC	297			
Dd 273	TACATTCGGTCCCTCAAGAGTCGAGTCACCATTTCAAAGAGTCCAAACCAAGTTC	332			
Qy 298	TTTCCTGAACCTTGAATTTCTGTGACCGAGCGGAGCACGGCCGCTCTATTACTGTGCGAGAGGC	357			

Db 333 TCCCTGAGGTTGACCTCTGTGACCGCCGACACGCGCGTGTATTACTGTGCCAGAGGG 392
QY 358 CTTCCGCCCTGATGACCAACCAITTTGTTATGCGGCTGGTTCGATGCTGTGGGCGCCGGA 417
Db 393 CTTGT-...TCATCGCAGGATTTGATACCCACGTTCTCGTTTACTACTGGGCGCAGGA 449
QY 418 GACCTGGTCACCGTCTCTCAGCTAGCACCAAGGCGCCATCGTCTTCCCTCGCACCC 477
Db 450 ACCCTGGTACCGCTCTCAGCTCACCACAGGCGCCATCGTCTTCCCTCGCACCC 509
QY 478 TCCTCAAGAGACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGAGACTACTTC 537
Db 510 TCCTCAAGAGACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGAGACTACTTC 569
QY 538 CCGGAACCGGTGACCGTCTCTGGAACCTCAGGCGCCCTGACACGCGCTGACACCTTC 597
Db 570 CCGGAACCGGTGACCGTCTCTGGAACCTCAGGCGCCCTGACACGCGCTGACACCTTC 629
QY 598 CCGGCTGCTCTACAGTCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTCC 657
Db 630 CCGGCTGCTCTACAGTCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTCC 689
QY 658 AGCAGCTTGGGACCCAGCTCCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTCC 717
Db 690 AGCAGCTTGGGACCCAGCTCCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTCC 749
QY 718 GTGGACAAGAGAGAGAGCCCAATCTTGTGACAAACTCACAATGACCGTGTGACCGTCC 777
Db 750 GTGGACAAGAGAGAGAGCCCAATCTTGTGACAAACTCACAATGACCGTGTGACCGTCC 809
QY 778 GCACCTGAACCTCTGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 837
Db 810 GCACCTGAACCTCTGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 869
QY 838 CTCATGATCTCCGGAACCCCTGAGGTCACATGCTGCTGTGCTGTGCTGTGCTGTGCTGT 897
Db 870 CTCATGATCTCCGGAACCCCTGAGGTCACATGCTGCTGTGCTGTGCTGTGCTGTGCTGT 929
QY 898 CTTGAGGTCAGATTTCACTGCTGCTGAGCGGCTGTGAGTGTGATTAATGCAAGCAAG 957
Db 930 CTTGAGGTCAGATTTCACTGCTGCTGAGCGGCTGTGAGTGTGATTAATGCAAGCAAG 989
QY 958 CCGCGGAGGAGCAGTACACAGCAGTCACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1017
Db 990 CCGCGGAGGAGCAGTACACAGCAGTCACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1049
QY 1018 CAGGACTGGCTGAATGGCAAGAGTACAAGTGAAGTCTTCCAAAGCCCTTCCAGCC 1077
Db 1050 CAGGACTGGCTGAATGGCAAGAGTACAAGTGAAGTCTTCCAAAGCCCTTCCAGCC 1109
QY 1078 CCGATCGAAGAACCTCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGTGTACACC 1137
Db 1110 CCGATCGAAGAACCTTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGTGTGTACACC 1169
QY 1138 CTGCCCCATCCCGGATGAGCTGACCAAGAACAGCTCAGCTGAGCTGCTGTGTCAA 1197
Db 1170 CTGCCCCATCCCGGATGAGCTGACCAAGAACAGCTCAGCTGAGCTGCTGTGTCAA 1229
QY 1198 GCGTCTATCCAGGACATCCGCTGAGTGGGAGGAGCAATGGGAGCGCGGAGACAC 1257
Db 1230 GCGTCTATCCAGGACATCCGCTGAGTGGGAGGAGCAATGGGAGCGCGGAGACAC 1289
QY 1258 TACAAGACACCGCTCCCGTGTGAGTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1317
Db 1290 TACAAGACACCGCTCCCGTGTGAGTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1349
QY 1318 ACCGTGGACAGAGCAGTGGCAGCGGAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1377
Db 1350 ACCGTGGACAGAGCAGTGGCAGCGGAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1409
QY 1378 GCTCTGCAACACCTACACGCAAGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1431

Db 1410 GGCTCCACCAACCACTACACGCAAGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1463

RESULT 6
A49389
LOCUS A49389
DEFINITION Sequence 7 from Patent WO9607740.
ACCESSION A49389
VERSION A49389.1
KEYWORDS GI:2302866
SOURCE unidentifed.
ORGANISM unidentifed.
REFERENCE 1 (bases 1 to 1418)
AUTHORS Edelman, L., Margaratte, C., Kaczorek, M. and Chaabihi, H.
TITLE MONOCLONAL RECOMBINANT ANTI-RHESUS D (D7C2) ANTIBODY
JOURNAL Patent: WO 9607740-A 7 14-MAR-1996;
PASTEUR INSTITUT (FR)
COMMENT Other publication FR 2724182 960308.
FEATURES
Location/Qualifiers
1..1418
/organism="unidentifed"
/db_xref="taxon:32644"
1..1418
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAA03180.1"
/translation="MGMSCLLELVATATGVHVSQVQLQWQAGLAKPSTLSLTCTVY
GGSPGYWIRQPGKGLIEINHSNSTNPSLRSVTISYDTSKQFSLKLN
SVTAADTAVYCARAPYKMYKHWDFDQWQGTTFVSSATKSPVPLAPSSKST
SGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSL
GTQVTCNVNHPKSTNKKDKKPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTL
MISLPTPEVTVVDVSHEDPEVKFNKYVDGVHNAKTPRBEQYNSTYRVPPVSLKVL
HQMINKKEYKCKVSNKALPAPIEKIKSAKGPQPREPQYITLPPSRDELTKNQVSLTLC
LVKGFYPSDIAVESWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRHQQGNVFC
SYMHEALHNHYTQKSLSLSPGK"
sig_peptide 1..57
mat_peptide 58..1418
BASE COUNT 333 a 458 c 378 g 249 t
ORIGIN
Query Match 85.4%; Score 1221.6; DB 6; Length 1418;
Best Local Similarity 92.9%; Pred. No. 1.3e-237;
Matches 1317; Conservative 0; Mismatches 89; Indels 12; Gaps 3;
QY 13 TGGTCT 72
Db 13 TGTATCATCT 72
QY 73 CAGTGGGCGAAGGACTTCTCGAGCCTTCGGAGACCTGTCCCGACCTCGGTGTCTCT 132
Db 73 CAGTGGGCGAAGGACTTCTCGAGCCTTCGGAGACCTGTCCCGACCTCGGTGTCTCTCTCT 132
QY 133 GGTGGCTCCATCAGCGGTTTACTTACTTGGACCTGGAGTCCCGCCAGACCCCGAGGAGGGA 192
Db 133 GGTGGCTCTCTCAGTGGT---TACTTCTGAGTGGATCCCGCAGCCCCCAGGGAAGGG 189
QY 193 CTGGAGTGGATGGCCATTTATTTGTTAGTGGTGGACACCACTACATCTCCCTCCTC 252
Db 190 CTGGAGTGGATGGGGAATCAA---TCATAGTGAAGACCACTACATCAACCCGCTCCTC 246
QY 253 AAGAGTCGAGTCACCATTTCAAAAGACACGTCGAAGAACAGTTCTTCTGAATTTGAAT 312
Db 247 AAGAGTCGAGTCACCATATCAGTAGACACGTCGAAGAACAGTTCTTCTGAATTTGAAT 306
QY 313 TCTGTACCGCAGCGGACACCGCGCTCTATTACTGTGGAGAGCCCTCCGCTGATTGC 372
Db 307 TCTGTACCGCAGCGGACACCGCGCTGTATTACTGTGGAGG-----CCCGAGAGTAT 360
QY 373 ACAACCATTTGTTATGGCGGCTTGGGTGATCTTGGGCGCCCGGAGACCTTGGTCAACCGTC 432

Db 156 TGCAAGTGTCTCTGGTGAATCCATCGCCCAAACTGGCTATTTCTGGGGTGTGTTCCGCAAG 215
QY 178 ACCCCAGGAGGGAGTGGAGTGGATTTGGCCCAATTTATGGTAATGGTGGACCAACCAAC 237
Db 216 CCCCAGGGAAGGAGCTGCAATTTATAGGAGTGTATTTATCTATG--GACCGCCAC 272
QY 238 TACAATCCCTCCCTCAAGAGTGAAGTACCAATTTCAAAGACAGCTCCAAAGAACAGTTTC 297
Db 273 CACAACCCGCTCCCTCAAGCGCGAGTCAACATATCGCAGACACATCCCAAGGCCCAAGTTTC 332
QY 298 TTCTGAACCTTGAATTTCTGTGACCGACGGGACACGGCGCTTATTTACTGTGCGAGAGGC 357
Db 333 TTCTGACACTGACCTCTGTGACCGCGGGATAGCGTGTCTATTACTGTGCGAGA--- 389
QY 358 CTTGCGCCCTGATTGACACACCAATTTGTTATGGCGGCTGGGTGCAATGTCTGGGGCCCGGGA 417
Db 390 ---CAITGGGTTCTTAGGTTCTGGAGTGGATGCTGTGTCGACCCCTGGGGCCCGGGA 446
QY 418 GACCTGGTCAACCGTCTCTCAGTACACCAAGGCCCATCGGTCTTCCCTCCGACCC 477
Db 447 ATCTCTGGTCAACCGTCTCTCAGTACACCAAGGCCCATCGGTCTTCCCTCCGACCC 506
QY 478 TCTTCAAGAGACCTCTCTGGGGGACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTC 537
Db 507 TCTTCAAGAGACCTCTCTGGGGGACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTC 566
QY 538 CCGCAACCCGTCAGCGTGTGCGAACTCAGCGCCCTGACCGGGGTCGACACCTTC 597
Db 567 CCGCAACCCGTCAGCGTGTGCGAACTCAGCGCCCTGACCGGGGTCGACACCTTC 626
QY 598 CCGGCTGTCTCAGTCTCAGGACTTACTCTCTCAGCAGCGTGTGACCGTCCCTTC 657
Db 627 CCGGCTGTCTCAGTCTCAGGACTTACTCTCTCAGCAGCGTGTGACCGTCCCTTC 686
QY 658 AGCAGCTTGGGACACAGACTTACTCTCAGCGTGAATCAAGGCCAGCAACCAAG 717
Db 687 AGCAGCTTGGGACACAGACTTACTCTCAGCGTGAATCAAGGCCAGCAACCAAG 746
QY 718 GTGGAACAAGAGAGAGCCCAAACTTTGTGACAAACTCAACATGCCACCGTGCCCA 777
Db 747 GTGGAACAAGAGTGTGAGCCCAAACTTTGTGACAAACTCAACATGCCACCGTGCCCA 806
QY 778 GCACCTGAATCTCTGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 837
Db 807 GCACCTGAATCTCTGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 866
QY 838 CTCAATGATCTCCCGGACCCCTCAGGTCACATGCGTGTGGTGGAGCGTGAAGAC 897
Db 867 CTCAATGATCTCCCGGACCCCTCAGGTCACATGCGTGTGGTGGAGCGTGAAGAC 926
QY 898 CTTGAGGTCAAGTTCACTGTTGATCGTGACCGCGTGGAGTGCATATGCGCAAGAAC 957
Db 927 CTTGAGGTCAAGTTCACTGTTGATCGTGACCGCGTGGAGTGCATATGCGCAAGAAC 986
QY 958 CCGCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTGGAGTGCATATGCGCAAGAAC 1017
Db 987 CCGCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTGGAGTGCATATGCGCAAGAAC 1046
QY 1018 CAGGACTGCTGAATGGCAAGAGTACAAAGTGAAGTGTCTCAACAAAGCCCTCCAGCC 1077
Db 1047 CAGGACTGCTGAATGGCAAGAGTACAAAGTGAAGTGTCTCAACAAAGCCCTCCAGCC 1106
QY 1078 CCGATCGAAGAAACCATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1137
Db 1107 CCGATCGAAGAAACCATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1166
QY 1138 CTGCCCCCATCTCCGGGATGAGTGAACAAAGAACAGGTCAGCTGACCTGCTGGTCAAA 1197
Db 1167 CTGCCCCCATCTCCGGGATGAGTGAACAAAGAACAGGTCAGCTGACCTGCTGGTCAAA 1226
QY 1198 GGTCTTATCTCCAGCAGATCCCTGCGAGTGGGAGAGCAATGGGAGCCGCGGAGAAC 1257
Db 1227 GGTCTTATCTCCAGCAGATCCCTGCGAGTGGGAGAGCAATGGGAGCCGCGGAGAAC 1286

QY 1258 TACAAGACACAGCCCTCCGTCCTGGACTCCGACGGCTCTCTTCTCTTACACGAAGCTC 1317
Db 1287 TACAAGACACAGCCCTCCGTCCTGGACTCCGACGGCTCTCTTCTCTTACACGAAGCTC 1346
QY 1318 ACCGTGGACAGAGCAGTGGCAGCAGGGGAAAGTCTCTCATGCTCCGTGATGCATGAG 1377
Db 1347 ACCGTGGACAGAGCAGTGGCAGCAGGGGAAAGTCTCTCTCATGCTCCGTGATGCATGAG 1406
QY 1378 GCTCTGCACAACTACTACACGACAGAGAGCTCTCCCTGTCTCCGGGTAATGA 1431
Db 1407 GCTCTGCACAACTACTACACGACAGAGAGCTCTCCCTGTCTCCGGGTAATGA 1460

RESULT 8
ARI76296

LOCUS ARI76296 1418 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6312690.

ACCESSION ARI76296

VERSION ARI76296.1 GI:17918651

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1418)

AUTHORS Edelman, L., Margaratte, C., Kaczorek, M. and Chaabih, H.

TITLE Monoclonal recombinant anti-rhesus D (D7C2) antibody

JOURNAL Patent: US 6312690-A 7 06-NOV-2001;

FEATURES Location/Qualifiers

source 1..1418

BASE COUNT 332 a 454 c 379 g 253 t

ORIGIN

/organism="unknown"

Query Match 84.6%; Score 1210.4; DB 6; Length 1418;

Best Local Similarity 92.4%; Pred. No. 2.5e-235;

Matches 1310; Conservative 0; Mismatches 96; Indels 12; Gaps 3;

QY 13 TGGTTTCT 72

Db 13 TGTATCATCT 72

QY 73 CAGTGGGGGAGAGACTTCTGACGCTTCCGAGACCTGTCCGACCTCTCTCTCTCTCTCTCTCT 132

Db 73 CAGTGGGGGAGAGACTTCTGAGCCTTCCGAGACCTGTCTCTCTCTCTCTCTCTCTCTCTAT 132

QY 133 GGTGCTCCATCAGCGGTACTACTGACCTGGATCCGACAGACCCCGAGGAGGGGA 192

Db 133 GGTGCTCCATCAGTGGT---TACTACTGGAGCTGGATCCGACAGACCCCGAGGAGGGG 189

QY 193 CTGGAGTGGATGGCCATATTTATGGTAATGGTGGAGACCAACCAACTACAACTCCCTCCCTC 252

Db 190 CTGGAGTGGATGGGGAATCAA---TCATAGTGAAGACCAACCAACTACAACTCCCTCCCTC 246

QY 253 AAGAGTCGAGTCACATTTCAAAAGACACGTCACAAAGAACAGTTCTCTCTGAACTTGAAT 312

Db 247 AAGAGTCGAGTCACATATCAGTAGACACGTCACAAAGAACAGTTCTCTCTGAACTTGAAC 306

QY 313 TCTGTGACCGACCGGACACGGCGTCTATTATGTGCGAGAGGCGCTCGCCCTGATTCG 372

Db 307 TCTGTGACCGCGGACACGGCTGTGTATTACTGTGCGAGGG-----CCCCAGAGTAT 360

QY 373 ACAACCATTTCTTATGGCGGTGGTGCATGTCTGGGGCCCGGAGACCTGGTCCACCGTC 432

Db 361 AAATGGAAGTATATGGGAGCTGGTTCGACCCCTGGGGCCCAAGGTACCACTGTACCGTC 420

QY 433 TCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCTGGACCCCTCTCTCAAGAGACCC 492

Db 421 TCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCTGGACCCCTCTCTCAAGAGACCC 480

QY 493 TCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGAGTACTTCCCGAACCGGTGAGC 552

Db 481 TCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGAGTACTTCCCGAACCGGTGAGC 540

	Qy	553	GTGTCGTGGAACTCAGGCGCCCTGACGAGCGCGTGCACACTTCCC GGCTGTCTCTACAG	612
	Db	541		
	Db	541	GTGTCGTGGAACTCAGGCGCCCTGACGAGCGCGTGCACACTTCCC GGCTGTCTCTACAG	600
	Qy	613	TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTTGGGCACC	672
	Db	601		
	Db	601	TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTTGGGCACC	660
	Qy	673	CAGACCTTAATCTGCAACGTTGAATACAAGCCCCAGCAAACCAAGGTGGACAAGAAGCA	732
	Db	661		
	Db	661	CAGACCTTAATCTGCAACGTTGAATACAAGCCCCAGCAAACCAAGGTGGACAAGAAGCA	720
	Qy	733	GAGCCCAATCTTTGACAAAACCTCACATATGCCACCGTGCACGACCTTGAACCTCTG	792
	Db	721		
	Db	721	GAGCCCAATCTTTGACAAAACCTCAGCATATGCCACCGTGCACGACCTTGAACCTCTG	780
	Qy	793	GGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCTCATGATCTCCCGG	852
	Db	781		
	Db	781	GGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCTCATGATCTCCCGG	840
	Qy	853	ACCCCTGAGGTCAATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTC	912
	Db	841		
	Db	841	ACCCCTGAGGTCAATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTC	900
	Qy	913	AACCTGTTAGTGGACGGCGTGGAGTGATTAATGCAAGAACCCGCGGAGGAGCAG	972
	Db	901		
	Db	901	AACCTGTTAGTGGACGGCGTGGAGTGATTAATGCAAGAACCCGCGGAGGAGCAG	960
	Qy	973	TACAACGACGTAACCGTGTGTCAGCGTCTCACCGTCTGCAACGAGGACTGGCTGAAT	1032
	Db	961		
	Db	961	TACAACGACGTAACCGGCGTGTGTCAGCGTCTCAAAGTCTGTCACGAGGACTGGCTGAAT	1020
	Qy	1033	GGCAAGGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGAGCCCATCGAAGAAACC	1092
	Db	1021		
	Db	1021	GGCAAGGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGAGCCCATCGAAGAAACC	1080
	Qy	1093	ATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGG	1152
	Db	1081		
	Db	1081	ATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGG	1140
	Qy	1153	GATGAGCTGACCAAGAACCCAGGTGAGCTGACCTGACCTGCTGCTCAAGGCTTCTATCCGAC	1212
	Db	1141		
	Db	1141	GATGAGCTGACCAAGAACCCAGGTGAGCTGACCTGACCTGCTGCTCAAGGCTTCTATCCGAC	1200
	Qy	1213	GACATCGCGGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAAACAATAAGACACACGCT	1272
	Db	1201		
	Db	1201	GACATCGCGGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAAACAATAAGACACACGCT	1260
	Qy	1273	CCGTGTGTGACTCCGACGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGC	1332
	Db	1261		
	Db	1261	CCGTGTGTGACTCCGACGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGC	1320
	Qy	1333	AGTGGGACGAGGGGAGAGCTTCTCATGTCTCCGTGATGATGAGGCTCTGCACACAC	1392
	Db	1321		
	Db	1321	AGTGGGACGAGGGGAGAGCTTCTCATGTCTCCGTGATGATGAGGCTCTGCACACAC	1380
	Qy	1393	TACACGAGAGAGAGGCTCTCCCTGTCTCCGGGTAAATG	1430
	Db	1381		
	Db	1381	TACACGAGAGAGGCTCTCCCTGTCTCCGGGTAAATG	1418
	RESULT	9		
	LOCUS	AK057775		
	DEFINITION	Homo sapiens cDNA FLJ25046 fis, clone CBL03624, highly similar to Ig gamma immunoglobulin heavy chain.	1589 bp mRNA linear PRI 26-MAR-2002	
	ACCESSION	AK057775		
	VERSION	AK057775.1		
	KEYWORDS	oligo cloning; fis (full insert sequence).		
	SOURCE	Homo sapiens cerebellum cDNA to mRNA, clone lib:CBL clone: CBL03624.		
	ORGANISM	Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

[illegible]

QY 961 CGGGAGGACAGTACAACAGCAGTACCGTGTGGTCAAGTCTTCCAGGTCCTGACCCAG 1020
Db 934 CGGGAGGACAGTACAACAGCAGTACCGTGTGGTCAAGTCTTCCAGGTCCTGACCCAG 993
QY 1021 GACTCGCTGAATGGCAAGAGTACAAGTGCAGAGTCTCAACAAAGCCCTCCAGCCCC 1080
Db 994 GACTCGCTGAATGGCAAGAGTACAAGTGCAGAGTCTCAACAAAGCCCTCCAGCCCC 1053
QY 1081 ATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACAGAGTGTACACCCCTG 1140
Db 1054 ATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACAGAGTGTACACCCCTG 1113
QY 1141 CCCCATCCCGGAGTGAAGTGAACAAAGAACAGAGTCAAGCTGCTGGTCAAGGCG 1200
Db 1114 CCCCATCCCGGAGTGAAGTGAACAAAGAACAGAGTCAAGCTGCTGGTCAAGGCG 1173
QY 1201 TTCTATCCCGAGGACATCGCGTGGAGTGGGAGAGCAATGGCGAGCCCGAGAACAACTAC 1260
Db 1174 TTCTATCCCGAGGACATCGCGTGGAGTGGGAGAGCAATGGCGAGCCCGAGAACAACTAC 1233
QY 1261 AAGACCGCTCCCGTGTGAGTCTCCAGCGCTCTTCTTCTCTACAGCAAGCTCACC 1320
Db 1234 AAGACCGCTCCCGTGTGAGTCTCCAGCGCTCTTCTTCTCTACAGCAAGCTCACC 1293
QY 1321 GTGGACAAGAGCAGTGGCAGAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGCT 1380
Db 1294 GTGGACAAGAGCAGTGGCAGAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGCT 1353
QY 1381 CTGCAACCACTACACAGAGAGCCTCTCCCTGTCTCTGGGTAAATGA 1431
Db 1354 CTGCAACCACTACACAGAGAGCCTCTCCCTGTCTCTGGGTAAATGA 1404

RESULT 13
ARI135376
LOCUS ARI135376 1404 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 9 from patent US 6136310.
ACCESSION ARI135376
VERSION ARI135376.1 GI:14476048
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Hanna,N., Newman,R.,Anthony. and Reff,M.,Elliot.
TITLE Recombinant anti-CD4 antibodies for human therapy
JOURNAL Patent: US 6136310-A 9 24-OCT-2000;
FEATURES Location/Qualifiers
source 1..1404
BASE COUNT 313 a 446 c 379 g 266 t
ORIGIN

Query Match 81.5%; Score 1166.6; DB 6; Length 1404;
Best Local Similarity 89.8%; Pred. No. 1.9e-226;
Matches 1285; Conservative 0; Mismatches 119; Indels 27; Gaps 2;
QY 1 ATGAACACCTGTGGTCTTCTCTCTCTGTGGCAGCTCCAGATGGTCTGTGCCAG 60
Db 1 ATGAACACCTGTGGTCTTCTCTCTCTGTGGCAGCTCCAGATGGTCTGTGCCAG 60
QY 61 GTGAAGTGCAGCAGTGGGGGGAAGAGTCTCTGAGCCTTCGGAGACCTGTCCCGACC 120
Db 61 GTGAGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
QY 121 TGGCTGTCTCTGTGTCTCCATCAGCGGTGTACTACTTGGACCTGGATCCGCGAGCC 180
Db 121 TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGTACTATTATGGTCTGGATCCGCGAGTCC 180
QY 181 CCAGGAGGGGACCTGGAGTGGGCAATATTTATGGTAATGGTGGGACCACTAC 240
Db 181 CCAGGAGGGGACCTGGAGTGGGCAATATTTATGGTAATGGTGGGACCACTAC 240

QY 241 AATCCCTCCCTCAAGTCCAGTCAACATTTCAAAGACACGCTCCAAAGACACGTTCTTTC 300
Db 241 AATCCCTCCCTCAACATTTCAAAGTCTCAATTTCAATAGACACGCTCCAAAGACACCTTTCTCC 300
QY 301 CTGAACCTGAATTTCTGTGACCGGACACGCGCGTCTATTACTGTGCGAGAGGCGCT 360
Db 301 CTGAACCTGAAGTCTGTGACCGGCGGACACGCGCGTCTATTACTGTGCGA----- 352
QY 361 CGCCCTGATTTGCAACACCATTTGTTATGGGGCTGGGTGATGTCTGGGGCCCGGAGAC 420
Db 353 -----GTAATATATTGAATATCTTCACTGGTTATTATCTGGGGCCAGGGAGTC 402
QY 421 CTGGTCAACCGTCTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCC 480
Db 403 CTGGTCAACCGTCTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGGGCCCTGC 462
QY 481 TCAAGAGACACCTCTGGGGGACACGCGGCCCTGGGCTGCTTGGTCAAGGACTACTTCCCC 540
Db 463 TCCAGGAGCACCTCCGAGAGACACGCGGCCCTGGGCTGCTTGGTCAAGGACTACTTCCCC 522
QY 541 GAACCGGTGACGGTGTGCTGGAACTCAGGGCGCCCTGACCCAGCGGGGTGCACACCTTCCCG 600
Db 523 GAACCGGTGACGGTGTGCTGGAACTCAGGGCGCCCTGACCCAGCGGGGTGCACACCTTCCCG 582
QY 601 GCTGTCTTACAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGTGTGTGACCGTGCCTCCAG 660
Db 583 GCTGTCTTACAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGTGTGTGACCGTGCCTCCAG 642
QY 661 AGTTGGGCAACCGACCTATCATCTGTCAACAGTGAATCACAAGCCCCAGCAACACCAAGGTG 720
Db 643 AGTTGGGCAACGAAGACCTACACCTGCAACGTAGATCACAAGCCCCAGCAACACCAAGGTG 702
QY 721 GACAAGAAAGAGAGAGCCCAATCTTGTGACAAATCTCACATATGCCACCGTGCACGCA 780
Db 703 GACAAGAGAGTTGAGTCCAAATATGG-----TCCCCCATGCCCCTCATGTGCCAGCA 753
QY 781 CCTGAACTCTCTGGGGGAGCCGTCACTCTTCTTCTTCCCCCAGGAGGAGGAGGAGGAGGAGG 840
Db 754 CCTGAGTTCGAGGGGGGACCATCAGTCTTCTTCTTCCCCCAGGAGGAGGAGGAGGAGGAGG 813
QY 841 ATGATCTCCCGGACCCCTGAGGTCAATCGTGTGGTGGAGCGTGAGCCAGCAAGAACCTT 900
Db 814 ATGATCTCCCGGACCCCTGAGGTCAATCGTGTGGTGGAGCGTGAGCGAGGAGGAGGAGGAG 873
QY 901 GAGGTCAAGTTCACACTGGTACCGTGGAGCGGCTGGAGGTGCATTAATCCCAAGCAAGCGCG 960
Db 874 GAGGTCCAGTTCACACTGGTACCGTGGATGGCGTGGAGGTGCATAATGCCAAGCAAGCGCG 933
QY 961 CGGGAGGAGCAGTACAACAGCAGCAGTACCGTGTGGTCAAGCGTCTTCAACCGTCTGACCCAG 1020
Db 934 CGGGAGGAGCAGTACAACAGCAGCAGTACCGTGTGGTCAAGCGTCTTCAACCGTCTGACCCAG 993
QY 1021 GACTGGCTGAATGGCAAGAGTACAAGTGCAGAGTCTTCAACAAAGCCCTCCAGCCCC 1080
Db 994 GACTGGCTGAACGGCAAGAGTACAAGTGCAGAGTCTTCAACAAAGGCGCTCCCGCTCTCC 1053
QY 1081 ATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACAGAGTGTACACCCCTG 1140
Db 1054 ATCGAGAAACCATCTTCAAGCCAAAGGCGAGCCCGAGAACACAGAGTGTACACCCCTG 1113
QY 1141 CCCCATCCCGGAGTGAAGTGAACAAAGAACAGGCTGACCTGCTGGTCAAGGCG 1200
Db 1114 CCCCATCCCGGAGGAGATGACCAAGAACAGGTCAGCTGACCTGCTGGTCAAGGCG 1173
QY 1201 TTCTATCCCGAGGACATCGCGTGGAGTGGGAGAGCAATGGGAGCGCCGAGAACAACTAC 1260
Db 1174 TTCTATCCCGAGGACATCGCGTGGAGTGGGAGAGCAATGGGAGCGCCGAGAACAACTAC 1233
QY 1261 AAGACCGCTCCCGTGTGAGTCTCCAGCGCTCTTCTTCTCTACAGCAAGCTCACC 1320
Db 1234 AAGACCGCTCCCGTGTGAGTCTCCAGCGCTCTTCTTCTCTACAGCAAGCTCACC 1293

[illegible]

```
Qy 1201 TTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTAC 1260
    |||||
Db 1170 TTCTATCCCGAGCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTAC 1229
    |||||
Qy 1261 AGACCAACGCTCCCGTGTGGACTCCGACGGGTCTTCTTCTCTACAGCAAGCTCACC 1320
    |||||
Db 1230 AGACCAACACCTCCCATGTGTGGACTCCGACGGGTCTTCTTCTCTACAGCAAGCTCACC 1289
    |||||
Qy 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGNAACGTCTTCTCATGTCTCCGTGATGCATGAGGCT 1380
    |||||
Db 1290 GTGGACAAGAGCAGGTGGCAGCAGGGGNAACGTCTTCTCATGTCTCCGTGATGCATGAGGCT 1349
    |||||
Qy 1381 CTGCACAACCACTACACGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1431
    |||||
Db 1350 CTGCACAACCACTACACGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1400
    |||||
```

Search completed: April 6, 2003, 01:56:00
Job time : 4496.25 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 8.31417 Seconds
(without alignments)
828.100 Million cell updates/sec

Title: US-09-758-173-2

Perfect score: 1243

Sequence: 1 MRVPAQLGLLLWLPGARCAVELTQPPSVSPQQTARITCGGDSNRNEVHHVYQOKPA 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1243	100.0	234	3	US-08-487-550-2
2	1015.5	81.7	233	4	US-08-523-894-6
3	973	78.3	236	3	US-08-487-550-10
4	880.5	70.8	236	4	US-09-049-672A-7
5	867.5	69.8	235	2	US-09-049-672A-10
6	861	69.3	235	2	US-08-378-939-12
7	855.5	68.8	238	4	US-08-793-450-6
8	835	68.8	235	4	US-09-049-672A-12
9	844	67.9	240	4	US-09-049-672A-11
10	812	65.3	235	4	US-09-152-060-70
11	809	65.1	235	4	US-09-152-060-88
12	658.5	53.0	229	4	US-08-751-359-22
13	658.5	53.0	229	4	US-08-907-146-22
14	567	45.6	109	2	US-08-761-277A-51
15	560.5	45.1	200	6	5189147-10
16	548	44.1	105	1	US-08-422-101-9
17	548	44.1	105	1	US-08-422-091-9
18	548	44.1	105	2	US-08-422-092-9
19	548	44.1	105	2	US-08-788-800-6
20	548	44.1	105	3	US-08-422-093-9
21	548	44.1	105	3	US-08-422-112-9
22	535	43.0	104	4	US-09-025-769B-170
23	503	40.5	241	4	US-07-916-098A-56
24	502.5	40.4	235	3	US-08-812-586-16
25	500.5	40.3	143	2	US-08-345-321-8
26	500.5	40.3	236	1	US-08-157-101A-5
27	487	39.2	235	1	US-08-276-852-153

28	487	39.2	235	1	US-08-899-575-153	Sequence 153, App
29	487	39.2	235	1	US-08-899-575-153	Sequence 153, App
30	487	39.2	235	5	PCT-US95-08743-153	Sequence 153, App
31	483.5	38.9	234	5	PCT-US94-07659-4	Sequence 4, Appl1
32	477.5	38.4	234	2	US-07-690-192-2	Sequence 2, Appl1
33	475	38.2	239	3	US-08-487-550-6	Sequence 6, Appl1
34	469.5	37.8	234	4	US-09-049-672A-6	Sequence 6, Appl1
35	467.5	37.6	128	1	US-08-478-039-110	Sequence 110, App
36	467.5	37.6	128	1	US-08-476-349A-110	Sequence 110, App
37	467.5	37.6	128	4	US-08-523-894-4	Sequence 4, Appl1
38	466	37.5	105	2	US-08-646-981-3	Sequence 3, Appl1
39	457	36.8	108	1	US-08-259-372A-10	Sequence 10, Appl1
40	457	36.8	108	1	US-08-468-671-10	Sequence 10, Appl1
41	456	36.7	235	4	US-09-423-439-58	Sequence 58, Appl1
42	456	36.7	235	4	US-09-011-769A-23	Sequence 23, Appl1
43	454	36.5	109	4	US-09-202-181-2	Sequence 2, Appl1
44	452	36.4	109	1	US-08-478-039-91	Sequence 91, Appl1
45	452	36.4	109	1	US-08-476-349A-91	Sequence 91, Appl1

ALIGNMENTS

RESULT 1

US-08-487-550-2

; Sequence 2, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 234 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-487-550-2

Query Match 100.0%; Score 1243; DB 3; Length 234;

Best Local Similarity 100.0%; Pred. No. 9.9e-103;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRVPAQLGLLLWLPGARCAVELTQPPSVSPQQTARITCGGDSNRNEVHHVYQOKPA 60

Db 1 MRVPAQLGLLLWLPGARCAVELTQPPSVSPQQTARITCGGDSNRNEVHHVYQOKPA 60

QY 61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDPVFG 120
DB 61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDPVFG 120
QY 121 GGTTRVTLGQPKAAPSVTLPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
DB 121 GGTTRVTLGQPKAAPSVTLPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
QY 181 VETTTPSKSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
DB 181 VETTTPSKSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
RESULT 2
US-08-523-894-6
; Sequence 6, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-6
Query Match 81.7%; Score 1015.5; DB 4; Length 233;
Best Local Similarity 86.0%; Pred. No. 1.4e-82;
Matches 196; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
QY 7 LLGILLWLPQARCAVELTQPPSVSVSPGQTARITCGGDNRSNEYVHWYQKPARAPILV 66
DB 7 LLGILLWLPQARCAVELTQPPSVSVSPGQTARITCGGDNRSNEYVHWYQKPARAPILV 66
QY 67 IYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDPVFGGTRVT 126
DB 67 IYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDPVFGGTRVT 126
QY 127 VLGQPKAAPSVTLPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTP 186
DB 127 VLGQPKAAPSVTLPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTP 186
QY 187 SKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
DB 187 SKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

DB 186 SKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233
RESULT 3
US-08-487-550-10
; Sequence 10, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-10
Query Match 78.3%; Score 973; DB 3; Length 236;
Best Local Similarity 80.1%; Pred. No. 8.3e-79;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;
QY 1 MRVPAQLGLLLWLPQARCAVELTQPPSVSVSPGQTARITCGGDNRSNEYVHWYQK 58
DB 1 MRVPAQLGLLLWLPQARCAVELTQPPSVSVSPGQTARITCGGDNRSNEYVHWYQK 58
QY 59 PARAPILVIYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDPV 118
DB 59 PARAPILVIYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDPV 118
QY 61 PGTPAKLLIYDINKRPSGISDRFSGSKSGTAAALITGLQTEDEADYYCQSDSLNAQV 120
DB 61 PGTPAKLLIYDINKRPSGISDRFSGSKSGTAAALITGLQTEDEADYYCQSDSLNAQV 120
QY 119 FCGGTRVTLGQPKAAPSVTLPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
DB 119 FCGGTRVTLGQPKAAPSVTLPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
QY 121 FCGGTRVTLGQPKAAPSVTLPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 121 FCGGTRVTLGQPKAAPSVTLPSPSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 179 AGVETTTPSKSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
DB 179 AGVETTTPSKSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
QY 181 AGVETTTPSKSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 181 AGVETTTPSKSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
RESULT 4
US-09-049-672A-7
; Sequence 7, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti

```

; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ADRETUT05
; CLONE: 2492122
; US-09-049-672A-7

Query Match 70.8%; Score 880.5; DB 4; Length 236;
Best Local Similarity 74.9%; Pred. No. 1.3e-70;
Matches 173; Conservative 17; Mismatches 38; Indels 3; Gaps 1;

Qy 7 LLGLLLWLPGARCAYELTPPPSVSPGQTARITCGDNR--NEYVHWYQQPARAP 63
Db 6 LLLTLAHC TGSAQSVLTQPPSVSGAPQRTVITCTGSSNIGAGYDVHWYQLPGTAP 65
Qy 64 ILIVYDDSDRPGIPERFSGSKGNATLTINGVEAGDEADYICQWDRASDHPVFGGTT 123
Db 66 KULIYGSNRPRGVPDRFSGSKGTSASLAITGLQADEADYICQSDSSISGVVFGGTT 125
Qy 124 RVTVLGQPKAAASVTLFPSPSEELQANKATLVCLISDFYPGAVTVAMKADSPVKAGVET 183
Db 126 KLTVLGQPKAAASVTLFPSPSEELQANKATLVCLISDFYPGAVTVAMKADSPVKAGVET 185
Qy 184 TTPSKQSNKNKYAASSYLSLTPPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 186 TTPSKQSNKNKYAASSYLSLTPPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 5
US-09-049-672A-10
; Sequence 10, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

```

```

; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYRNOT10
; CLONE: 2872705
; US-09-049-672A-10

Query Match 69.8%; Score 867.5; DB 4; Length 235;
Best Local Similarity 74.7%; Pred. No. 1.8e-69;
Matches 177; Conservative 16; Mismatches 29; Indels 15; Gaps 4;

Qy 7 LLGLLLL-----WLPGARCAYELTPPPSVSPGQTARITCGDNR---RNEYVHWYQQ 57
Db 5 LLFLTLTQTGTGSAQSA-----LTQPASVSGSPGSIITISCTGSDVGGYVSVWYQQ 59
Qy 58 KPARAPILVIYDDSDRPGIPERFSGSKGNATLTINGVEAGDEADYICQWDRASDHP 117
Db 60 SPGTAPKLMIEYVSNRPSGVSNNRPSGSKGNATLTISGLQADEADYICSSY-VGNIV 118
Qy 118 VFGGTRVTVLPGPKAAPSVTLFPSPSEELQANKATLVCLISDFYPGAVTVAMKADSPV 177
Db 119 VFGGTRVTVLPGPKAAPSVTLFPSPSEELQANKATLVCLISDFYPGAVTVAMKADSPV 178
Qy 178 KAGVETTTSPKQSNKNKYAASSYLSLTPPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 KAGVETTTSPKQSNKNKYAASSYLSLTPPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 6
US-08-378-939-12
; Sequence 12, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:

```

```

; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-378-939-12

Query Match 59.3%; Score 861; DB 2; Length 235;
Best Local Similarity 75.1%; Pred. No. 6.9e-69;
Matches 175; Conservative 16; Mismatches 38; Indels 4; Gaps 2;

QY 5 AQLGLLLLPAGCAYELTPPPSVSPGQTARITCGGDNS---RNEYVHVYQKPAR 61
DB 4 ALLLLTLTQGTGWAQSALTQPASVSGSQSITISCTGTNDVGSYLVSVYQQHPGK 63
QY 62 APILVYDSDRPSGIPERFSGSKGNATLTINGVAGDEADYQCQWDRADHPVFGG 121
DB 64 APKTMIEVSKRPSGVSNRFGSKSGNTASLITISGLQAEDEADYCCSY-AGSYTVVVF 122
QY 122 GTRVTVLGQPKAAPSVTLPSPSSSELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
DB 123 GTKLVTVLGQPKAAPSVTLPSPSSSELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 182
QY 182 ETTTPSKQSNKNKYAASSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
DB 183 ETTTPSKQSNKNKYAASSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 7
US-08-793-450-6
; Sequence 6, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

```

```

; ADDRESSEE: P. C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-793-450-6

Query Match 68.8%; Score 855.5; DB 4; Length 238;
Best Local Similarity 73.2%; Pred. No. 2.2e-68;
Matches 167; Conservative 14; Mismatches 32; Indels 15; Gaps 2;

QY 17 GARCAYELTPPPSVSPGQTARITCGGDNSRNEYVHVYQKPARAPILVIYDSDRPSG 76
DB 16 GVHSDIELTQDPVAVSVALGQTVRITCQGDSLRTYVASYWYQKPGQAPVLVIYGNRPSG 75
QY 77 IPERFSGSKGNATLTINGVAGDEADYQCQWDRADHPVFGGTRTVTLGQPKAAPS 136
DB 76 IPDRFSGSGNTASLITITGADEADYFCN-----SGGKVFGGTKLTVLGQPKAAPS 130
QY 137 VTLFPPS-----SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVEITTP 186
DB 131 VTLFPPSLEELQANKATLEELQANKATLVCLISDFYPGAVTVLAWKADGRPVKAGVEITNKP 190
QY 187 SKQSNKNKYAASSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
DB 191 SKQSNKNKYAASSYLSLTPQWKSHRSYSCQVTHEGSTAEKTVAPAECS 238

RESULT 8
US-09-049-672A-12
; Sequence 12, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

```

```

; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HERewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTUT13
; CLONE: 3116314
; US-09-049-672A-12

```

Query Match 68.8%; Score 855; DB 4; Length 235;

Best Local Similarity 72.6%; Pred. No. 2.4e-68; Indels 2; Gaps 1;

Matches 167; Conservative 17; Mismatches 44; Indels 2; Gaps 1;

```

QY 7 LLGLLLLPFGARCAVELTOPPSVSPGQTARITCG--DNSRNEYVHWYQKPARAPI 64
DB 6 LLLALLTHCAGSQAQSVLTQPPSASGTPGQRTISCGTTSNIASNVHWYQLVPGAAPK 65
QY 65 LVYIDSDRPSGIPERFSGSKGNATLTINGVEAGDEADYQCQWDRADHPVFGGTR 124
DB 66 LLIYANDQASGVPDRFSGSKGTSASLAISGLRPEDETDYYCATWDDSVSGWFMFGGTK 125
QY 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPCAVTVAMKADSSPKAGVETT 184
DB 126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPCAVTVAMKADSSPKAGVETT 185
QY 185 TPSSQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
DB 186 TPSSQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

```

RESULT 9

```

US-09-049-672A-11
; Sequence 11, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive

```

```

; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HERewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LNOODNOT08
; CLONE: 3056213
; US-09-049-672A-11

```

Query Match 57.9%; Score 844; DB 4; Length 240;

Best Local Similarity 71.4%; Pred. No. 2.3e-67; Indels 8; Gaps 3;

Matches 172; Conservative 16; Mismatches 45; Indels 8; Gaps 3;

```

QY 1 MRVPAQLLGLLLWL---PGARCAVELTOPPSVSPGQTARITCG--GDNSRNEYVH 53
DB 1 MSVTMAMMLLLGLLAYGSGVDSQTVTQEPFSVSPGGTVTLTCLSGSGSVSTSNPS 60
QY 54 WYQKPARAPILVIYDDSDRPSGIPERFSGSKGNATLTINGVEAGDEADYQCQWDR 113
DB 61 WYQTPGQAPRTLIVGTSSRSGVDRFSGSILGNKAGLITGAQADSDSYCVLY-RR 119
QY 114 SDHPVFGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPCAVTVAMKAD 173
DB 120 SGSWVFGGTKSLVGLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPCAVTVAMKAD 179
QY 174 SSPVKAGVETTTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
DB 180 SSPVKAGVETTTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 239

```

RESULT 10

```

US-09-152-060-70
; Sequence 70, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762

```

```

;
; TOPOLOGY:
; 110 00 751 350 33

```


Query Match 53.0%; Score 658.5; DB 4; Length 229;
Best Local Similarity 57.6%; Pred. No. 5.8e-51;
Matches 133; Conservative 32; Mismatches 59; Indels 7; Gaps 5;

QY 5 AQLGLLLWLPQARCAVELTOPPSVSPGOTARITCGDNRSEYVHWYQOK-PARAP 63
Db 4 APLLAVLAHTSGSLVQAAALTOPSSVSANPGETVKITCSGDRS---YYGWYQOKAPGSAP 60

QY 64 ILVIYDDSRPISGIPERFSGSKSGNTATLITINGVEAGDEADYYCQVMDRASDPVFGGCT 123
Db 61 VTVIYANTNRPSDIPSRFSGSKSGSTATLITGVQADDEAVYYCGSADSSSTAGIFGAGT 120

QY 124 RVTVLGQPKAAPSVTLFPPSSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
Db 121 TLTVLGPQKVPATITLFPSPSKEELNEATKATLVCLINDFYPSPTVDWVIDGS-TRSG-E 178

QY 183 TTPSPKSNKYAASSYLSITPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
Db 179 TTAQRQSNQYMASSYLSASDMSWSSHETYTCRVTHNGTSITKTLKRSEC 229

RESULT 13
US-08-907-146-22
; Sequence 22, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,146
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,359
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-907-146-22

Query Match 53.0%; Score 658.5; DB 4; Length 229;
Best Local Similarity 57.6%; Pred. No. 5.8e-51;
Matches 133; Conservative 32; Mismatches 59; Indels 7; Gaps 5;

QY 5 AQLGLLLWLPQARCAVELTOPPSVSPGOTARITCGDNRSEYVHWYQOK-PARAP 63
Db 4 APLLAVLAHTSGSLVQAAALTOPSSVSANPGETVKITCSGDRS---YYGWYQOKAPGSAP 60

QY 64 ILVIYDDSRPISGIPERFSGSKSGNTATLITINGVEAGDEADYYCQVMDRASDPVFGGCT 123
Db 61 VTVIYANTNRPSDIPSRFSGSKSGSTATLITGVQADDEAVYYCGSADSSSTAGIFGAGT 120

QY 124 RVTVLGQPKAAPSVTLFPPSSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
Db 121 TLTVLGPQKVPATITLFPSPSKEELNEATKATLVCLINDFYPSPTVDWVIDGS-TRSG-E 178

QY 183 TTPSPKSNKYAASSYLSITPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
Db 179 TTAQRQSNQYMASSYLSASDMSWSSHETYTCRVTHNGTSITKTLKRSEC 229

Db 4 APLLAVLAHTSGSLVQAAALTOPSSVSANPGETVKITCSGDRS---YYGWYQOKAPGSAP 60

QY 64 ILVIYDDSRPISGIPERFSGSKSGNTATLITINGVEAGDEADYYCQVMDRASDPVFGGCT 123
Db 61 VTVIYANTNRPSDIPSRFSGSKSGSTATLITGVQADDEAVYYCGSADSSSTAGIFGAGT 120

QY 124 RVTVLGQPKAAPSVTLFPPSSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
Db 121 TLTVLGPQKVPATITLFPSPSKEELNEATKATLVCLINDFYPSPTVDWVIDGS-TRSG-E 178

QY 183 TTPSPKSNKYAASSYLSITPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
Db 179 TTAQRQSNQYMASSYLSASDMSWSSHETYTCRVTHNGTSITKTLKRSEC 229

RESULT 14
US-08-761-277A-51
; Sequence 51, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOPE-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-761-277A-51

Query Match 45.8%; Score 567; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 TVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT 185
Db 1 TVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT 60

QY 186 PSKQSNKYAASSYLSITPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 61 PSKQSNKYAASSYLSITPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 109

RESULT 15
5189147-10

; Patent No. 5189147
; APPLICANT: SAITO, HARUO; KRAUS, DAVID M.; ELSEN, HERMAN N.;
; TONEGAWA, SUSUMU
; TITLE OF INVENTION: METEODIMERIC T LYMPHOCYTE RECEPTOR
; ANTIBODY
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO:10:
; LENGTH: 200
; 5189147-10

Query Match 45.1%; Score 560.5; DB 6; Length 200;
Best Local Similarity 53.3%; Pred. No. 2.4e-42;
Matches 112; Conservative 28; Mismatches 51; Indels 19; Gaps 4;
Qy 24 LTQPPSVSVSPGOTARITC---GGDNRNEYVHWYQKPARAPIL-VIYDDSDRPSGIPE 79
Db 4 VTQESALTTPGETVTLTCRSSTGAVTTSNYANWVQKPDHFLFTGLIGGTNNRAPGVPA 63
Qy 80 RFGSGSGNTATLTINGVEAGDEADYICQWDRASDPVFGGTRVTVLGPKAAPSVTL 139
Db 64 RFGSLIGNKAALTITGAQTEDEAIYFCALM---SNH-----WQPKSPSVTL 108
Qy 140 FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKSNKYNKYAASY 199
Db 109 FPPSSELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTPSKSNKYNKYMASSY 168
Qy 200 LSLTPEQWKSRSYSCQVTHEGSTVEKTV 229
Db 169 LTLTARAWERHSSYSCQVTHEGHTVEKSL 198

Search completed: March 29, 2003, 09:17:39
Job time : 10.3142 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 24.0673 Seconds
(without alignments)
1295.559 Million cell updates/sec

Title: US-09-758-173-2

Perfect score: 1243

Sequence: 1 MRVPAQLGLLLWLPQARC.....CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1243	100.0	234	18 AAW01817	Primatized anti-hu
2	1243	100.0	234	19 AAW63760	Macaque primatized
3	1243	100.0	234	23 AAU11538	Protein sequence o
4	1015.5	81.7	233	18 AAW14924	Ant-CD4 monkey-hum
5	991.5	79.8	247	22 ABG19295	Novel human diagno
6	979	78.8	228	22 ABG19299	Novel human diagno
7	976.5	78.6	232	22 AAU14412	Human novel protei
8	973	78.3	236	19 AAW63764	Macaque primatized
9	973	78.3	236	23 AAU11645	Protein sequence o
10	973	78.3	269	23 ABP41361	Human ovarian anti

11	970	78.0	236	18 AAW01821	Primatized anti-hu
12	959	77.2	231	22 AAU14176	Human novel protei
13	959	77.2	234	22 ABG23084	Novel human diagno
14	958.5	77.1	232	22 AAU14236	Human novel protei
15	944	75.9	218	22 AAU08381	Anti-OPGbp antibod
16	944	75.9	233	23 AAU82012	Human secreted pro
17	939.5	75.6	236	22 AAU14472	Human novel protei
18	936.5	75.3	244	21 AAB43979	Human cancer assoc
19	936	75.3	226	22 ABG19294	Novel human diagno
20	925	74.4	233	9 AAP81260	VDJC regions of hu
21	912	73.4	231	23 AAU81991	Human secreted pro
22	906.5	72.9	232	22 AAM23527	Human EST encoded
23	905	72.8	238	22 ABG19297	Novel human diagno
24	898.5	72.3	246	22 ABB12413	Human bone marrow
25	884.5	71.2	217	14 AAR42163	Anti-HIV-1 recomb
26	881	70.9	236	22 ABG23083	Novel human diagno
27	880.5	70.8	236	22 AAB36209	Human immune syste
28	880	70.8	235	20 AAW88465	Monoclonal antibod
29	879.5	70.8	217	19 AAW40533	Antibody HB4C5 lig
30	870	70.0	249	22 ABG12886	Novel human diagno
31	867.5	69.8	235	22 ABG19290	Novel human diagno
32	867.5	69.8	235	22 AAB36212	Human immune syste
33	865.5	69.6	219	21 AAB30594	Variable and first
34	864.5	69.5	236	22 ABG19293	Novel human diagno
35	864	69.5	235	22 AAG64474	Human type antihum
36	864	69.5	244	22 ABG19296	Novel human diagno
37	864	69.5	251	22 ABG19291	Novel human diagno
38	863	69.4	235	22 AAG64472	Human type antihum
39	861	69.3	235	14 AAR31024	Antibody D light c
40	860	69.2	235	22 AAM38953	Human polypeptide
41	860	69.2	235	22 AAG64476	Human type antihum
42	855.5	68.8	238	17 AAR93165	Anti-rhesus D reco
43	855	68.8	235	22 AAB36214	Human immune syste
44	853	68.6	614	23 ABB06275	Plasmid scfv(CC046
45	849	68.3	240	21 AAY96306	Human IGFAM-18 imm

ALIGNMENTS

RESULT 1

AAW01817

ID AAW01817 standard; Protein; 234 AA.

XX AAW01817;

XX AC

XX 25-MAY-1997 (first entry)

DT

XX

DE Primatized anti-human B7.1 antigen antibody 7C10 light chain.

XX

KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;

KW primatized antibody; B7 antigen; CD28; immunosuppressive;

KW autoimmune disease; idiopathic thrombocytopenia purpura;

KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;

KW type 1 diabetes mellitus; graft versus host disease;

KW hetero-hybridoma; transfectoma.

XX

OS Chimeric Macaca cynomolgus;

OS Chimeric Homo sapiens.

XX

FN WO9640878-A1.

XX

PD 19-DEC-1996.

XX

XX 06-JUN-1996; 96WO-US10053.

XX

PR 07-JUN-1995; 95US-0487550.

XX

PA (IDEC-) IDEC PHARM CORP.

XX

PI Anderson DR, Brams P, Hanna N, Shestowsky WS;

XX WPI; 1997-108638/10.

DR N-PSDB; AAT62509.

XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -

PT useful for treating autoimmune disease or graft-versus-host disease

XX Claim 6; Fig 8A; 81pp; English.

XX 2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised

CC forms of the light and heavy chains of cynomolgus monkey anti-human

CC B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy

CC variable genes (see also AAT62509 and AAT62510) are inserted into

CC an expression vector (pref. NEOSPLA) which contains human light and

CC heavy chain constant region genes to allow prodn. of the primatised

CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1

CC antibodies have also been produced (see also AAW01819-22). The

CC primatised antibodies inhibit the B7:CD28 pathway, making them

CC useful immunosuppressants for the treatment of autoimmune disorders

CC and graft-versus-host disease.

XX Sequence 234 AA;

Query Match 100.0%; Score 1243; DB 18; Length 234;

Best Local Similarity 100.0%; Pred. No. 1e-70;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLGLLLWLPFCARCAVELTOPPSVSVPQTARITCGDNRNRYVHWYQKPA 60

DB 1 MRVPAQLGLGLLLWLPFCARCAVELTOPPSVSVPQTARITCGDNRNRYVHWYQKPA 60

QY 61 RAPILVIYDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYICQVMDRASHDPVFG 120

DB 61 RAPILVIYDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYICQVMDRASHDPVFG 120

QY 121 GGRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

DB 121 GGRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

QY 181 VETTPSKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234

DB 181 VETTPSKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 2

AAW63760

ID AAW63760 standard; Protein; 234 AA.

XX AAW63760;

XX 29-SEP-1998 (first entry)

DE Macaque primatised 7C10 light chain protein.

XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;

XX CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;

XX T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;

XX immunogen; anti-idiotype reagent; interleukin-2; IGF; immunoglobulin G;

XX T cell proliferation.

XX Macaca fascicularis.

XX WO9819706-A1.

XX 14-MAY-1998.

XX 29-OCT-1997; 97WO-US19906.

XX 08-NOV-1996; 96US-0746361.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Brams P, Hanna N;

XX WPI; 1998-286601/25.

DR N-PSDB; AAV35484.

XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and

PT inhibiting binding to CD28 - useful as specific immunosuppressants

PT for treating diseases that involve interactions between T and B

PT cells, e.g. graft rejection or tumours

XX Example 7; Fig 3a; 87pp; English.

XX This sequence represents a primatised form of the antibody 7C10 light

CC chain from macaque. This sequence is used in a method which studies new

CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to

CC B7.2 (CD86) antigens and inhibit binding of these antigens to CD28. Such

CC Mab's are specific immunosuppressants for treatment of diseases involving

CC T cell/B cell interactions, particularly autoimmune disease, specifically

CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type

CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,

CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.

CC host diseases, B cell lymphoma, infections (including by human immune

CC deficiency virus) or inflammatory disease and tumours. Optionally the

CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can

CC also be used as imaging agents and as vaccines or immunogens to develop

CC anti-idiotype reagents. Mab's are optionally combined with other proteins

CC or small molecule immunosuppressants. Blocking B7/CD28 interactions

CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits

CC production of interleukin-2 (IL-2), T cell proliferation and

CC antigen-specific immunoglobulin G (IgG) responses.

XX Sequence 234 AA;

Query Match 100.0%; Score 1243; DB 19; Length 234;

Best Local Similarity 100.0%; Pred. No. 1e-70;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLGLLLWLPFCARCAVELTOPPSVSVPQTARITCGDNRNRYVHWYQKPA 60

DB 1 MRVPAQLGLGLLLWLPFCARCAVELTOPPSVSVPQTARITCGDNRNRYVHWYQKPA 60

QY 61 RAPILVIYDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYICQVMDRASHDPVFG 120

DB 61 RAPILVIYDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYICQVMDRASHDPVFG 120

QY 121 GGRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

DB 121 GGRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

QY 181 VETTPSKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234

DB 181 VETTPSKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 3

AAU11538

ID AAU11538 standard; Protein; 234 AA.

XX AAU11538;

XX 12-MAR-2002 (first entry)

DE Protein sequence of primatised form of the light chain of 7C10 antibody.

XX Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;

XX neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;

XX B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;

XX tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;

XX graft-vs-host disease; immunosuppression; organ rejection;

XX interleukin-2; IL-2; mutant; mutein.

XX Chimeric - Homo sapiens.

XX Chimeric - Macaca sp.

XX Synthetic.

XX WO200189567-A1.

XX PD 29-NOV-2001.
 XX PF 22-MAY-2001; 2001WO-US16364.
 XX PR 22-MAY-2000; 2000US-0576424.
 XX PA (IDEC-) IDEC PHARM CORP.
 XX PI Anderson DR, Hanna N, Brans P;
 XX DR WPI; 2002-089895/12.
 XX DR N-PSDB; AAS17242.
 XX PT Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease such as
 PT allergy
 XX PS Example 8; Fig 3a; 89pp; English.
 XX CC The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present protein
 CC sequence represents the light chain of 7C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).
 XX SQ Sequence 234 AA;
 Query Match 100.0%; Score 1243; DB 23; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1e-70;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRVPAQLGLLLWLPGARCAVELTPPPSVSPGQTARITCGDNRNRYVHWYQKPA 60
 Db 1 MRVPAQLGLLLWLPGARCAVELTPPPSVSPGQTARITCGDNRNRYVHWYQKPA 60
 QY 61 RAPLVYDDSDRPSGIPERPSGKSGNTATLTINGVEAGDEADYYCQVWDRASHPVFG 120
 Db 61 RAPLVYDDSDRPSGIPERPSGKSGNTATLTINGVEAGDEADYYCQVWDRASHPVFG 120
 QY 121 GGTRTVTLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTAVKADSSPVKAG 180
 Db 121 GGTRTVTLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTAVKADSSPVKAG 180
 QY 181 VETTPSKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234
 Db 181 VETTPSKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234
 RESULT 4
 AAW14924
 ID AAW14924 standard; Protein; 233 AA.
 XX AC AAW14924;
 XX DT 18-OCT-1997 (first entry)
 XX DE Ant-CD4 monkey-human chimeric antibody CE9.1.

XX CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
 KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
 KW leukaemia; lymphoma; graft-versus-host disease; asthma;
 XX transplant rejection; HIV; therapy; CE9.1.
 OS Chimaeric Macaca cynomolgus;
 OS Chimaeric Homo sapiens.
 XX WO9709351-A1.
 XX 13-MAR-1997.
 XX 05-SEP-1996; 96WO-US14324.
 XX 06-SEP-1995; 95US-0523894.
 XX (IDEC-) IDEC PHARM CORP.
 XX Hanna N, Newman RA, Reff ME;
 XX WPI; 1997-201913/18.
 XX N-PSDB; AAT62867.
 XX Chimeric antibody comprising monkey variable domains and human
 PT constant domains - affects CD4-mediated immune functions, esp.
 PT useful for treatment of autoimmune disease, e.g. rheumatoid
 PT arthritis
 XX Claim 6; Page 79-80; 155pp; English.
 XX A polypeptide (AAW14924) comprises the lambda variable and constant
 CC domains of anti-human CD4 monkey/human chimeric antibody CE9.1.
 CC This antibody contains the antigen binding domains (see also
 CC AAW14922-23) of a cynomolgus monkey anti-CD4 monoclonal antibody, a
 CC human heavy chain constant region of gamma 1 isotype and Gm1a, Gm1z
 CC allotype, and a human lambda light constant region of the Oz minus,
 CC mcg minus genotype and Ke minus allotype. The immunoglobulin genes
 CC (see also AAT62867) were cloned into mammalian expression vector
 CC TCAC 6, and chimeric antibody was produced in CHO cells. CE9.1
 CC binds to domain 1 of human, but not macaque, CD4, a region involved
 CC in the interaction with MHC Class II molecules on antigen-
 CC presenting cells. It shows potent immunomodulatory activity with
 CC low immunogenicity in humans, and can be used to treat autoimmune
 CC diseases such as rheumatoid arthritis.
 XX SQ Sequence 233 AA;
 Query Match 81.7%; Score 1015.5; DB 18; Length 233;
 Best Local Similarity 86.0%; Pred. No. 1.8e-56;
 Matches 196; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
 QY 7 LIGLILLWLPGARCAVELTPPPSVSPGQTARITCGDNRNRYVHWYQKPARAPILV 66
 Db 7 LIGLILAHFTDSA-ASYELSQPRSVSPGQTARITCGDNRNRYVHWYQKPARAPILV 65
 QY 67 IYDDSDRPSGIPERPSGKSGNTATLTINGVEAGDEADYYCQVWDRASHPVFGGTRVT 126
 Db 66 IYADSERPSGIPARPSGNSGNTATLTISGVEAGDEADYYCQVWDRASHPVFGGTRLT 125
 QY 127 VLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTAVKADSSPVKAGVETTTT 186
 Db 126 VLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTAVKADSSPVKAGVETTTT 185
 QY 187 SKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234
 Db 186 SKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 233
 RESULT 5
 ABG19295
 ID ABG19295 standard; Protein; 247 AA.
 XX


```

Query Match          78.6%; Score 976.5; DB 22; Length 232;
Best Local Similarity 80.3%; Pred. No. 5.le-54;
Matches 187; Conservative 14; Mismatches 21; Indels 11; Gaps 2;

QY    12 LMLP-----GARCAYELTPPSVSPSGQTARITCGDNSRNEYVHWYQQKPAR 61
DB     1 MAWIPFLGLVAICTGSVASVELTQPSPSVSPSQATISITCGDNLGNKYVAWYQQKAGQ 60
      :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY    62 APLIVTYDDSDPPSICIPERFSGSKSGNTATTITINGVEAGDEADYYCOWDRASDPHVEGG 121
DB     ||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY    61 SPVLVIYQDKRKPSIPIERFGSGNSGNTALTITSGTOAMDEADYYCQAWD-SSTAVMFFG 119
DB     ||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY    122 GTRVTYLGPQAAPSVTILFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAHV 181
DB    120 GTKLTVLGPQAAPSVTILFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAHV 179
      ||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY    182 ETTTFKSQNKNYAASSVLSLTPQWKSRSYSQCVTHEGSTVEKTVAPTPCS 234
DB    180 ETTTFKSQNKNYAASSVLSLTPQWKSRSYSQCVTHEGSTVEKTVAPTBES 232
      ||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
AAW63764
ID AAW63764 standard; Protein; 236 AA.
AC AAW63764;
XX DT
XX DT 29-SEP-1998 (first entry)
XX Macaque primatized 16ClO light chain protein.
XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
XX CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
XX T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
XX immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
XX T cell proliferation.
XX Macaca fascicularis.
OS
XX WO9819706-A1.
PN
XX
XX 14-MAY-1998.
PD
XX
XX 29-OCT-1997; 97WO-U91906.
PF
XX
XX 08-NOV-1996; 96US-0746361.
PR
XX
PA (IDEC-) IDEC PHARM CORP.
PX
XX Anderson DR, Brams P, Hanna N;
PI
XX WPI; 1998-286601/25.
XX N-P8DB; AAV35488.
DR
XX
XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
XX inhibiting binding to CD28 - useful as specific immunosuppressants
XX for treating diseases that involve interactions between T and B
XX cells, e.g. graft rejection or tumours
XX Example 7; Fig 5a; 87pp; English.
XX
XX This sequence represents a primatized form of the antibody 16ClO light

```

chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionallly the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.

XX Sequence 236 AA;

Query Match 78.3%; Score 973; DB 19; Length 236;
Best Local Similarity 80.1%; Pred. No. 8.6e-54;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

Qy 1 MRVPAQLGLLLWLPGARCAVELTQPPSVSPGQTARITCGGDSNR--NEYVHWYQOK 58
Db 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQOL 60
Qy 59 PARAPILVIYDDSDRPSGIPERFSGSGNTATLTNGVEAGDEADYCYQWDRASDPV 118
Db 61 PGTAPEKLLIYDINKRPSGISDRFSGSGKTAASLAITGLQTEDEADYCYQSDSSNAQV 120
Qy 119 FGGGTRTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
Db 121 FGGGTRTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
Qy 179 AGVETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 181 AGVETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 9
AAU11645

ID AAU11645 standard; Protein; 236 AA.

AC AAU11645;

XX 12-MAR-2002 (first entry)

DE Protein sequence of primatised form of the light chain of 16C10 antibody.

XX Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW graft-vs-host disease; immunosuppression; organ rejection;
KW interleukin-2; IL-2; mutant; mutein.

OS Chimeric - Homo sapiens.

OS Chimeric - Macaca sp.

OS Synthetic.

XX WO2001189567-A1.

XX 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US16364.

XX 22-MAY-2000; 2000US-0576424.

XX (IDEC-) IDEC PHARM CORP.

PI Anderson DR, Hanna N, Brans P;

XX WPI; 2002-089895/12.
DR N-PSDB; AAS17246.
XX Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT treating cancer, graft-vs-host disease and autoimmune disease such as
PT allergy -
XX Example 8; Fig 5a; 89pp; English.

XX The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus,
CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host disease. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present protein
CC sequence represents the light chain of 16C10, a primatised antibody
CC used in the invention to induce apoptosis and inhibit production of
CC interleukin-2 (IL-2).

XX Sequence 236 AA;

Query Match 78.3%; Score 973; DB 23; Length 236;
Best Local Similarity 80.1%; Pred. No. 8.6e-54;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

Qy 1 MRVPAQLGLLLWLPGARCAVELTQPPSVSPGQTARITCGGDSNR--NEYVHWYQOK 58
Db 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQOL 60
Qy 59 PARAPILVIYDDSDRPSGIPERFSGSGNTATLTNGVEAGDEADYCYQWDRASDPV 118
Db 61 PGTAPEKLLIYDINKRPSGISDRFSGSGKTAASLAITGLQTEDEADYCYQSDSSNAQV 120
Qy 119 FGGGTRTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
Db 121 FGGGTRTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
Qy 179 AGVETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 181 AGVETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 10

ABP41361

ID ABP41361 standard; Protein; 269 AA.

XX AC ABP41361;

XX 22-AUG-2002 (first entry)

XX Human ovarian antigen HCN5F57, SEQ ID NO:2493.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;

antiinflammatory; gynaecological; reproductive.

Homo sapiens.

WO200200677-A1.

03-JAN-2002.

07-JUN-2001; 2001WO-US18569.

07-JUN-2000; 2000US-209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI: 2002-147878/19.

N-PSDB; AB054438.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -

Claim 11; SEQ ID No 2493; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 269 AA;

Query Match 78.3%; Score 973; DB 23; Length 269;

Best Local Similarity 79.8%; Pred. No. 9.8e-54;

Matches 186; Conservative 14; Mismatches 21; Indels 12; Gaps 2;

Qy 12 LLWLP-----GARCAYELTOPPSVSPGQTARITCGDNRNRYVHWYQKPAR 61

Db 39 MANIPLFLGLVACTGSVASYELTOPPSVSPGQTARITCGDNRNRYVHWYQKPAR 98

Qy 62 APILVIYDDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 121

Db 99 SPVLVIYQDNKRSGIPERFSGSGNTATLTISGQAMDEADYYCQAND--SXTVVF 156

Qy 122 GTRVTVLQGPKAAPSVTLFPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV 181

Db 157 GTKLTVLQGPKAAPSVTLFPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV 216

Qy 182 ETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

Db 217 ETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 269

RESULT 11

AAW01821

ID AAW01821 standard; Protein; 236 AA.

XX AC AAW01821;

XX DT 25-MAY-1997 (first entry)

XX DE Primatised anti-human B7.1 antigen antibody 16C10 light chain.

XX KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;

XX KW Primatised antibody; B7 antigen; CD28; immunosuppressive;

XX KW autoimmune disease; idiopathic thrombocytopenia purpura;

XX KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;

XX KW type 1 diabetes mellitus; Graft versus host disease;

XX KW hetero-hybridoma; transflectoma.

XX OS Chimeric Macaca cynomolgus;

XX OS Chimeric Homo sapiens.

XX PN WO9640878-A1.

XX PD 19-DEC-1996.

XX PF 06-JUN-1996; 96WO-US10053.

XX PR 07-JUN-1995; 95US-0487550.

XX PA (IDEC-) IDEC PHARM CORP.

XX PI Anderson DR, Brams P, Hanna N, Sheatsowsky WS;

XX WPI; 1997-108638/10.

XX DR N-PSDB; AAT62512.

XX PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen - useful for treating autoimmune disease or graft-versus-host disease

XX PS Claim 14; Fig 10A; 81pp; English.

XX CC 2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.

XX SQ Sequence 236 AA;

Query Match 78.0%; Score 970; DB 18; Length 236;

Best Local Similarity 79.7%; Pred. No. 1.3e-53;

Matches 188; Conservative 14; Mismatches 32; Indels 2; Gaps 1;

Qy 1 MRVPAQLLGLLLLPAGRCAYELTOPPSVSPGQTARITCGDNR--NEYVHWYQK 58

Db 1 MRVPAQLLGLLLLPAGRCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQL 60

Qy 59 PARAFILVIYDDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118

Db 61 PGTAPKLLIYDINKRSGISDRFSGSGTAAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy 119 FGGGTRVTVLQGPKAAPSVTLFPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178

Db 121 FGGCTRLTVLGQPKAAPSVTLFPPSSSELOANKATLVCLISDYIPGAVTVAMKADSSPVK 180
AAU14176
Qy 179 AGVETTTPSQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
AAU14176
Db 181 AGVETTTPSQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
AAU14176
RESULT 12
ID AAU14176 standard; Protein; 231 AA.
XX
AC AAU14176;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #47.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
immunomodulatory; cytostatic; neuroprotective; vulnerrary; nootropic;
anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-451939/48.
DR N-PSDB; AAS22481.
XX
Isolated polypeptides useful for treating anti-inflammatory diseases,
nervous system disorders, and for regenerating bone and cartilage -
Example 4; Page 553; 894pp; English.
XX
The invention relates to polynucleotides encoding novel human
proteins or their active domains. The polypeptides, polynucleotides and
antibodies raised against the polypeptides are used in a method of
treatment of a mammal and prevention of disorders caused by the aberrant
protein expression or activity. The polypeptides can be used as
molecular weight markers, food supplements, and in antibody production.
The polypeptides are used to identify compounds which bind to the
polypeptides. Polynucleotides of the invention are used as probes and
primers, for sequencing, for chromosome or gene mapping, in the
production of recombinant proteins, and in generating anti-sense DNA or
RNA and in gene therapy. Polypeptides of the invention can be used to
target drugs to a tumour, in assays to determine biological activity, to
raise antibodies/ elicit an immune response, to determine quantitative
protein levels, as tissue markers, and to isolate receptors or ligands.
Polypeptides of the invention may also be useful in treating platelet
disorders, stem cell disorders, regenerating bone, cartilage, tendon,
ligament and/or nerve tissue, wound healing, treating burns, promoting
the proliferation, differentiation and survival of stem cells, as a
contraceptive, treating osteoporosis and osteoarthritis, anaemia,
Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
fungal infection or from autoimmunity, cancer, allergy, asthma,
graft-versus-host disease, eczema, haemophilia, thrombosis,
anti-inflammatory diseases, nervous system disorders, and infection.
The present sequence represents a protein of the invention.

XX SQ Sequence 231 AA;
Query Match 77.2%; Score 959; DB 22; Length 231;
Best Local Similarity 79.0%; Pred. No. 6.4e-53;
Matches 184; Conservative 14; Mismatches 23; Indels 12; Gaps 2;
Qy 12 LLWLP-----GARCAYELTQPPSVSVSGQTARITCCGDNRSRNYVHWYQOKPAR 61
Db 1 MAWIFLFLGLVAYCTGVSASVELTQPPSVSVSGKTASITCSDGLGDKYASWYQOKAGQ 60
Qy 62 APILVYDDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYYCQVDRASHPVFGG 121
Db 61 SPVLVIYRHSKRPSGIPERFSGSGNTATLTISGTQVMEADYYCQAWD--SSIVVFGG 118
Qy 122 GTRVTVLGOPKAAPSVTLPFPSSSELOANKATLVCLISDFYPGAVTVAMKADSSPVKAGV 181
Db 119 GTKUTVLGQPKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAVTVAMKADSSPVKAGV 178
Qy 182 ETTTPSQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 ETTTPSQSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231
RESULT 13
ID ABG23084
XX ABG23084 standard; Protein; 234 AA.
AC ABG23084;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23075.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS87271.
XX
New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity -
Claim 20; SEQ ID No 53443; 103pp; English.
XX
The invention relates to isolated polynucleotide (I) and
polypeptide (II) sequences. (I) is useful as hybridisation probes,
polymerase chain reaction (PCR) primers, oligomers, and for chromosome
and gene mapping, and in recombinant production of (II). The
polynucleotides are also used in diagnostics as expressed sequence tags
for identifying expressed genes. (I) is useful in gene therapy techniques
to restore normal activity of (II) or to treat disease states involving
(II). (II) is useful for generating antibodies against it, detecting or
quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.
The polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. ABG00010-ABG03077 represent novel human
diagnostic amino acid sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

Query Match 77.2%; Score 959; DB 22; Length 234;
Best Local Similarity 78.5%; Pred. No. 6.5e-53;
Matches 183; Conservative 17; Mismatches 21; Indels 12; Gaps 2;
SQ Sequence 234 AA;

12 LMLP-----GARCAYELTOPPSVSPGQTARITCGGDSNRNEYVHHYQKQPAR 61
4 MAWIPFLGLVLAICTGSVASVELTQPPSVSPGQTASITCGDKLGDYKYSWTQKPGQ 63
62 APILVIYDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYYCQWDRASDPVFGG 121
64 SPLVLVYQDTPNRPSPGIPERFSGSGNTATLTISTQAMDEADYYCQWDRASDPVFGG 121
122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
182 ETTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
182 ETTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 14
AAU14236
ID AAU14236 standard; Protein; 232 AA.
XX
AC AAU14236;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #107.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
immunomodulatory; cytosolic; neuroprotective; vulnery; nootropic;
anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-451939/48.
DR N-PSDB; AAS22541.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
nervous system disorders, and for regenerating bone and cartilage -
XX
PS Example 4; Page 582; 894pp; English.

The invention relates to polynucleotides encoding novel human
proteins or their active domains. The polypeptides, polynucleotides and
antibodies raised against the polypeptides are used in a method of
treatment of a mammal and prevention of disorders caused by the aberrant
protein expression or activity. The polypeptides can be used as
molecular weight markers, food supplements, and in antibody production.
The polypeptides are used to identify compounds which bind to the
polypeptides. Polynucleotides of the invention are used as probes and
primers, for sequencing, for chromosome or gene mapping, in the
production of recombinant proteins, and in generating anti-sense DNA or
RNA and in gene therapy. Polypeptides of the invention can be used to
target drugs to a tumour, in assays to determine biological activity, to
raise antibodies/elicit an immune response, to determine quantitative
protein levels, as tissue markers, and to isolate receptors or ligands.
Polypeptides of the invention may also be useful in treating platelet
disorders, stem cell disorders, regenerating bone, cartilage, tendon,
ligament and/or nerve tissue, wound healing, treating burns, promoting
the proliferation, differentiation and survival of stem cells, as a
contraceptive, treating osteoporosis and osteoarthritis, anaemia,
Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
fungal infection or from autoimmunity, cancer, allergy, asthma,
graft-versus-host disease, eczema, haemophilia, thrombosis,
anti-inflammatory diseases, nervous system disorders, and infection.
The present sequence represents a protein of the invention.

Query Match 77.1%; Score 958.5; DB 22; Length 232;
Best Local Similarity 78.5%; Pred. No. 6.9e-53;
Matches 183; Conservative 16; Mismatches 23; Indels 11; Gaps 2;
SQ Sequence 232 AA;

12 LMLP-----GARCAYELTOPPSVSPGQTARITCGGDSNRNEYVHHYQKQPAR 61
1 MAWIPFLGLVLAICTGSVASVELTQPPSVSPGQTASITCGDKLGDYKYSWTQKPGQ 60
62 APILVIYDSDRPSGIPERFSGSGNTATLTINGVEAGDEADYYCQWDRASDPVFGG 121
61 SPVLVIYQDSDRPSGIPERFSGSGNTATLTISTQAMDEADYYCQWDRASDPVFGG 119
122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
120 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 179
182 ETTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
180 ETTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 232

RESULT 15
AAU08381
ID AAU08381 standard; Peptide; 218 AA.
XX
AC AAU08381;
XX
DT 17-DEC-2001 (first entry)
XX
DE Anti-OPGbp antibody light chain, S.
XX
KW Antibody; OPGbp; human; S light chain; osteopathic;
osteoprotegerin binding protein; osteoclast formation; bone resorption;
loss of bone mass; bone tumour; osteoporosis; bone cancer;
rheumatoid arthritis; hypercalcaemia of malignancy;
steroid-induced osteoporosis; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT Region 5..26
FT /label= FR1
FT /note= "Framework region"

FT Misc-difference 5..7 /note= "Wild-type Ser-Tyr-Glu substituted by
FT Gln-Ser-Val"
FT Misc-difference 9 /note= "Wild-type Met substituted by Thr"
FT Misc-difference 23 /note= "Wild-type Arg substituted by Thr"
FT Region 27..37 /label= CDR1
FT /note= "Complementarity determining region"
FT Misc-difference 36 /note= "Wild-type Ala substituted by Val"
FT Region 38..52 /label= FR2
FT /note= "Framework region"
FT Misc-difference 40 /note= "Wild-type Gln substituted by Arg"
FT Misc-difference 48 /note= "Wild-type Val substituted by Leu"
FT Region 53..59 /label= CDR2
FT /note= "Complementarity determining region"
FT Misc-difference 53 /note= "Wild-type Lys substituted by Glu"
FT Region 60..91 /label= FR3
FT /note= "Framework region"
FT Misc-difference 73 /note= "Wild-type Thr substituted by Glu"
FT Misc-difference 77 /note= "Wild-type Thr substituted by Ser"
FT Region 92..102 /label= CDR3
FT /note= "Complementarity determining region"
FT Misc-difference 94 /note= "Wild-type Ala substituted by Ile"

WO200162932-A1.

30-AUG-2001.

23-FEB-2001; 2001WO-US05973.

23-FEB-2000; 2000US-051139.

22-FEB-2001; 2001US-0791153.

(AMGE-) AMGEN INC.

Deshpande RV, Hitz A, Boyle WJ, Sullivan JK;

WPI; 2001-557706/62.

N-PSDB; AAS13364.

XX Antibodies that bind antagonistically to osteoprotegerin binding
PT protein, useful for treating osteoporosis, metastasis of cancer to
PT bone, rheumatoid arthritis, hypercalcaemia of malignancy and
PT steroid-induced osteoporosis -

XX Claim 10; Fig 8; 239pp; English.

XX The invention relates to an antibody or antigen binding domain (or
CC fragment, variant or derivative), which binds to an osteoprotegerin
CC binding protein (OPGbp) and which is an antagonistic antibody.
CC The antibody or antigen binding domain may be administered to inhibit
CC osteoclast formation or activation, inhibit bone resorption in a mammal,
CC prevent or treat loss of bone mass in a mammal and to prevent or treat
CC tumour cell growth in bone. The loss of bone mass results from
CC osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
CC hypercalcaemia of malignancy and steroid-induced osteoporosis. The
CC present sequence is a full length, cloned anti-OPGbp antibody light
CC chain, S.

XX Sequence 218 AA;

SQ

Query Match 75.9%; Score 944; DB 22; Length 218;
Best Local Similarity 84.4%; Pred. No. 5.2e-52;
Matches 178; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
QY 24 LTQPPSVSVPGQTARITCGGDNSEYVHYQKPARAPILVIYDDSDRPSGIPERFSG 83
DB 8 LTQPPSVSVPGQTATITCSGDALPKQVYVYRQKPGQAPLLVIYEDSERPSGIPERFSG 67
QY 84 SKSGNTALTITNGVEAGDEADYICQVWDRASDHPVFGGTRVTVLGQPKAAPSVTLFPPPS 143
DB 68 SSSGTEVTLSISGVQAEADYICQSTDSSGTYVYVFGGTTKTLVLSQPKAAPSVTLFPPPS 127
QY 144 SEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTTTPSKQSNKKAASSYLSLT 203
DB 128 SEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTTTPSKQSNKKAASSYLSLT 187
QY 204 PEQWKSHRSYSQCVTHEGSTVEKTVAPTECS 234
DB 188 PEQWKSHRSYSQCVTHEGSTVEKTVAPTECS 218

Search completed: March 29, 2003, 09:10:14
Job time : 26.0673 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 8.97055 Seconds
(without alignments)
1531.829 Million cell updates/sec

Title: US-09-758-173-2

Perfect score: 1243

Sequence: 1 MRVPQLLGLLLMLPGARC.....QVTHGSEVTEKTVAPTECS 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB_PEP.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB_PEP.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB_PEP.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB_PEP.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB_PEP.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB_PEP.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243	100.0	234	9	US-10-124-905-2
2	1243	100.0	234	9	US-09-948-429B-2
3	973	78.3	236	9	US-10-124-905-10
4	973	78.3	236	9	US-09-948-429B-10
5	936.5	75.3	244	10	US-09-925-301-1424
6	880	70.8	235	10	US-09-747-669-6
7	873.5	70.3	221	9	US-10-001-857-202
8	865.5	69.6	219	10	US-09-974-449-38
9	812	65.3	235	9	US-09-852-797-70
10	812	65.3	235	10	US-09-853-161-70
11	812	65.3	235	10	US-09-852-659A-70
12	809	65.1	235	9	US-09-852-797-88
13	809	65.1	235	10	US-09-853-161-88
14	809	65.1	235	10	US-09-852-659A-88
15	804	64.7	216	10	US-09-736-371B-19
16	749	60.3	239	9	US-09-828-995B-26
17	746.5	60.1	246	9	US-09-908-567B-49
18	691.5	55.6	216	10	US-09-291-299A-8
19	665	53.5	217	10	US-09-291-299A-7

20	646.5	52.0	216	10	US-09-291-299A-10	Sequence 10, Appl
21	637.5	51.3	216	10	US-09-291-299A-9	Sequence 9, Appl
22	631	50.8	139	9	US-09-796-692-901	Sequence 901, App
23	616	49.6	143	9	US-09-796-692-742	Sequence 742, App
24	613	49.3	123	9	US-09-796-692-683	Sequence 683, App
25	613	49.3	123	9	US-09-796-692-838	Sequence 838, App
26	613	49.3	123	9	US-09-796-692-859	Sequence 859, App
27	613	49.3	123	9	US-09-796-692-993	Sequence 993, App
28	613	49.3	123	9	US-09-796-692-1011	Sequence 1011, App
29	613	49.3	123	9	US-09-796-692-1041	Sequence 1041, App
30	613	49.3	123	9	US-09-796-692-1138	Sequence 1138, App
31	613	49.3	123	9	US-09-796-692-1142	Sequence 1142, App
32	613	49.3	154	9	US-09-796-692-706	Sequence 706, App
33	610	49.1	123	9	US-09-796-692-931	Sequence 931, App
34	609	49.0	127	9	US-09-796-692-836	Sequence 836, App
35	608	48.9	123	9	US-09-796-692-896	Sequence 896, App
36	608	48.9	123	9	US-09-796-692-982	Sequence 982, App
37	608	48.9	123	9	US-09-796-692-991	Sequence 991, App
38	608	48.9	123	9	US-09-796-692-1021	Sequence 1021, App
39	608	48.9	123	9	US-09-796-692-1095	Sequence 1095, App
40	606	48.8	123	9	US-09-796-692-810	Sequence 810, App
41	606	48.8	123	9	US-09-796-692-1062	Sequence 1062, App
42	606	48.8	123	9	US-09-796-692-1105	Sequence 1105, App
43	603	48.5	125	9	US-09-796-692-843	Sequence 843, App
44	600	48.3	125	9	US-09-796-692-737	Sequence 737, App
45	591	47.5	121	9	US-09-796-692-998	Sequence 998, App

ALIGNMENTS

RESULT 1

US-10-124-905-2

; Sequence 2, Application US/10124905

; Patent No. US20020166136A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 234 amino acids

Db 1 MRVPAQLLGLLLWLPARCESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQQL 60
QY 59 PARAPILVIYDDSDRPSGIPERFSGSKGNTATLTINGVEAGDEADYYCQVWDRADHPV 118
Db 61 PGTAPELLIYDINKRPSGIDSRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
QY 119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
Db 121 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 179 AGVETTTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 181 AGVETTTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 4
US-09-948-429B-10
; Sequence 10, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMARIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-10

Query Match 78.3%; Score 973; DB 9; Length 236;
Best Local Similarity 80.1%; Pred. No. 1.3e-42;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

QY 1 MRVPAQLLGLLLWLPARCAVELTOPPSVSPGQTARITCGDNR--NEYVHTQOK 58
Db 1 MRVPAQLLGLLLWLPARCESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQQL 60
QY 59 PARAPILVIYDDSDRPSGIPERFSGSKGNTATLTINGVEAGDEADYYCQVWDRADHPV 118

Db 61 PGTAPELLIYDINKRPSGIDSRFSGSKGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
QY 119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
Db 121 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 179 AGVETTTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 181 AGVETTTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 5
US-09-925-301-1424
; Sequence 1424, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1424
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (62)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (221)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1424

Query Match 75.3%; Score 936.5; DB 10; Length 244;
Best Local Similarity 75.4%; Pred. No. 9.2e-41;
Matches 184; Conservative 15; Mismatches 34; Indels 11; Gaps 2;

QY 2 RVPAQLLG-LLLLWLP-----GARCAYELTOPPSVSPGQTARITCGDLPXK 60
Db 1 RVRRQSSGNLTMAWTPLLLTFTCTVSEAYELTOPPSVSPGQTARITCGDLPXK 60
QY 51 YVHWYQOKPARAPILVIYDDSDRPSGIPERFSGSKGNTATLTINGVEAGDEADYYCQVW 110
Db 61 YVHWYQOKGQAPVLVIYEDTRRPSAIPERFSASSGNTATLTISGAQVEADYYCYST 120
QY 111 DRASDPVFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW 170
Db 121 DSSSYVRVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW 180
QY 171 KADSSPVKAGVETTTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAP 230
Db 181 KADSSPVKAGVETTTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAP 240
QY 231 TECS 234
Db 241 TECS 244

RESULT 6
US-09-747-669-6
; Sequence 6, Application US/09747669
; Patent No. US20020122807A1
; GENERAL INFORMATION:

APPLICANT: Dan, Michael D.
APPLICANT: Saleh, Mansoor
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
TITLE OF INVENTION: 4BS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
TITLE OF INVENTION: AND DETECTION OF CANCERS
FILE REFERENCE: 316082001001
CURRENT APPLICATION NUMBER: US/09/747,669
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/111,286
PRIOR FILING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 235
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-747-669-6
Query Match 70.8%; Score 880; DB 10; Length 235;
Best Local Similarity 73.9%; Pred. No. 6.1e-38;
Matches 170; Conservative 21; Mismatches 37; Indels 2; Gaps 1;
Qy 7 LGLLLLLWLPACAYELTOPPSVSPGQTARITCGDNR--NEVHHYQOKPARAPI 64
Db LLLLLTHCAGSAQSVLTOPPSASGTGQRTVLTSCGSNSNLTGSKTVNYYQLPGTAPK 65
Qy 65 LVIVDDSDRPSGIPERTSGSGKNTATLTNGVEAGDEADYYCQVMDRASHDPVFGGTR 124
Db 66 FLIYNNQRPSEVDPDRSGSGKNTATLTNGVEAGDEADYYCQVMDRASHDPVFGGTR 125
Qy 125 VTLVGGQKAAPSVTLFPPSSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVET 184
Db 126 LTVLGGQKAAPSVTLFPPSSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVET 185
Qy 185 TPKSQNNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 186 TPKSQNNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235
RESULT 7
US-10-001-857-202
Sequence 202, Application US/10001857
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Pro
FILE REFERENCE: DEX-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 202
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapien
US-10-001-857-202
Query Match 70.3%; Score 873.5; DB 9; Length 221;
Best Local Similarity 76.9%; Pred. No. 1.2e-37;
Matches 170; Conservative 16; Mismatches 18; Indels 17; Gaps 3;
Qy 24 LTQPPSVSPGQTARITCGDNR----NEVHHYQOKPARAPILVIYDDSDRPSGIPE 79
Db 8 LTQPPSVGAPGQRTVISTCGSSNIGAGDYVHHYQQLPGTAPKLMYEVAKRPSGVSD 67

Qy 80 RFGSKSGNTATLTNGVEAGDEADYYC-----QVMDRASHDPVFGGTRVTVLGPKA 133
Db 68 RFGSKSGNTASLTISGLQADEADYYCCSVAGSYTW-----VFGGGTKLVTLVGPKA 120
Qy 134 APSVTLFPPSSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTPSKQSNK 193
Db 121 APSVTLFPPSSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTPSKQSNK 180
Qy 194 YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 181 YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 221
RESULT 8
US-09-974-449-38
Sequence 38, Application US/09974449
Patent No. US20020141989A1
GENERAL INFORMATION:
APPLICANT: Kricek, Franz
APPLICANT: Stadler, Beda
APPLICANT: Vogel, Monique
TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST
TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO
TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR
FILE REFERENCE: 4-30888A
CURRENT APPLICATION NUMBER: US/09/974,449
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: PCT/EP00/03288
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-449-38
Query Match 69.6%; Score 865.5; DB 10; Length 219;
Best Local Similarity 78.7%; Pred. No. 3.1e-37;
Matches 170; Conservative 16; Mismatches 25; Indels 5; Gaps 2;
Qy 24 LTQPPSVSPGQTARITCGG---DNSRNEYVHHYQOKPARAPILVIYDDSDRPSGIPE 80
Db 4 VTQPASVSGSPGQSITISCTGTRSDVGGYVSMYQQHPGAPKLMYDVSNRPSGVNR 63
Qy 81 FSGSKSGNTATLTNGVEAGDEADYYCQVMDRASHDPVFGGTRVTVLG--OPKAAPSVT 138
Db 64 FSGSKSGNTASLTISGLQADEADYYCSTYSSSTLGVFGGGTKLVTLVGPKAAPSVT 123
Qy 139 LFPSSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTPSKQSNKYAASS 198
Db 124 LFPSSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTPSKQSNKYAASS 183
Qy 199 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 184 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 219
RESULT 9
US-09-852-797-70
Sequence 70, Application US/09852797
Patent No. US20020172994A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P2
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11

RESULT 11

RESULT 11

```

/ CURRENT FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: 60/265,583
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 09/152,060
/ PRIOR FILING DATE: 1998-09-11
/ PRIOR APPLICATION NUMBER: PCT/US98/04858
/ PRIOR FILING DATE: 1998-03-12
/ PRIOR APPLICATION NUMBER: 60/040,762
/ PRIOR FILING DATE: 1997-03-14
/ PRIOR APPLICATION NUMBER: 60/040,710
/ PRIOR FILING DATE: 1997-03-14
/ PRIOR APPLICATION NUMBER: 60/050,934
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: 60/048,100
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: 60/048,357
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: 60/048,189
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: 60/057,765
/ PRIOR FILING DATE: 1997-09-05
/ PRIOR APPLICATION NUMBER: 60/048,970
/ PRIOR FILING DATE: 1997-06-06
/ PRIOR APPLICATION NUMBER: 60/068,368
/ PRIOR FILING DATE: 1997-12-19

```


QY 142 PSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTTTPSKOSNNKYAASSYLS 201
Db 143 PSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTTTPSKOSNNKYAASSYLS 202
QY 202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 203 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 14

US-09-852-659A-88
; Sequence 88, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-88

Query Match 65.1%; Score 809; DB 10; Length 235;
Best Local Similarity 74.2%; Pred. No. 2.2e-34;
Matches 158; Conservative 20; Mismatches 33; Indels 2; Gaps 1;

QY 24 LTQPPSVSVSPGQTARITCGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
Db 23 LTQPPSVKDLROTATLTCTGNNNNVGDQAAWLQHQHPPKLLSYRNNRPSGISERL 82
QY 82 SGKSGNTATLTINGVEAGDEADYYCQVWDRADSDHPVFGGTRVTVLGQPKAAPSVTLPP 141
Db 83 SASRSGATSLTITGLQPEDEADYYCAAYDSSLAIVWFGGTTKLTVLGQPKAAPSVTLPP 142
QY 142 PSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTTTPSKOSNNKYAASSYLS 201
Db 143 PSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTTTPSKOSNNKYAASSYLS 202
QY 202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 203 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 15

US-09-736-371B-19
; Sequence 19, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736,371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Rattus
US-09-736-371B-19
Query Match 64.7%; Score 804; DB 10; Length 216;
Best Local Similarity 74.0%; Pred. No. 3.7e-34;
Matches 159; Conservative 15; Mismatches 35; Indels 6; Gaps 3;
QY 24 LTQPPSVSVSPGQTARITC--GGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
Db 4 VTQANSYSTSLGISTVKLSCTLSGNIENNVHWYQLVEGRSPITMIYDDDKRPDGVDFR 63
QY 82 SGS--KSGNTATLTINGVEAGDEADYYCQVWDRADSDHPVFGGTRVTVLGQPKAAPSVTL 139
Db 64 SGSIDRSSNSAFLTIHNVAIEDEALYFCHSY--VSSFNVFGGTTKLTVLGQPKAAPSVTL 121
QY 140 FPPSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTTTPSKOSNNKYAASSY 199
Db 122 FPPSSEELQANKATLVCLISDFYFGAVTVAVKADSSPVKAGVETTTTPSKOSNNKYAASSY 181
QY 200 LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 182 LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 216

Search completed: March 29, 2003, 09:38:36
Job time : 10.9705 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 5.57924 Seconds
(without alignments)
1739.566 Million cell updates/sec

Title: US-09-758-173-2

Perfect score: 1243

Sequence: 1 MRVPAQLGLLLWLPQARC.....CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	44.1	105	1	LAC HUMAN
2	522	42.0	213	1	ILLI HUMAN
3	472	38.0	111	1	LV3B_HUMAN
4	444	35.7	108	1	LV5A_HUMAN
5	417	33.5	107	1	LV4C_HUMAN
6	415	33.4	105	1	LAC FIG
7	412	33.1	105	1	LAC1 MOUSE
8	407	32.7	106	1	LV4A_HUMAN
9	400	32.2	111	1	LV7A_HUMAN
10	399	32.1	105	1	LAC RABBIT
11	399	32.1	106	1	LV4B_HUMAN
12	397	31.9	106	1	LV4E_HUMAN
13	385.5	31.0	104	1	LAC1 RAT
14	380.5	30.6	104	1	LAC2 RAT
15	378	30.4	106	1	LV4D_HUMAN
16	377	30.3	105	1	LAC5 MUSSP
17	374.5	30.1	104	1	LAC3 MOUSE
18	369.5	29.7	104	1	LAC2 MOUSE
19	368	29.6	130	1	LV1G_HUMAN
20	360	29.0	108	1	LV3A_HUMAN
21	357	28.7	111	1	LV1D_HUMAN
22	347	27.9	105	1	LAC5 MOUSE
23	342	27.5	111	1	LV1C_HUMAN
24	331	26.6	111	1	LV6C_HUMAN
25	328	26.4	109	1	LV1I_HUMAN
26	327	26.3	111	1	LV2G_HUMAN
27	326.5	26.3	103	1	LAC CHICK
28	326.5	26.3	112	1	LV1B_HUMAN
29	325.5	26.2	112	1	LV2K_HUMAN
30	325	26.1	111	1	LV1A_HUMAN
31	322.5	25.9	112	1	LV6A_HUMAN
32	320.5	25.8	117	1	KV1J_HUMAN
33	318.5	25.6	129	1	KV1W_HUMAN

ALIGNMENTS

RESULT 1

ID	LAC HUMAN	STANDARD;	PRT;	105 AA.
AC	P01842; P80423;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig lambda chain C regions.			
GN	IGLC1 AND IGLC2 AND IGLC3.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (BENCE-JONES PROTEIN SH).			
RX	MEDLINE=70166723; PubMed=4909564;			
RA	Titani K., Wikler M., Shinoda T., Putnam F.W.;			
RT	"The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide bridges.";			
RT	J. Biol. Chem. 245:2171-2176(1970).			
RN	[2]			
RP	SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.			
RX	MEDLINE=69088380; PubMed=4883841;			
RA	Milstein C., Clegg J.B., Jarvis J.M.;			
RT	"Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jones protein.";			
RT	Biochem. J. 110:631-652(1968).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN NIG-64).			
RX	MEDLINE=83186114; PubMed=6404900;			
RA	Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T., Shimizu A.;			
RT	"Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subgroup.";			
RT	J. Biochem. 93:421-429(1983).			
RN	[4]			
RP	SEQUENCE (BENCE-JONES PROTEIN KERN).			
RX	MEDLINE=71150336; PubMed=5549568;			
RA	Ponstingl H., Hess M., Hilschmann N.;			
RT	"Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones protein Kern). V. The complete amino acid sequence and its genetic interpretation.";			
RT	Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).			
RN	[5]			
RP	PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).			
RX	MEDLINE=74109253; PubMed=4814727;			
RA	Chen B.L., Poljak R.J.;			
RT	"Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobulin (IgG New).";			
RT	Biochemistry 13:1295-1302(1974).			
RN	[6]			
RP	SEQUENCE (DOT).			
RX	MEDLINE=95255298; PubMed=7737190;			
RA	Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;			

34	318	25.6	111	1	LV2F_HUMAN	P01709 homo sapien
35	314.5	25.3	131	1	LV6E_HUMAN	P06319 homo sapien
36	313	25.2	109	1	LV1F_HUMAN	P04208 homo sapien
37	313	25.2	111	1	LV2C_HUMAN	P01706 homo sapien
38	310.5	25.0	112	1	LV1H_HUMAN	P06887 homo sapien
39	310	24.9	109	1	LV2E_HUMAN	P01708 homo sapien
40	310	24.9	111	1	LV2I_HUMAN	P01712 homo sapien
41	303	24.4	111	1	LV2A_HUMAN	P01704 homo sapien
42	302	24.3	111	1	LV2B_HUMAN	P01705 homo sapien
43	298.5	24.0	129	1	KV1X_HUMAN	P04432 homo sapien
44	298	24.0	111	1	LV2D_HUMAN	P01707 homo sapien
45	298	24.0	113	1	LV1_CHICK	P04210 gallus gall

RT "Characterization of the two unique human anti-flavin monoclinal
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWN.
RX MEDLINE=75046825; PubMed=4215080;
RA Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA Saul P.;

RT "The three-dimensional structure of the fab' fragment of a human
myeloma immunoglobulin at 2.0-A resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
RN [8]

RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX MEDLINE=75013804; PubMed=4415202;
RA Felt J.W., Deusch H.F.;

RT "Primary structure of the MCG lambda chain.";
RL Biochemistry 13:4102-4114(1974).
RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RX Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA Panagiotopoulos N.;

RT "Rotational allomerism and divergent evolution of domains in
immunoglobulin light chains.";
RL Biochemistry 14:3953-3961(1975).
RN [10]

RP X-RAY CRYSTALLOGRAPHY OF MCG.
RX MEDLINE=90133913; PubMed=2515285;
RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;

RT "Three-dimensional structure of a light chain dimer crystallized in
water. Conformational flexibility of a molecule in two crystal
forms.";
RL J. Mol. Biol. 210:601-615(1989).
RN [11]

RP SEQUENCE FROM N.A.
RX MEDLINE=82080680; PubMed=6273747;
RA Hietter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;

RT "Clustered arrangement of immunoglobulin lambda constant region genes
in man.";
RL Nature 294:536-540(1981).
RN [12]

CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN
FOUND IN PROTEINS SH, X, AND NIG-84. THE KERN PROTEIN HAS THE

CC KERN+ MARKER, THE NEWN PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN
HAS THE KERN+ MARKER, AND THE MCG+ MARKER.

CC -1- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE
3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE

CC (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
SEQUENCE (LAMBDA-3).
CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----

DR EMBL; J00253; AAA59107.1; -;
DR EMBL; L38562; AAB36581.1; ALT_INIT.

DR EMBL; X51754; CAB38569.1; ALT_INIT.
DR EMBL; X51755; CAA36049.1; -;

DR EMBL; X51755; CAA36051.1; -;
DR PIR; A02125; L2HU.

DR PDB; 2MCG; 15-JUL-92.
DR PDB; 7FAB; 31-JAN-94.

DR Genew; HGNC:5855; IGLC1.
DR Genew; HGNC:5856; IGLC2.

DR Genew; HGNC:5857; IGLC3.
DR MIM; 147220; -;

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.

DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGL1; 1.

DR PROSITE; PS00290; IG_MHC; 1.
DR

KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 1

FT DISULFID 27 86

FT DISULFID 104 104

FT VARIANT 5 5

FT VARIANT 7 7

FT VARIANT 45 45

FT VARIANT 56 56

FT VARIANT 82 82

FT STRAND 4 4

FT STRAND 7 11

FT HELIX 15 19

FT TURN 20 21

FT STRAND 23 33

FT STRAND 38 43

FT TURN 44 45

FT STRAND 46 48

FT TURN 50 51

FT STRAND 52 54

FT STRAND 58 59

FT TURN 61 62

FT STRAND 65 73

FT HELIX 75 79

FT TURN 80 80

FT STRAND 84 90

FT TURN 91 92

FT STRAND 93 99

SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;

Query Match 44.1%; Score 548; DB 1; Length 105;

Best Local Similarity 100.0%; Pred. No. 9.6e-38;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPTSKQ 189

Db 1 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPTSKQ 60

Oy 190 SNKYAASSYLSTLPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

Db 61 SNKYAASSYLSTLPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 105

RESULT 2

ILLI HUMAN

ID ILLI HUMAN STANDARD; PRT; 213 AA.

AC P15814;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)

DE (CD179b antigen).

GN IGLL1 OR IGL1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89315835; PubMed=2501791;

RA Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
McKearn J.P.;

RT "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
expressed in pre-B cells and may encode the human immunoglobulin
omega light-chain protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1989).
RN [2]

RP SEQUENCE FROM N.A.

```

RC TISSUE=lymphoid;
RX MEDLINE=91108327; PubMed=1703205;
RA Evans R.J., Hollis G.F.;
RT "Genomic structure of the human Ig lambda 1 gene suggests that it may
RT be expressed as an Ig lambda 14.1-like protein or as a canonical B
RT cell Ig lambda light chain: implications for Ig lambda gene
RT evolution";
RL J. Exp. Med. 173:305-311(1991).
CC -!- SUBUNIT: Associates non-covalently with VPB1.
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL
CC B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- DATABASE: NAME=PRO; NOTE=PROW 1.64-67(2000);
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/696419174.g.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M27749; AAA36100.1; -
DR EMBL; M34513; AAA36096.1; -
DR EMBL; M34511; AAA36096.1; JOINED.
DR EMBL; M34512; AAA36096.1; JOINED.
DR PIR; A33911; A33911.
DR HSSP; P01842; 7FAB.
DR Genew; HGNC:5870; IGLL1.
DR MIM; 146770; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; B-cell; Signal.
FT SIGNAL 1 37
FT CHAIN 38 213
FT DOMAIN 97 108
FT DOMAIN 109 213
FT C REGION (BY SIMILARITY TO LAMBDA
FT LIGHT-CHAIN).
SQ SEQUENCE 213 AA; 22963 MW; 9133A742B943C79 CRC64;

Query Match 42.0%; Score 522; DB 1; Length 213;
Best Local Similarity 77.1%; Pred. No. 2.8e-35;
Matches 101; Conservative 8; Mismatches 16; Indels 6; Gaps 2;

QY 110 WDRA--SDH-----PVFGGTRTVLGGPKAAPSVTLFPPSSEELQANKATLVCLISDFYP 163
Db 83 WPRGFQSKHNSVTHVFGSGTQTLVLSQPKATPSVTLFPPSSEELQANKATLVCLMDFYP 142

QY 164 GAVTVAMKADSSPVKAGVETTPPSKSNKKAASSYLSLTPEQWKSHRYSQVTHGEGST 223
Db 143 GLTWTWKADGPTITQGVEMITTPPSKSNKKAASSYLSLTPEQWRRSRYSQVTHGEGST 202

QY 224 VEKTVAPTECS 234
Db 203 VEKTVAPAECS 213

RESULT 3
LV3B_HUMAN
ID LV3B_HUMAN STANDARD; PRT; 111 AA.
AC P80748;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig lambda chain V-III region LOI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.
RC TISSUE=Urine;
RX MEDLINE=99441384; PubMed=10510403;
RA Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
RT "Nephritogenic lambda light chain dimer: a unique human
RT miniautoantibody against complement factor H.";
RL J. Immunol. 163:4590-4596(1999).
CC -!- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING
CC TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.
CC -!- SUBUNIT: HOMODIMER.
CC -!- DISEASE: THE BLOCKING OF FACTOR H BY LOI PROTEIN LEADS TO THE
CC DEVELOPMENTAL OF MEMBRANOPROLIFERATIVE GLOMERULONEPHRITIS (MPGN).
DR PDB; 2LOI; 29-DEC-99.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; 3D-structure.
FT BINDING 15 15 SCR3.
FT BINDING 25 25 SCR3.
FT BINDING 29 29 SCR3.
FT BINDING 48 51 SCR3.
FT BINDING 94 94 SCR3.
FT DISULFID 21 86 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11935 MW; 69498EBEFD82053 CRC64;

Query Match 38.0%; Score 472; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 1.4e-31;
Matches 85; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 22 YELTOPSVSVSPGQTARITCGGDSNRNEVHWYQKPARAPILVYDSDRSGIPERF 81
Db 1 YVLTQPPSVSVAPGEVETARLTCGGNDIGSESVHWYQKPGQAPVLVYFDRDRSGIPERF 60

QY 82 SGKSGNATLTITNGVEAGDEADYVQVMDRASHDPVFGGTRTVTLGQPK 132
Db 61 SGNSGNATLTITSRVEAGDEADYVQLWDSSEHVVFGGTRTVTLVLSQPK 111

RESULT 4
LV5A_HUMAN
ID LV5A_HUMAN STANDARD; PRT; 108 AA.
AC P01719;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-V region DEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75112179; PubMed=4452363;
RA Bulitz M.;
RT "A new subgroup of human L-chains of the lambda-type. Primary
RT structure of Bence-Jones protein DEL.";
RL Eur. J. Biochem. 50:49-69(1974).
CC -!- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
CC CHAIN SUBGROUP V.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01985; L5HIDL.
DR HSSP; P80748; 2LOI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11342 MW; B8E8ED9C09C9B451 CRC64;

```

```

RP SEQUENCE.
RX MEDLINE=78000254; PubMed=409425;
RA Novotny J., Franek F., Margolies M.N., Haber E.;
RT "Amino acid sequence of normal (microheterogeneous) porcine
RT immunoglobulin lambda chains.";
RL Biochemistry 16:3765-3772(1977).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MIXTURE OF NORMAL
IMMUNOGLOBULINS.
DR PIR; A02129; L1PG.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_c1.
DR Pfam; PF00447; ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
CC FT NON_TER 1
FT DISULFID 27 86
FT DISULFID 104 104 INTERCHAIN (WITH HEAVY CHAIN).
SQ SEQUENCE 105 AA; 11003 MW; 3817AAEBD747C396 CRC64;

Query Match 33.4%; Score 415; DB 1; Length 105;
Best Local Similarity 74.3%; Pred. No. 4.9e-27;
Matches 78; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAADSSPVKAGVETTPTSKQ 189
DB 1 QPKAAPVTLFPPSSEELQNKATLVCLISDFYPGAVTVAWKAAGTTVTQGVETTPSKQ 60

QY 190 SNKYAASSYLSLTPEQWKSRSYSCQVTHEGTSVEKTVAPTSCS 234
DB 1 SNKYAASSYLSLTPEQWKSRSYSCQVTHEGTSVEKTVAPTSCA 105

RESULT 7
LACI_MOUSE STANDARD; PRT; 105 AA.
ID ID LACI_MOUSE
AC P01843;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ig lambda-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83014953; PubMed=6812053;
RA Selsing E., Miller J., Wilson R., Storb U.;
RT "Evolution of mouse immunoglobulin lambda genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
RN [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE=81148806; PubMed=6259534;
RA Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA Geffer M.L., Baltimore D.;
RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RL Nature 290:65-67(1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE=82220143; PubMed=6283385;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382(1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=71107854; PubMed=5276767;
RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
CC -!- MISCELLANEOUS: THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1

```



```
CC NORMAL LAMBDA-2 CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING
CC A LARGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
CC APPEARS COMPLETELY NORMAL.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00582; AA051636.1; -
DR EMBL: J00587; AA059672.1; -
DR PIR: A02126; LIMS.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00407; IgC1; 1.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 27 86
FT CONFLICT 19 104
FT CONFLICT 56 56
FT CONFLICT 75 75
FT CONFLICT 81 82
FT CONFLICT 85 85
FT CONFLICT 96 96
FT CONFLICT 96 96
FT SEQUENCE 105 AA; 11575 MW; A89F2B09BCFCA018 CRC64;
Query Match 33.1%; Score 412; DB 1; Length 105;
Best Local Similarity 71.4%; Pred. No. 8.6e-27;
Matches 75; Conservative 12; Mismatches 18; Indels 0; Gaps 0;
QY 130 QPKAAPSVTLFPPSSEELQANKTLVLISDFYGVAVTAAWKADSSPVKAGVETTTFSKQ 189
DB 1 QPKSPSVTLFPPSSEELQANKTLVLITDFYGVAVTAAWKADSSPVKAGVETTTFSKQ 60
QY 190 SNKYAASYSLLTPPEOWKSHRSYSCVTHSGSTVEKTVAPTECS 234
DB 61 SNKYMASSYLTLTARAWERHSSYSQCVTHSGHTVEKSLRADCS 105
RESULT 8
LV4A HUMAN
ID LV4A_HUMAN STANDARD; PRT; 106 AA.
AC P01715;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-IV region Bau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
MEDLINE=75059189; PubMed=4435717;
RA Bacsko K., Braun D., Hilschmann N.;
RT "Pattern of antibody structure, the primary structure of monoclonal
RT immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
RT protein Bau.)."
RL Hoppe-Sevler's Z. Physiol. Chem. 355:131-154 (1974).
CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR: A01981; LAHUB.
DR HSSP: P80748; 2LOI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT NON_TER 106
FT SEQUENCE 106 AA; 11305 MW; 4B6A688E0EC46571 CRC64;
Query Match 32.7%; Score 407; DB 1; Length 106;
Best Local Similarity 71.3%; Pred. No. 2.2e-26;
Matches 77; Conservative 10; Mismatches 19; Indels 2; Gaps 1;
QY 22 YELTOPPSVSUSPGQFARITCGDNRNEYVHWYQKPARAPILVIYDSDRPSGIPERF 81
DB 1 YGTQPPSLVSUSPGQFASITCSGDKLGEQVVCWYQKQSPVLVIYHDSKRPISGIPERF 60
QY 82 SGSKSGNTATLTINGVEAGDEADYVCQVMDRASDHPVFGGTRTVLG 129
DB 61 SGNSGTTATLTISGTQAMDEADYVQAWD--SYTVIFGGTKLTVLG 106
RESULT 9
LV7A HUMAN
ID LV7A_HUMAN STANDARD; PRT; 111 AA.
AC P01720;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VII region MOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
MEDLINE=81122740; PubMed=6780787;
RA Kojima M., Odani S., Ikenaka T.;
RT "Amino acid sequence of the lambda type light chain of a human IgG1
RT myeloma protein (MOT) with unusual antigenicity: a possible new
RT subgroup of lambda chain having a unique N-terminal sequence.";
RL Mol. Immunol. 17:1407-1414 (1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE REPRESENTS A NEW LAMBDA CHAIN
CC SUBGROUP. IT HAS AN AMINO-TERMINAL EXTENSION OF THREE RESIDUES
CC COMPARED WITH OTHER HUMAN LAMBDA CHAINS.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
CC MARKERS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01986; L7HUNT.
DR HSSP: P80748; 2LOI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT NON_TER 111
FT SEQUENCE 111 AA; 11942 MW; 140A28A2F86A6911 CRC64;
Query Match 32.2%; Score 400; DB 1; Length 111;
Best Local Similarity 69.4%; Pred. No. 8.5e-26;
Matches 75; Conservative 10; Mismatches 23; Indels 0; Gaps 0;
QY 22 YELTOPPSVSUSPGQFARITCGDNRNEYVHWYQKPARAPILVIYDSDRPSGIPERF 81
DB 4 YELTOPPSVSUSPGQFATMITCEGNDIGERSVHWYQKQAPVPVIVYDDADRPSCGPARF 63
QY 82 SGSKSGNTATLTINGVEAGDEADYVCQVMDRASDHPVFGGTRTVLG 129
DB 64 SGYNSGSAITLTINVEAGDEADYFCQSDWNGSVEVFGTGMTVLG 111
RESULT 10
LAC RABBIT
ID LAC_RABBIT STANDARD; PRT; 105 AA.
AC P01847;
DT 21-JUL-1986 (Rel. 01, Created)
DE 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
```

```

DE Ig lambda chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RN SEQUENCE.
RP MEDLINE=82091105; PubMed=6797414;
RX Garcia J., Jaton J.-C.;
RA "The primary structure of the constant region of Basilea-rabbit
RT immunoglobulin lambda-chains.";
RL Biochem. J. 197:177-183(1981).
CC -1- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC
CC SPECIFICITY.
DR PIR; A02130; LTRB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGL; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER 1
FT DISULFID 27 86
FT DISULFID 104 104 INTERCHAIN (WITH HEAVY CHAIN).
SQ SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;

Query Match 32.1%; Score 399; DB 1; Length 105;
Best Local Similarity 72.4%; Pred. No. 9.6e-26;
Matches 76; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVETTTPSKQ 189
DB 1 QPVTSPVILFPPSSEELKONKATLVCLISDFYPRTVYKWKADGNSVTGVTTPSKQ 60
QY 190 SNKYAASSLSLTPEQWKSHRSYSCQVTHGSTEKTVKTAFTCS 234
DB 61 SNKYAASSFLHLTANQWKSQSVTCQVTHGTVKSLAPAECS 105

RESULT 11
LV4B HUMAN STANDARD; PRT; 106 AA.
AC P01716;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-IV region X.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE.
RP MEDLINE=69088380; PubMed=4883841;
RX Milstein C., Clegg J.B., Jarvis J.M.;
RA "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT Bence-Jones protein.";
RL Biochem. J. 110:631-652(1968).
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01982; L4HUX.
DR HSSP; P80748; 2LOI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT NON TER 106
FT NON TER 106
SQ SEQUENCE 106 AA; 11334 MW; 24D04344AA812855 CRC64;

Query Match 32.1%; Score 399; DB 1; Length 106;
Best Local Similarity 71.0%; Pred. No. 9.7e-26;
Matches 76; Conservative 11; Mismatches 18; Indels 2; Gaps 1;

```

```

QY 22 YELTOPPSVSPGQTARITCGGDSNRNEYVHWYQKPARAPILVIYDSDRSGIPERF 81
DB 1 YDLTOPPSVSPGQTASITCSGDKGKDVWCYQRPQSPVLVIYQDNQRSGIPERF 60
QY 82 SGSKSGNTALTITNGVEAGDEADYYCQVMDRASDPHPVFGGGRVTVL 128
DB 61 SGSNSGNTALTITSGTQAMDEADYYCQAWDSMS--VVFGGGTRLTVL 105

RESULT 12
LV4E HUMAN STANDARD; PRT; 106 AA.
AC P06889;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-IV region MOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE.
RP MEDLINE=87156515; PubMed=3103603;
RX Holm E., Sletten K., Husby G.;
RA "Structural studies of a carbohydrate-containing
RT immunoglobulin-lambda-light-chain amyloid-fibril protein (AL) of
RT variable subgroup III.";
RL Biochem. J. 239:545-551(1986).
CC -1- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY
CC HOMOLOGU.
DR PIR; A26019; L4HUML.
DR HSSP; P80748; 2LOI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Amyloid; Glycoprotein.
FT DISULFID 21 86
FT CARBOHYD 90 90 BY SIMILARITY.
FT NON TER 106 106 N-LINKED (GLCNAC. .) (PROBABLE).
SQ SEQUENCE 106 AA; 11272 MW; D9BB77D4797D2123 CRC64;

Query Match 31.9%; Score 397; DB 1; Length 106;
Best Local Similarity 67.6%; Pred. No. 1.4e-25;
Matches 73; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY 22 YELTOPPSVSPGQTARITCGGDSNRNEYVHWYQKPARAPILVIYDSDRSGIPERF 81
DB 1 YELTOPPSVSPGQTATISCGDKLGESYDWMYQQSPGQSPLLVIYEGDKRPSGIPZRF 60
QY 82 SGSKSGNTALTITNGVEAGDEADYYCQVMDRASDPHPVFGGGRVTVL 129
DB 61 SGSNSGNTALTITSGTESMDEADYYCQAWNSS--VLFGGGTRLTVL 106

RESULT 13
LV4L RAT STANDARD; PRT; 104 AA.
AC P20766;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=87305594; PubMed=3114047;
RX Steen M.L., Hellman L., Pettersson U.;

```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 21.223 Seconds
(without alignments)
2271.829 Million cell updates/sec

Title: US-09-758-173-2

Perfect score: 1243

Sequence: 1 MRVPAQLGLLLWLPQARG.....CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	981	78.9	233	4	Q8TBC9
2	917.5	73.8	233	4	Q96169
3	885	71.2	237	4	Q8WUK4
4	883	71.0	237	4	Q8WTU6
5	856.5	68.9	236	4	Q96E61
6	763	61.4	240	4	Q8WUK3
7	700	56.3	235	11	Q99M11
8	551	44.3	106	4	Q8TCJ5
9	479.5	38.6	234	11	Q8VCP0
10	468.5	37.7	130	11	Q9DBW4
11	464	37.3	239	4	Q8TCD0
12	462.5	37.2	238	11	Q8VC16
13	449.5	36.2	234	11	Q8R062
14	444	35.7	235	11	Q91W12
15	441.5	35.5	238	11	Q99W37
16	432.5	34.8	234	11	Q91WF8

ALIGNMENTS

RESULT 1

ID	Q8TBC9	PRELIMINARY;	PRT;	233 AA.
AC	Q8TBC9;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Hypothetical 24.9 kDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PRIMARY B-CELLS;			
RA	Strausberg R.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; BC022823; AAH22823.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;			
Query Match 78.9%; Score 981; DB 4; Length 233;				
Best Local Similarity 79.4%; Pred. No. 1.7e-80;				
Matches 185; Conservative 17; Mismatches 21; Indels 10; Gaps 1;				
QY	12	LWLP-----GARCAYELTPPSVSPGQTARITCGGDSRNEYVHWYQOKPAR	61	
Db	1	MAWIPLLPLLLTCTGSEASYELTPPSVSPGQTARITCGSDALPKQYAYWYQOKPQ	60	
QY	62	APLIVYDSDRSPGIPERFSGSKGNTALTINGVEACDEADYVCQWDRADHPVFG	121	
Db	61	APVLVYKDNERPSPGIPERFSGSSGTTVLTISGVAEDEADYTCQSADSGTYWVFG	120	
QY	122	GTRVTVLGPKAAPSVTLPSPSSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGV	181	
Db	121	GTKLTVLGGPKAAPSVTLPSPSSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGV	180	
QY	182	ETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	234	

```
Db 181 ETTTPSKQSNKYYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 233
RESULT 2
ID Q96I69 PRELIMINARY; PRT; 233 AA.
AC Q96I69;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:12849).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RP TISSUE=B-CELL;
RC Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007782; AA07782.1; -.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00047; ig_2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;

Query Match 73.8%; Score 917.5; DB 4; Length 233;
Best Local Similarity 78.1%; Pred. No. 9.1e-75;
Matches 178; Conservative 17; Mismatches 32; Indels 1; Gaps 1;

Qy 7 LLGLLLWLPGARCAVELTOPPSVSPGQTARITCGDNSRNEYVHWYQOKPARAPILV 66
Db 7 LLG-LLSHCTGSGTSVLTOPASVSPAGQTARITCGGSLGSKSVNWLQREGQAPILV 65

Qy 67 IYDSDRPSGIPERFSGSKGNATLTINGVEAGDEADYQCQWDRASDHVPFGGTRVT 126
Db 66 VYENKERPAGIPERLSALTSEETATLTISVVAGDEADYFCQVMDTTSQQYVFGTGQVT 125

Qy 127 VLGPQKAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTP 186
Db 126 VLGPQKAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTP 185

Qy 187 SKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 186 SKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 3
Q8WUK4
ID Q8WUK4 PRELIMINARY; PRT; 237 AA.
AC Q8WUK4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RP TISSUE=TONSIL;
RC Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022098; AAH22098.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_IG_MHC.
SQ SEQUENCE 237 AA; 24884 MW; B6CF371E753968E8 CRC64;

Query Match 71.0%; Score 883; DB 4; Length 237;
Best Local Similarity 75.9%; Pred. No. 1.2e-71;
Matches 176; Conservative 17; Mismatches 35; Indels 4; Gaps 2;

Qy 7 LLGLLLWLPGARCAVELTOPPSVSPGQTARITCGDNSR---NEWVHWYQOKPARAP 63
Db 6 LLLTLAHCCTGSAQSVLTQPPSVSGAPQQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65

Qy 64 ILVIYDSDRPSGIPERFSGSKGNATLTINGVEAGDEADYQCQWDRASDHVPFGG 122
Db 66 KLLIYGNNSRPSGVPDRFSGSKSGTSASLAITGLQAEADYQCQSYDYSLSASGVFGG 125

Qy 123 TRVTVLGPQKAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
Db 126 TKLTVLGPQKAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185

Qy 183 TTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 186 TTTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 237

RESULT 4
Q8WTU6
ID Q8WTU6 PRELIMINARY; PRT; 237 AA.
AC Q8WTU6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RP TISSUE=TONSIL;
RC Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022098; AAH22098.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_IG_MHC.
SQ SEQUENCE 237 AA; 24884 MW; B6CF371E753968E8 CRC64;

Query Match 71.0%; Score 883; DB 4; Length 237;
Best Local Similarity 75.9%; Pred. No. 1.2e-71;
Matches 176; Conservative 17; Mismatches 35; Indels 4; Gaps 2;

Qy 7 LLGLLLWLPGARCAVELTOPPSVSPGQTARITCGDNSR---NEWVHWYQOKPARAP 63
Db 6 LLLTLAHCCTGSAQSVLTQPPSVSGAPQQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65

Qy 64 ILVIYDSDRPSGIPERFSGSKGNATLTINGVEAGDEADYQCQWDRASDHVPFGG 122
Db 66 KLLIYGNNSRPSGVPDRFSGSKSGTSASLAITGLQAEADYQCQSYDYSLSASGVFGG 125

Qy 123 TRVTVLGPQKAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
```

```

Db 126 TKTLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVE 185
QY 183 TTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTECS 234
Db 186 TTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTECS 237

RESULT 5
Q96E61
ID Q96E61 PRELIMINARY; PRT; 236 AA.
AC Q96E61;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:17259).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 24712 MW; 75C9FB3622FED957 CRC64;

Query Match 68.9%; Score 856.5; DB 4; Length 236;
Best Local Similarity 72.7%; Pred. No. 2.9e-69;
Matches 168; Conservative 19; Mismatches 41; Indels 3; Gaps 1;

QY 7 LIGLLLLMLPGARCAYELTOPPSVSPGQTARITCGDNR---NEVHYQOKPARAP 63
Db 6 LUTLLAHCTGSAQSVLAQPPSVSGAFQGVTTISCTGSGTIGAGYAVHYQYQPPGAAP 65

QY 64 ILVIYDDSDRPSGIPERFSGSGKSGNTATLTINGVEAGDEADYYCQVMDRSDHPVFGGT 123
Db 66 KVLIVGNYNRPSGVDRPSGSGKSGTSASLAITGLQAEADYYCQSYDGSLSGVFGNGT 125

QY 124 RVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVET 183
Db 126 KVTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVET 185

QY 184 TTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTECS 234
Db 186 TKPSQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTECS 236

RESULT 6
Q8WUK3
ID Q8WUK3 PRELIMINARY; PRT; 240 AA.
AC Q8WUK3;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical 26.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=IONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020236; AAH020236.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.

```

```

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;

Query Match 61.4%; Score 763; DB 4; Length 240;
Best Local Similarity 67.4%; Pred. No. 7.8e-61;
Matches 155; Conservative 20; Mismatches 33; Indels 22; Gaps 6;

QY 20 CAYE-LTQPPSVSPGQTARITCGDNRNEY-VHYQOKPARAPILVIYDDSD---R 73
Db 18 CALPVLTPPSASAFILGASIKLTCTLSREHSSYTIEMWQORPGRSPQYIMKVKSDGSHNK 77

QY 74 PSGIPERFSGSGKSGNTATLTINGVEAGDEADYYC-----QV-WDRASDHPVFGGT 124
Db 78 GDGIPDRFMGSSSGADRYLTLSNLQSDDEAEYHCGSHTIDGQGVW-----VFGG 130

QY 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVET 184
Db 131 LTVLSQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVET 190

QY 185 TPKSQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTECS 234
Db 191 TPKSQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTECS 240

RESULT 7
Q99M11
ID Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Hypothetical 25.4 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 56.3%; Score 700; DB 11; Length 235;
Best Local Similarity 60.7%; Pred. No. 3.6e-55;
Matches 142; Conservative 28; Mismatches 58; Indels 6; Gaps 3;

QY 5 AQLGLLLMLPGARCAYELTOPPSVSPGQTARITCGD---NSRNEVHYQOKPARA 62
Db 4 APLLLVFLHLLTGSCAQLVLTQPSVSTSLGSTAKLPCKASTGNIGDSYVNYQYWGSR 63

QY 63 PILVIYDDSDRPSGIPERFSGS--KSGNTATLTINGVEAGDEADYYCQVMDRSDHPVFG 120
Db 64 PTNMIYGDLLRPSGVDRPSGSGSIDSSNSAFLTIQNVQADDEADYYCQSY--SSGIRVFG 121

```



```
Matches 87; Conservative 14; Mismatches 19; Indels 7; Gaps 1;
QY 108 QVWDRADHPVFGGTRVTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVT 167
Db 11 QCW-----VFGGGTKLTVLQPKSSPSVTLFPPSSEELQANKATLVCLISDFYPGAVT 63
QY 168 VAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPTQWKSRRSYSCQVTHGSTEVT 227
Db 64 VDMKVDGTPVTQGMETTPQSKQSNNKYAASSYLSLTPTARAWERHSSYSCQVTHGSTEVT 123
QY 228 VAPTECS 234
Db 124 LSRADCS 130
RESULT 11
Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1 MRVPAQLLGLLLMLPGARCAYELTQPP-SVSVSPGQTARITCGDNS-----RNEYVHW 54
RP TISSUE=LUNG;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC022362; AAH22362.1; -.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;
Query Match 37.3%; Score 464; DB 4; Length 239;
Best Local Similarity 41.8%; Pred. No. 6.6e-34;
Matches 102; Conservative 52; Mismatches 74; Indels 16; Gaps 8;
QY 1 MRVPAQLLGLLLMLPGARCAYELTQPP-SVSVSPGQTARITCGDNS-----RNEYVHW 54
Db 1 MRLPAQLLGLLLMLVPGSGDVMVTQPSLPLVTLQGPASISCRSTQSLVYSDGNTVLNW 60
QY 55 YQOKPARAPILVIYDDSDRPSGIPERFSGSKGNTATLTINGVEAGDEADYYCQVWDRAS 114
Db 61 FQORPGQSPRLIYKVNRDGVDPDRFSGSGGTDFTLKIRVEAEDGVYFCN---QGT 117
QY 115 DHP-VFVGGRTRVTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAKAD 173
Db 118 HWPSTFGGQTKLEI-KRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFYPREAKVQWKVD 176
QY 174 SSPVKAG--VETTPSKQSNNKYAASSYLSLTPTQWKSRRSYSCQVTHG--STVEKTV 229
Db 177 NA-LQSGNSQESVTEQDSKDSYSLSTLTLSKADYKHVYACEVTHQGLSSPVTKSFN 235
QY 230 PTEC 233
Db 236 RGE 239
RESULT 12
Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```

RN 1 MRVPAQLLGLLLMLPGARCAYELTQPP-SVSVSPGQTARITCGDNS-----RNEYVHW 54
RP TISSUE=COLON;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG. 2.
DR SMART; SM00409; IG. 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
Query Match 37.2%; Score 462.5; DB 11; Length 238;
Best Local Similarity 41.4%; Pred. No. 9e-34;
Matches 101; Conservative 49; Mismatches 77; Indels 17; Gaps 8;
QY 1 MRVPAQLLGLLLMLPGARCAYELTQPP-SVSVSPGQTARITCGDNS-----RNEYVHW 54
Db 1 MKLUPVRL-LVLMFWIPASSDDVVMVTQPSLPLVSLDQASISCRSQSLVHSGNTYLHW 59
QY 55 YQOKPARAPILVIYDDSDRPSGIPERFSGSKGNTATLTINGVEAGDEADYYCQVWDRAS 114
Db 60 YLQKPGQSPKLLIYKVNRDGVDPDRFSGSGGTDFTLKIRVEAEDLVYFCS----QS 115
QY 115 DH--PVFGGRTRVTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAKA 172
Db 116 THVPPTFGGQTKLEI-KRADAAPTIVFPPSSEQLTSGGASVVCFLNNFYPRKDVNKKI 174
QY 173 DSSPVKAGV-ETTPSKQSNNKYAASSYLSLTPTQWKSRRSYSCQVTHGSGT--VEKTV 229
Db 175 DGSERQNGVLNSWTQDQSKDSTYSMSSTLTLTQKDEYRHSNTCEATHKTSTSPIVKSFN 234
QY 230 PTEC 233
Db 235 RNEC 238
RESULT 13
Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1 MRVPAQLLGLLLMLPGARCAYELTQPP-SVSVSPGQTARITCGDNSRNEYVHWYQKQP 59
RP TISSUE=COLON;
RA Strauberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC027418; AAH27418.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;
Query Match 36.2%; Score 449.5; DB 11; Length 234;
Best Local Similarity 41.6%; Pred. No. 1.3e-32;
Matches 99; Conservative 43; Mismatches 87; Indels 9; Gaps 6;
QY 1 MRVPAQLLGLLLMLPGARCAYELTQPP-SVSVSPGQTARITCGDNSRNEYVHWYQKQP 59
Db 1 MMSAQLGLLLLCFQGTICDQTTSSLSASLGDRVTISCSASQGISNLYNNYQKQP 60
QY 60 ARAPILVIYDDSDRPSGIPERFSGSKGNTATLTINGVEAGDEADYYCQVWDRASDHP-V 118
```

Db 61 DGVKLLIYVTSLSHGVSFRSGSGTHYSLTIGNLEPDIATYCCQY---SQFPPT 117
Qy 119 FGCGTRVTLGQPKAPSVTLPPSSEELQANKATVLCVLSDFYPCAVTVAMKADSSPVK 178
Db 118 FSGGTLKLEI--KRADAAPTIVSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQ 176
Qy 179 AGV-ETTPSKQNNKYAASSYLSLTPQWKSHRSYSCQVTHEGST--VEKTVAPTEC 233
Db 177 NGVLNSWTDQDSKDYMSSTLTLTLDKDEYERHNSYTCEATHKTSPIVKSFNNEC 234

RESULT 14
Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE=BREAST TUMOR;
RC Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
Query Match 35.7%; Score 444; DB 11; Length 235;
Best Local Similarity 43.0%; Pred. No. 4.1e-32;
Matches 92; Conservative 45; Mismatches 69; Indels 8; Gaps 6;

Qy 24 LTQPPSV-SVSPGOTARITCGDNRNEYVHWYQKPARAPILVIYDDSDRPSGIPERES 82
Db 26 LTQSPALMSASPGERVMTTCASSSVS-HHWHYQKSGTSPKRWIYDTFKLTSGVDPDRFS 84
Qy 83 GSKSGNTATLTNGVEAGDEADYICQVWDRASDHPFGGTRVTLGQPKAPSVTLFPP 142
Db 85 GSGSGTSYSLTISNWEADVATYCCQMSR--NPPTFGVGTGLE-LKRADAAPTIVSIFPP 141
Qy 143 SSELQANKATVLCVLSDFYPCAVTVAMKADSSPVKAGV-ETTPSKQNNKYAASSYLS 201
Db 142 SSELTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLNSWTDQDSKDYMSSTLT 201
Qy 202 LTPQWKSHRSYSCQVTHEGST--VEKTVAPTEC 233
Db 202 LTKDEYERHNSYTCEATHKTSPIVKSFNNEC 235

RESULT 15
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -

DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
Query Match 35.5%; Score 441.5; DB 11; Length 238;
Best Local Similarity 40.7%; Pred. No. 7e-32;
Matches 99; Conservative 49; Mismatches 80; Indels 15; Gaps 8;
Qy 1 MRVPAQLGLGLLLWLPGARCAVELTQPP-SVSVSPGOTARITCGDNR-----RNEYVHW 54
Db 1 MKLPVRL--VLMFWIPASSDDVVMVTQPLSLPVSLGQASISCRSSQSIVHNSNGNTYLEW 59
Qy 55 YQKPARAPILVIYDDSDRPSGIPERESGSKSGNTATLTNGVEAGDEADYICQVWDRAS 114
Db 60 YLQKPGOSPCLLYKVSNNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGVIYC---FGS 116
Qy 115 DHP-VFGGTRVTLGQPKAPSVTLFPPSSEELQANKATVLCVLSDFYPCAVTVAMKAD 173
Db 117 HVPYTFSGGTLKLEI-KRADAAPTIVSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWID 175
Qy 174 SSPVKAGV-ETTPSKQNNKYAASSYLSLTPQWKSHRSYSCQVTHEGST--VEKTVAP 230
Db 176 GSERQNGVLNSWTDQDSKDYMSSTLTLTLDKDEYERHNSYTCEATHKTSPIVKSFN 235
Qy 231 TEC 233
Db 236 NEC 238

Search completed: March 29, 2003, 09:14:34
Job time : 24.223 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 10.5021 Seconds
(without alignments)
2141.995 Million cell updates/sec

Title: US-09-758-173-2

Perfect score: 1243

Sequence: 1 MRVPAQLLGLLLWLPQARC.....CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1016	81.7	232	2 S25756	Ig lambda chain -
2	1012.5	81.5	233	2 S25747	Ig lambda chain -
3	979	78.8	231	2 S25738	Ig lambda chain -
4	959	77.2	231	2 S25751	Ig lambda chain -
5	959	77.2	231	2 S25753	Ig lambda chain -
6	936	75.3	226	2 S25745	Ig lambda chain -
7	923	74.3	213	2 JE0247	Ig lambda chain -
8	920	74.0	233	2 S25748	Ig lambda chain -
9	920	74.0	235	2 S05270	Ig lambda chain -
10	910	73.2	232	2 S25742	Ig lambda chain pr
11	905	72.8	233	2 S25741	Ig lambda chain -
12	883	71.0	233	2 S25752	Ig lambda chain -
13	881	70.9	235	2 S25750	Ig lambda chain -
14	873	70.2	234	2 S25757	Ig lambda chain -
15	871.5	70.1	213	2 S21066	Ig lambda chain -
16	871.5	70.1	236	2 S25746	Ig lambda chain V
17	870	70.0	233	2 S25744	Ig lambda chain -
18	870	70.0	235	2 S14675	Ig lambda chain -
19	867.5	69.8	235	2 S25759	Ig lambda chain -
20	867	69.8	216	2 A42193	Ig lambda chain -
21	862.5	69.4	217	2 JE0246	Ig lambda chain (B
22	859	69.1	216	2 S29258	Ig lambda chain NI
23	850.5	68.4	235	2 S25754	Ig lambda chain V
24	846	68.1	216	2 S03401	Ig lambda chain (K
25	840.5	67.6	225	2 S25758	Ig lambda chain -
26	835	67.2	190	2 S25740	Ig lambda chain -
27	833.5	67.1	212	2 S70431	Ig lambda chain -
28	822	66.1	216	2 JE0245	Ig lambda chain NI
29	820.5	66.0	235	2 S25749	Ig lambda chain -

30	818	65.8	216	2 S69130	Ig lambda chain (D
31	799	64.3	208	2 B49444	Ig lambda chain (N
32	785	63.2	243	2 S25755	Ig lambda chain -
33	639.5	51.4	181	2 PT0220	Ig lambda chain V-
34	639.5	51.4	232	2 S17399	Ig lambda chain pr
35	635.5	51.1	214	2 PC4156	Ig lambda chain V
36	632	50.8	230	2 S49449	Ig lambda chain -
37	622.5	50.1	213	2 A21177	Ig light chain pre
38	603	48.5	118	2 S12441	Ig lambda chain (K
39	600	48.3	118	2 S12442	Ig lambda chain (K
40	579	46.6	118	2 S12440	Ig lambda chain (M
41	578	46.5	118	2 S12443	Ig lambda chain (K
42	576	46.3	118	2 A39949	Ig lambda chain J-
43	559	45.0	234	2 A39956	Ig lambda chain pr
44	548	44.1	105	1 L2HU	Ig lambda chain C
45	542.5	43.6	146	2 S02083	Ig lambda chain V-

ALIGNMENTS

RESULT 1

S25756

Ig lambda chain - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25756

R:Combriato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt

A:Reference number: S16439; MUID:91257162; PMID:1904362

A:Accession: S25756

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-232 <COM>

A:Cross-references: EMBL:X57821; NID:G33741; PIDN:CAA40958.1; PID:G33742

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:147-215/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.7%; Score 1016; DB 2; Length 232;

Matches 196; Conservative 14; Mismatches 16; Indels 2; Gaps 2;

QY 7 LLGLLLLPGLARCAVELTOPPSVSPGQTARITCGDINSREYVHWYQOKPARAPILV 66

Db 7 LLG-LLSHCTGVTSLVLTQPPSVAPGKTASITCGGNIGSKSVHWYQOKPGQAPVLV 65

QY 67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRAHPVFGGTRVT 126

Db 66 VYDDSDRPSGIPERFSGSGNTATLTISRVEAGDEADYYCQVWSSD-VVFGGTRVT 124

QY 127 VLGPQKAAAPSVTLFPSSBELQANKATLVCLISDPYAGVAVWAKADSSPVKAGVETTP 186

Db 125 VLGPQKAAAPSVTLFPSSBELQANKATLVCLISDPYAGVAVWAKADSSPVKAGVETTP 184

QY 187 SKQSNKKAASLYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234

Db 185 SKQSNKKAASLYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 232

RESULT 2

S25747

Ig lambda chain - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25747

R:Combriato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt

A:Reference number: S16439; MUID:91257162; PMID:1904362

A:Accession: S25747

A:Status: preliminary; translation not shown

```
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57812; NID:g33723; PIDN:CAA40949.1; PID:g33724
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match      81.5%; Score 1012.5; DB 2; Length 233;
Best Local Similarity 85.1%; Pred. No. 1.6e-60; Indels 1; Gaps 1;
Matches 194; Conservative 13; Mismatches 20;

Qy 7 LLGLLLWLPACAYELTOPPSVSPGQTARITCGGDSNRNEYVHMYQOKPARAPILV 66
Db 7 LLG-LLSHTGTSVTSVLTOPPSPSVAPGKAARITCGGINIAKSVHMYQOKPGAPLV 65

Qy 67 IYDSDRPSGIPERFSGSKSGNTATITINGVEAGDEADYYCQWDRASDHPVFGGTRV 126
Db 66 VYGDSDRPSGIPERFSGSKSGNTATINISRVEAGDEADYYCQWDRASDHPVFGGTRV 125

Qy 127 VLGPQKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTP 186
Db 126 VLGPQKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTP 185

Qy 187 SKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 186 SKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 3
S25738
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25738
R:Combratio, G.; Klobbeck, H.G.
A:Title: V(lambda) 21, 1513-1522, 1991
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25738
A:Molecule type: mRNA
A:Status: preliminary; translation not shown
A:Residues: 1-231 <COM>
A:Cross-references: EMBL:X57802; NID:g33701; PIDN:CAA40940.1; PID:g33702
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:146-214/Domain: immunoglobulin homology <IMM>

Query Match      78.8%; Score 979; DB 2; Length 231;
Best Local Similarity 80.3%; Pred. No. 2.7e-58;
Matches 187; Conservative 13; Mismatches 21; Indels 12; Gaps 2;

Qy 12 LLWLP-----GACAYELTOPPSVSPGQTARITCGGDSNRNEYVHMYQOKPAR 61
Db 1 MAWIPFLGLVLAICTGSVASYELTOPPSVSPGQTASITCGDGLGDKYACWTQKPGH 60

Qy 62 APILVIYDSDRPSGIPERFSGSKSGNTATITINGVEAGDEADYYCQWDRASDHPVFGG 121
Db 61 SPVLVIFQDSKRPSGIPERFSGSKSGNTATITISGTQWDEADYYCQAWD--SSTA VFGG 118

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
Db 119 GTKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy 182 ETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 ETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

RESULT 4
S25751
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
```

```
C:Accession: S25751
R:Combratio, G.; Klobbeck, H.G.
A:Title: V(lambda) 21, 1513-1522, 1991
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25751
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-231 <COM>
A:Cross-references: EMBL:X57816; NID:g33731; PIDN:CAA40953.1; PID:g33732
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:146-214/Domain: immunoglobulin homology <IMM>

Query Match      77.2%; Score 959; DB 2; Length 231;
Best Local Similarity 79.0%; Pred. No. 5.7e-57;
Matches 184; Conservative 14; Mismatches 23; Indels 12; Gaps 2;

Qy 12 LLWLP-----GACAYELTOPPSVSPGQTARITCGGDSNRNEYVHMYQOKPAR 61
Db 1 MAWIPFLGLVLAICTGSVASYELTOPPSVSPGQTASITCGDGLGDKYASWYQKAGQ 60

Qy 62 APILVIYDSDRPSGIPERFSGSKSGNTATITINGVEAGDEADYYCQWDRASDHPVFGG 121
Db 61 SPVLVIVRHSKRPSGIPERFSGSKSGNTATITISGTQWDEADYYCQAWD--SSIVVFGG 118

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
Db 119 GTKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy 182 ETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 ETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

RESULT 5
S25753
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25753
R:Combratio, G.; Klobbeck, H.G.
A:Title: V(lambda) 21, 1513-1522, 1991
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25753
A:Molecule type: mRNA
A:Status: preliminary; translation not shown
A:Residues: 1-231 <COM>
A:Cross-references: EMBL:X57818; NID:g33735; PIDN:CAA40955.1; PID:g33736
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:146-214/Domain: immunoglobulin homology <IMM>

Query Match      77.2%; Score 959; DB 2; Length 231;
Best Local Similarity 78.5%; Pred. No. 5.7e-57;
Matches 183; Conservative 17; Mismatches 21; Indels 12; Gaps 2;

Qy 12 LLWLP-----GACAYELTOPPSVSPGQTARITCGGDSNRNEYVHMYQOKPAR 61
Db 1 MAWIPFLGLVLAICTGSVASYELTOPPSVSPGQTASITCGDGLGDKYASWYQKPGQ 60

Qy 62 APILVIYDSDRPSGIPERFSGSKSGNTATITINGVEAGDEADYYCQWDRASDHPVFGG 121
Db 61 SPVLVLYQDTRPSGIPERFSGSKSGNTATITISGTQWDEADYYCQAWD--SNTWVFGG 118

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
Db 119 GTKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy 182 ETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 ETTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231
```

RESULT 6

S25745
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25745
R:Combrato, G.; Klobbeck, H.G.
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25745
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-226 <COM>
A:Cross-references: EMBL:X57810; NID:g33717; PIDN:CAA40947.1; PID:g33718
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:141-209/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 936; DB 2; Length 226;
Best Local Similarity 79.0%; Pred. No. 1.9e-55;
Matches 177; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

QY 11 LLLWLPGARCAVELTQPPSVSPGQTARITCGDNRNRYVHWYQOKPARAPILVIYDD 70

DB 3 LLTFTCTVSEASYELTQPPSGVSPGKTARITCSGDALPKKYAYWYQKSGQSPVLVIYED 62

QY 71 SRPSPGIPRPSGSGKNTATLTINGVEAGDEADYICQVWDRAADHPVFGGGRVTVLQG 130

DB 63 TRKPSGIPRPSGSGKNTATLTISGAQVEADYICVSTDRGNHRVFGGGRVTVLQG 122

QY 131 PKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAATVAVKADSSPVKAGVETTTSPKOS 190

DB 123 PKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAATVAVKADSSPVKAGVETTTSPKOS 182

QY 191 NNKYAASSYLSLTPQWKSRSYSCQVTHEGSTVEKTVAPTECS 234

DB 183 NNKYAASSYLSLTPQWKSRSYSCQVTHEGSTVEKTVAPTECS 226

RESULT 7

JE0247
Ig lambda chain NIC250 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0247
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Takashi, I.; Shinoda,
submitted to JIPID, November 1998
A:Description: Structural relationship of lambda type light chains with AL amyloidosis.
A:Reference number: JE0245
A:Accession: JE0247
A:Molecule type: protein
A:Residues: 1-213 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:128-196/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 923; DB 2; Length 213;
Best Local Similarity 82.9%; Pred. No. 1.3e-54;
Matches 175; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

QY 24 LTQPPSVSPGQTARITCGDNRNRYVHWYQOKPARAPILVIYDDSRPSPGIPRPSFG 83

DB 3 LTQPPSVSPGQTARITCGDNLGTRNVHWYQOKPARAPILVIYDDSRPSPGIPRPSFG 62

QY 84 SKSGNTATLTINGVEAGDEADYICQVWDRAADHPVFGGGRVTVLQPKAAPSVTLFPPS 143

DB 63 SNSVTAATLAISEVAGDEADYICVWDRAANHFVFGGGRVTVLQPKAAPSVTLFPPS 122

QY 144 SELOANKATLVCLISDFYPGAATVAVKADSSPVKAGVETTTSPKOSNNKYAASSYLSLT 203

DB 123 SELOANKATLVCLISDFYPGAATVAVKADSSPVKAGVETTTSPKOSNNKYAASSYLSLT 182

QY 204 PEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

DB 183 PEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 213

RESULT 8

S25748
Ig lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25748
R:Combrato, G.; Klobbeck, H.G.
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25748
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 920; DB 2; Length 233;
Best Local Similarity 77.6%; Pred. No. 2.2e-54;
Matches 177; Conservative 16; Mismatches 29; Indels 6; Gaps 1;

QY 13 LMLP-----GARCAYELTQPPSVSPGQTARITCGDNRNRYVHWYQOKPARAPILV 66

DB 6 LMLTLLTLCIGSVSELSTQDPASVALGQVTRITCQGDLSURAYVSWYQHKPGQAPILV 65

QY 67 IYDSDRPSGIPRPSGSGKNTATLTINGVEAGDEADYICQVWDRAADHPVFGGGRVTV 126

DB 66 IYGENRPPSGIPRPSGSGKNTATLTINGVEAGDEADYICNSRDSDGQVLPFGGGRVTV 125

QY 127 VLQPKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAATVAVKADSSPVKAGVETTTTP 186

DB 126 VLQPKAAPSVTLFPPSSSELOANKATLVCLISDFYPGAATVAVKADSSPVKAGVETTTTP 185

QY 187 SKOSNNKYAASSYLSLTPQWKSRSYSCQVTHEGSTVEKTVAPTECS 234

DB 186 SKOSNNKYAASSYLSLTPQWKSRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 9

S05270
Ig lambda chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: S05270; S04601
R:Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05270
A:Molecule type: mRNA
A:Residues: 1-235 <KIS1>
A:Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of ϵ
A:Reference number: S04601; MUID:89296497; PMID:2500644
A:Accession: S04601
A:Molecule type: mRNA
A:Residues: 1-130 <KIS2>
A:Cross-references: EMBL:X14583
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted -SIG>
F:21-235/Product: Ig lambda chain #status predicted <NAT>
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 920; DB 2; Length 235;
 Best Local Similarity 77.4%; Pred. No. 2.3e-54;
 Matches 178; Conservative 15; Mismatches 35; Indels 2; Gaps 1;

QY 7 LLGALLLWLPGARCAVELTQPPSVSPGQTARITCGDNSR--NEYVHWYQKPARAPI 64
 DB 6 LLLTLLIHTCTGSAQSVLTQPPSVSAAPGQKVITSCSGSSNIGNNYVSWYQQLPGTAPK 65

QY 65 LVYDDSDRSPGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDHVPFGGTR 124
 DB 66 LLIYDNNKRPSPGIPDRFSGSKSGTSATLTGTLQTDGADYYCGTWDSSLNAGVFGGTR 125

QY 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
 DB 126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

QY 185 TPSKSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTEKTVAPTPCS 234
 DB 186 TPSKSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTEKTVAPTPCS 235

RESULT 10
 S25742
 Ig lambda chain - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S25742
 R:Combrato, G.; Klobbeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
 A:Reference number: S16439; MUID:91257162; PMID:1904362
 A:Accession: S25742
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-232 <COM>

C:Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:147-215/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 910; DB 2; Length 232;
 Best Local Similarity 76.5%; Pred. No. 1e-53;
 Matches 176; Conservative 17; Mismatches 35; Indels 2; Gaps 1;

QY 7 LLGALLLWLPGARCAVELTQPPSVSPGQTARITCGDNSR--NEYVHWYQKPARAPI 64
 DB 3 LLLTLLIHTCTGSAQSVLTQPPSVSAAPGQKVITSCSGSSNIGNNYVSWYQQLPGTAPK 62

QY 65 LVYDDSDRSPGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDHVPFGGTR 124
 DB 63 LLIFENNNKRPSPGIPDRFSGSKSGTSATLTGTLQTDGADYYCGTWDSSLNAGVFGGTR 122

QY 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
 DB 123 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 182

QY 185 TPSKSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTEKTVAPTPCS 234
 DB 183 TPSKSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTEKTVAPTPCS 232

RESULT 11
 S25741
 Ig lambda chain - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S25741
 R:Combrato, G.; Klobbeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
 A:Reference number: S16439; MUID:91257162; PMID:1904362
 A:Accession: S25741
 A:Status: preliminary; translation not shown

A:Molecule type: mRNA
 A:Residues: 1-233 <COM>
 A:Cross-references: EMBL:X57805; NID:g33707; PIDN:CAA40943.1; PID:g33708
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 905; DB 2; Length 233;
 Best Local Similarity 77.2%; Pred. No. 2.2e-53;
 Matches 176; Conservative 15; Mismatches 31; Indels 6; Gaps 1;

QY 13 LMLP-----GARCAYELTQPPSVSPGQTARITCGDNSRNEYVHWYQKPARAPI 66
 DB 6 LMLTLLTICIGSVSSELTDPTVSVAGQTLRIKCGDTRIRSYASWYQKPGCAPTLL 65

QY 67 IVYDDSDRSPGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDHVPFGGTR 126
 DB 66 INKDNRPSPGIPDRFSGSKSGTSATLTGTLQTDGADYYCQVMDRASDHVPFGGTR 125

QY 127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
 DB 126 VLSQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

QY 187 SKQSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTEKTVAPTPCS 234
 DB 186 SKQSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTEKTVAPTPCS 233

RESULT 12
 S25752
 Ig lambda chain - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S25752
 R:Combrato, G.; Klobbeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
 A:Reference number: S16439; MUID:91257162; PMID:1904362
 A:Accession: S25752
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-233 <COM>

C:Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 71.0%; Score 883; DB 2; Length 233;
 Best Local Similarity 74.3%; Pred. No. 6.4e-52;
 Matches 171; Conservative 21; Mismatches 36; Indels 2; Gaps 1;

QY 7 LLGALLLWLPGARCAVELTQPPSVSPGQTARITCGDNSR--NEYVHWYQKPARAPI 64
 DB 4 LLLTLLTICAGSAQSVLTQPPSVSAAPGQKVITSCSGSSNIGNNYVSWYQQLPGTAPK 63

QY 65 LVYDDSDRSPGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDHVPFGGTR 124
 DB 64 LLIYNNRPSPGIPDRFSGSKSGTSATLTGTLQTDGADYYCQVMDRASDHVPFGGTR 123

QY 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
 DB 124 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 183

QY 185 TPSKSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTEKTVAPTPCS 234
 DB 184 TPSKSNKNKYAASYSLSLTPEQWKSRSYSCQVTHEGSTEKTVAPTPCS 233

RESULT 13
 S25750
 Ig lambda chain - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

```
C:Accession: S25750
R:Combricato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25750
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57815; NID:G33729; PIDN:CAA40952.1; PID:G33730
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-219/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 881; DB 2; Length 235;
Best Local Similarity 74.3%; Pred. No. 8.8e-52;
Matches 171; Conservative 20; Mismatches 37; Indels 2; Gaps 1;

Qy 7 LLGLLLWLPGARCAVELTOPPSVSPGQTARITCGDNR--NEYVHWYQKPARAPI 64
Db 6 LLLTLLTHCAGWAQSVLTPPSASGTPGQRTVISCSSGSSNIGTNDVYVYQQLTGTPAK 65

Qy 65 LVIIYDDSRPSGIPERFSGSKGNATLTINGVEAGDEADYICQVMDRASDHVPFGGTR 124
Db 66 LLIYRNQRPQGVDPFRFSGSKSGSSASLITGLQSEADYICAWDDSLSGVPVGGTK 125

Qy 125 VTLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 184
Db 126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 185

Qy 185 TPSKQSNKYAASVLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTCS 234
Db 186 TPSKQSNKYAASVLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTCS 235

RESULT 14
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
A:Accession: S25757
R:Combricato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25757
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-234 <COM>
A:Cross-references: EMBL:X57822; NID:G33743; PIDN:CAA40959.1; PID:G33744
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:149-217/Domain: immunoglobulin homology <IMM>

Query Match 70.2%; Score 873; DB 2; Length 234;
Best Local Similarity 72.6%; Pred. No. 3e-51;
Matches 167; Conservative 25; Mismatches 36; Indels 2; Gaps 1;

Qy 7 LLGLLLWLPGARCAVELTOPPSVSPGQTARITCGDNR--NEYVHWYQKPARAPI 64
Db 5 LLLTLLTHCAGWAQSVLTPPSASGTPGQRTVISCSSGSSNIGTNDVYVYQQLTGTPAK 64

Qy 65 LVIIYDDSRPSGIPERFSGSKGNATLTINGVEAGDEADYICQVMDRASDHVPFGGTR 124
Db 65 VLIYNNRSPGVDPFRFSGSKSGSSASLITGLQSEADYICAWDDSLNGRLGGTK 124

Qy 125 VTLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 184
Db 125 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 184

Qy 185 TPSKQSNKYAASVLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTCS 234
Db 185 TPSKQSNKYAASVLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTCS 234
```

```
RESULT 15
S21066
Ig lambda chain V region - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
A:Accession: S21066
R:Diouha, A.; Lecroisey, A.; Henschen, A.; Ruttyn, Y.; Rouger, P.; Keil, B.
Protein Seq. Data Anal. 4, 319-324, 1991
A:Title: Partial amino acid sequence of the light chain of human anti-Rh(D) monoclonal an
A:Reference number: S21066; MUID:92253545; PMID:1812484
A:Accession: S21066
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-213 <DIO>
A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 74-Thr &
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:128-196/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 871.5; DB 2; Length 213;
Best Local Similarity 78.5%; Pred. No. 3.4e-51;
Matches 168; Conservative 16; Mismatches 23; Indels 7; Gaps 2;

Qy 24 LTQPPSVSPGQTARITCGDNR--NEYVHWYQKPARAPILVIYDDSRPSGIPER 80
Db 4 LTQPPSVSPGQRTVISCSSNIGARYDVNYYQQLPGTAPKLLIYNTIRPSGVPDR 63

Qy 81 FSGSKGNATLTINGVEAGDEADYICQVMDRASDHVPFGGTRTVLQPKAAPSVTLF 140
Db 64 FSGSKGTSASLITGLQAEDEGDIYCIW----DIVVFGGTKLTVLQPKAAPSVTLF 119

Qy 141 PPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPSKQSNKYAASVYL 200
Db 120 PPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPSKQSNKYAASVYL 179

Qy 201 SLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTCS 234
Db 180 SLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTCS 213

Search completed: March 29, 2003, 09:16:15
Job time : 11.5021 secs
```


GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 16.9836 Seconds
(without alignments)
828.100 Million cell updates/sec

Title: US-09-758-173-8
Perfect score: 2561
Sequence: 1 MGWSLLILFLVAVATRVQCE.....MHEALHNHYTQKLSLSGPK 478

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2561	100.0	478	3	US-08-487-550-8
2	2184.5	85.3	452	3	US-09-027-449-71
3	2184.5	85.3	452	4	US-09-026-985-71
4	2184.5	85.3	452	4	US-09-131-952A-71
5	2184.5	85.3	452	4	US-09-234-340A-71
6	2146.5	83.8	449	4	US-09-679-397-2
7	2146.5	83.8	449	4	US-09-680-148-2
8	2138.5	83.5	459	1	US-08-157-101A-7
9	2135	83.4	451	2	US-08-887-352B-18
10	2135	83.4	451	4	US-09-109-207C-18
11	2135	83.4	451	4	US-09-282-505-2
12	2135	83.4	451	4	US-09-054-255-2
13	2135	83.4	451	4	US-09-296-005-18
14	2132	83.2	451	2	US-08-887-352B-14
15	2132	83.2	451	2	US-08-887-352B-16
16	2132	83.2	451	3	US-08-466-151-65
17	2132	83.2	451	4	US-09-109-207C-14
18	2132	83.2	451	4	US-09-109-207C-16
19	2132	83.2	451	4	US-09-296-005-14
20	2132	83.2	451	4	US-09-296-005-16
21	2132	83.2	453	3	US-08-466-151-8
22	2132	83.2	453	4	US-08-466-163B-8
23	2100	82.0	476	2	US-08-378-339-10
24	2089.5	81.6	467	4	US-09-409-672A-8
25	2078	81.1	472	4	US-08-793-450-8
26	2073	80.9	476	3	US-08-487-550-4
27	2069	80.8	449	1	US-08-458-516-13

28	2064	80.6	472	4	US-09-301-593-43	Sequence 43, Appl
29	2058.5	80.4	467	1	US-08-704-744-81	Sequence 81, Appl
30	2056.5	80.3	446	3	US-08-197-411-7	Sequence 7, Appl
31	2054	80.2	468	4	US-09-485-737B-67	Sequence 67, Appl
32	2054	80.2	472	4	US-09-301-593-30	Sequence 30, Appl
33	2054	80.2	711	4	US-09-485-737B-90	Sequence 90, Appl
34	2053	80.2	476	3	US-08-487-550-12	Sequence 12, Appl
35	2046.5	79.9	473	4	US-09-049-672A-4	Sequence 4, Appl
36	2040.5	79.7	552	5	PCT-US93-07832-23	Sequence 23, Appl
37	2037.5	79.6	469	2	US-07-934-373C-23	Sequence 23, Appl
38	2037.5	79.6	469	3	US-08-437-642B-23	Sequence 23, Appl
39	2037.5	79.6	469	4	US-08-146-206C-23	Sequence 23, Appl
40	2030	79.3	451	4	US-09-247-352-3	Sequence 3, Appl
41	2030	79.3	451	4	US-09-466-635-3	Sequence 3, Appl
42	2024.5	79.1	453	4	US-09-301-593-18	Sequence 18, Appl
43	2023.5	79.0	454	2	US-07-934-373C-22	Sequence 22, Appl
44	2023.5	79.0	454	3	US-08-437-642B-22	Sequence 22, Appl
45	2023.5	79.0	454	4	US-08-146-206C-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-8
; Sequence 8, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-8

Query Match 100.0%; Score 2561; DB 3; Length 478;

Best Local Similarity 100.0%; Pred. No. 9.7e-199;

Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSLLILFLVAVATRVQCEVOLVESGGLVQPGGSLRVSCAVSGTFTSDHYMYWFRQAP 60

Db 1 MGWSLLILFLVAVATRVQCEVOLVESGGLVQPGGSLRVSCAVSGTFTSDHYMYWFRQAP 60

QY 61 GKPEWVGFTIRNKPNGGTTTEAASVKDRFTISRDDSKSIAYLQMSLKIETDAVYCTTS 120
DB 61 GKPEWVGFTIRNKPNGGTTTEAASVKDRFTISRDDSKSIAYLQMSLKIETDAVYCTTS 120
QY 121 Y1SHCRGGVCYCYFFFWGOGALVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDY 180
DB 121 Y1SHCRGGVCYCYFFFWGOGALVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDY 180
QY 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKPSNT 240
DB 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKPSNT 240
QY 241 KVDKAEPKSCDKTHCTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVDSHE 300
DB 241 KVDKAEPKSCDKTHCTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVDSHE 300
QY 301 DPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALP 360
DB 301 DPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALP 360
QY 361 APTKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
DB 361 APTKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
QY 421 NYKTPPVLDSDGFFLYSKLTVDKSRWQOGNVFSCSVMEALHNNHYTKLSLSPGK 478
DB 421 NYKTPPVLDSDGFFLYSKLTVDKSRWQOGNVFSCSVMEALHNNHYTKLSLSPGK 478

RESULT 2

US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid

; TOPOLOGY: Linear
US-09-027-449-71
Query Match 85.3%; Score 2184.5; DB 3; Length 452;
Best Local Similarity 89.2%; Pred. No. 2.le-168;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;
QY 20 EVOLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWMPROAPGKGPENWVGFIIRNKPNGGTT 79
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSSHYMHWRQAPGKGLEWVGI--DPSNGET 58
QY 80 EYAASVKDRFTISRDDSKSIAYLQMSLKIETDAVYCTTSYISHCRGGVCYCG--YFEF 137
DB 59 TYNQKFKGRFTLSRDNSKNTAYLQMSLRAEDTAVYYC-----ARGDYRYNGDMFFDV 111
QY 138 WGQALVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSG 197
DB 112 WGQGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSG 171
QY 198 VHTFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKPSNTKVDKAEPKSCDKTHCT 257
DB 172 VHTFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKPSNTKVDKAEPKSCDKTHCT 231
QY 258 PPCAPELILGGPSVFLFPKPKDTLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHN 317
DB 232 PPCAPELILGGPSVFLFPKPKDTLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHN 291
QY 318 AKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREP 377
DB 292 AKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREP 351
QY 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSSFFL 437
DB 352 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSSFFL 411
QY 438 YSKLTVDKSRWQOGNVFSCSVMEALHNNHYTKLSLSPGK 478
DB 412 YSKLTVDKSRWQOGNVFSCSVMEALHNNHYTKLSLSPGK 452
RESULT 3
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530

```
; TELFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-71

Query Match      85.3%; Score 2184.5; DB 4; Length 452;
Best Local Similarity 89.2%; Pred. No. 2.1e-168;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;

QY 20 EVLVESGGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPWVGFIRNKPNGGTT 79
Db 1 EVQLVQSGGGLVQPGSLRLSCAASGYSPFSHYMHWVRQAPGKGLEWGYI--DPSNGET 58
QY 80 EYAAASVKDRFTISRDSKSIAYLQWSSLIKIEDTAVYCTTSYISHCRGGVCYGG--YPEF 137
Db 59 TYNQFKGRFTLSRDNSKNTAYLQNSLRADTAIVYC-----ARGDYRYNGDWFFDV 111
QY 138 WQGGALVTVSSASTKGPVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSG 197
Db 112 WQGGTLVTVSSASTKGPVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSG 171
QY 198 VHTPEAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKAEPKSCDKTHTC 257
Db 172 VHTPEAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKAEPKSCDKTHTC 231
QY 258 PPCAPELGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 317
Db 232 PPCAPELGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 291
QY 318 AKTKPREQYNSTYRVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 377
Db 292 AKTKPREQYNSTYRVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 351
QY 378 QVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 437
Db 352 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 411
QY 438 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
Db 412 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 4
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A

; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-121-952A-71

Query Match      85.3%; Score 2184.5; DB 4; Length 452;
Best Local Similarity 89.2%; Pred. No. 2.1e-168;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;

QY 20 EVLVESGGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPWVGFIRNKPNGGTT 79
Db 1 EVQLVQSGGGLVQPGSLRLSCAASGYSPFSHYMHWVRQAPGKGLEWGYI--DPSNGET 58
QY 80 EYAAASVKDRFTISRDSKSIAYLQWSSLIKIEDTAVYCTTSYISHCRGGVCYGG--YPEF 137
Db 59 TYNQFKGRFTLSRDNSKNTAYLQNSLRADTAIVYC-----ARGDYRYNGDWFFDV 111
QY 138 WQGGALVTVSSASTKGPVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSG 197
Db 112 WQGGTLVTVSSASTKGPVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSG 171
QY 198 VHTPEAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKAEPKSCDKTHTC 257
Db 172 VHTPEAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKAEPKSCDKTHTC 231
QY 258 PPCAPELGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 317
Db 232 PPCAPELGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 291
QY 318 AKTKPREQYNSTYRVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 377
Db 292 AKTKPREQYNSTYRVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 351
QY 378 QVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 437
Db 352 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 411
QY 438 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
Db 412 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; NUMBER OF SEQUENCES: 72
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/234,340A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/121,952
;; FILING DATE: 24-Jul-1998
;; APPLICATION NUMBER: 60/074330
;; FILING DATE: 22-JAN-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/075467
;; FILING DATE: 20-FEB-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P1085R4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 71:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 452 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; US-09-234-340A-71

Query Match 85.3%; Score 2184.5; DB 4; Length 452;
Best Local Similarity 89.2%; Pred. No. 2.1e-168;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;

QY 20 EVQLVESGGGLVPGGSLRVSQAVSGFTFSDHYMYWFRQAPGKGPWVGFIKPKNGGTT 79
DB 1 EVQLVQSGGGLVPGGSLRLSCAASGYSSSHYMHVWRQAPGKLEWGVYI--DPSNGET 58

QY 80 EYAASVKDRFTISRDDSKSTAYLQMSLKIEDTAVYCTTSYISHCRGGVCYGG--YEPF 137
DB 59 TYNQKFKGRFTLSRDNSKNTAYLQMSLRAEDTAVYYC-----ARGDYRYNGDWFFDV 111

QY 138 WGQALVTYSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDDPVKFNWYVDGVEV 197
DB 112 WGQGLTVTVSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDDPVKFNWYVDGVEV 171

QY 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKAEKPSCKDKTHTC 257
DB 172 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKAEKPSCKDKTHTC 231

QY 258 PCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDPVKFNWYVDGVEV 317
DB 232 PCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDPVKFNWYVDGVEV 291

QY 318 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
DB 292 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351

QY 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPL 437
DB 352 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPL 411

QY 438 YSKLTVDKSRWQOGNFCSCVMHEALHNHYTQKSLSLSPGK 478
DB 412 YSKLTVDKSRWQOGNFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 6
US-09-679-397-2
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D2
; CURRENT APPLICATION NUMBER: US/09/679,397
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-09-679-397-2

Query Match 83.8%; Score 2146.5; DB 4; Length 449;
Best Local Similarity 88.3%; Pred. No. 2.5e-165;
Matches 408; Conservative 12; Mismatches 25; Indels 17; Gaps 3;

QY 20 EVQLVESGGGLVPGGSLRVSQAVSGFTFSDHYMYWFRQAPGKGPWVGFIKPKNGGTT 79
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFIKDTYIHWVROAPGKLEWVA--RIYPTNGYT 58

QY 80 EYAASVKDRFTISRDDSKSTAYLQMSLKIEDTAVYCTTSYISHCRGGVCYGG----YF 135
DB 59 RYADSVKGRFTISADTSKNTAYLQMSLRAEDTAVYYCSR-----WGGDGFYAM 107

QY 136 EFWQGGALVTYSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDDPVKFNWYVDGVEV 195
DB 108 DYWGQGLTVTVSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDDPVKFNWYVDGVEV 167

QY 196 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKAEKPSCKDKTH 255
DB 168 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKAEKPSCKDKTH 227

QY 256 TCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDPVKFNWYVDGVEV 315
DB 228 TCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDPVKFNWYVDGVEV 287

QY 316 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 375
DB 288 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 347

QY 376 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSF 435
DB 348 EPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSF 407

QY 436 FLYSKLTVDKSRWQOGNFCSCVMHEALHNHYTQKSLSLSPG 477
DB 408 FLYSKLTVDKSRWQOGNFCSCVMHEALHNHYTQKSLSLSPG 449

RESULT 7
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D1
; CURRENT APPLICATION NUMBER: US/09/680,148

; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
US-09-680-148-2

Query Match 83.8%; Score 2146.5; DB 4; Length 449;
Best Local Similarity 88.3%; Pred. No. 2.5e-165;
Matches 408; Conservative 12; Mismatches 25; Indels 17; Gaps 3;

QY 20 EVLVESGGLVQPGSLRVSCAVSGFTSDHYMYWFRQAPGKPEWVGFI RNKPNGGTT 79
DB 1 EVLVESGGLVQPGSLRVSCAVSGFTSDHYMYWFRQAPGKPEWVGFI RNKPNGGTT 58
QY 80 EYAAVKDRFTISRDSKSIAYLQSSLIKIEDTAVYCTTSYISHCRGGVCYGG----YF 135
DB 59 RYADSVKGRFTISADTSKNTAYLQNSLRADTAVYCSR-----WGSDGFYAM 107
QY 136 EFWGQALVTSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVVSNWNSGALT 195
DB 108 DYWGQGLTVTSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVVSNWNSGALT 167
QY 196 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKAEKPKSCDKTH 255
DB 168 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKAEKPKSCDKTH 227
QY 256 TCPGPCAPPELLGPGSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 315
DB 228 TCPGPCAPPELLGPGSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 287
QY 316 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIKAKKGOPR 375
DB 288 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIKAKKGOPR 347
QY 376 EPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSF 435
DB 348 EPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSF 407
QY 436 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 477
DB 408 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 449

RESULT 8

US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K.
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437/204199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-157-101A-7

Query Match 83.5%; Score 2138.5; DB 1; Length 459;
Best Local Similarity 87.2%; Pred. No. 1.1e-164;
Matches 409; Conservative 14; Mismatches 35; Indels 11; Gaps 3;

QY 11 VAVATRVQCVQLVQPGSLRVSCAVSGFTSDHYMYWFRQAPGKPEWVGFI 70
DB 1 VGLLRGVQCVQLVQPGSLRVSCAVSGFTSDHYMYWFRQAPGKPEWVGFI 60
QY 71 RNKPNGGTTTAYAAVKDRFTISRDSKSIAYLQSSLIKIEDTAVYCTTSYISHCRGGVC 130
DB 61 LY--DGNHKKFYADSVKGRFTISRDSKNTLYLEVSKLQTEDTGVYYCIRDQ-----T 110
QY 131 YGGV-PEFWGQALVTSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 189
DB 111 YGVHRFDSWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 170
QY 190 NSGALTSVGHVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKAEKPK 249
DB 171 NSGALASGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKAEKPK 230
QY 250 SCDKTHTCPCAPPELLGPGSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY 309
DB 231 SCDKTHTCPCAPPELLGPGSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY 290
QY 310 VDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIK 369
DB 291 VDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIK 350
QY 370 AKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVVL 429
DB 351 AKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVVL 410
QY 430 DSDGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 478
DB 411 DSDGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 459

RESULT 9
US-08-887-352B-18
; Sequence 18, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

```

; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-18

Query Match      83.4%; Score 2135; DB 2; Length 451;
Best Local Similarity 88.5%; Pred. No. 2.1e-164;
Matches 408; Conservative 14; Mismatches 27; Indels 12; Gaps 4;

Qy 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFROAPKGPGEWGFIRNKNPGGT 78
Db 1 EVQLVESGGGLVQPGGSLRVSCAVSGVTSITSGYSNWIRQAPKGLWEVASIK---YSGE 57
Qy 79 TEYAASVKDRFTISRDDSKSIAYLQMSLLKIEDTAVYYCTTSYISHCRGVCYV-GYFEF 137
Db 58 TKYNPSVKGRITISRDDSKNTFYLQMSLRAEDTAVYYC-----ARGSHYFGHWHFAV 110
Qy 138 WGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSMNSGALTSG 197
Db 111 WGGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSMNSGALTSG 170
Qy 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTC 257
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTC 230
Qy 258 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
Db 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
Qy 318 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
Db 291 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
Qy 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFFL 437
Db 351 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFFL 410
Qy 438 YSKLTVDKSRWQOGNPFSCSVMEALHNHYTQKSLSLSPGK 478
Db 411 YSKLTVDKSRWQOGNPFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 10
US-09-109-207C-18
; Sequence 18, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1

; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-18

Query Match      83.4%; Score 2135; DB 2; Length 451;
Best Local Similarity 88.5%; Pred. No. 2.1e-164;
Matches 408; Conservative 14; Mismatches 27; Indels 12; Gaps 4;

Qy 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFROAPKGPGEWGFIRNKNPGGT 78
Db 1 EVQLVESGGGLVQPGGSLRVSCAVSGVTSITSGYSNWIRQAPKGLWEVASIK---YSGE 57
Qy 79 TEYAASVKDRFTISRDDSKSIAYLQMSLLKIEDTAVYYCTTSYISHCRGVCYV-GYFEF 137
Db 58 TKYNPSVKGRITISRDDSKNTFYLQMSLRAEDTAVYYC-----ARGSHYFGHWHFAV 110
Qy 138 WGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSMNSGALTSG 197
Db 111 WGGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSMNSGALTSG 170
Qy 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTC 257
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTC 230
Qy 258 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
Db 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
Qy 318 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
Db 291 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
Qy 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFFL 437
Db 351 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFFL 410
Qy 438 YSKLTVDKSRWQOGNPFSCSVMEALHNHYTQKSLSLSPGK 478
Db 411 YSKLTVDKSRWQOGNPFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 11
US-09-282-505-2
; Sequence 2, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
; US-09-282-505-2
```

```

; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-18

Query Match      83.4%; Score 2135; DB 4; Length 451;
Best Local Similarity 88.5%; Pred. No. 2.1e-164;
Matches 408; Conservative 14; Mismatches 27; Indels 12; Gaps 4;

Qy 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFROAPKGPGEWGFIRNKNPGGT 78
Db 1 EVQLVESGGGLVQPGGSLRVSCAVSGVTSITSGYSNWIRQAPKGLWEVASIK---YSGE 57
Qy 79 TEYAASVKDRFTISRDDSKSIAYLQMSLLKIEDTAVYYCTTSYISHCRGVCYV-GYFEF 137
Db 58 TKYNPSVKGRITISRDDSKNTFYLQMSLRAEDTAVYYC-----ARGSHYFGHWHFAV 110
Qy 138 WGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSMNSGALTSG 197
Db 111 WGGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPETVSMNSGALTSG 170
Qy 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTC 257
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTC 230
Qy 258 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
Db 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
Qy 318 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
Db 291 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
Qy 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFFL 437
Db 351 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFFL 410
Qy 438 YSKLTVDKSRWQOGNPFSCSVMEALHNHYTQKSLSLSPGK 478
Db 411 YSKLTVDKSRWQOGNPFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 11
US-09-282-505-2
; Sequence 2, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
; US-09-282-505-2
```

Query Match	83.4%	Score 2135	DB 4	Length 451
Best Local Similarity	88.5%	Pred. No. 2.1e-164		
Matches	408	Conservative	14	Mismatches 27; Indels 12; Gaps
Qy	20	EVQLVESGGGLVPGGSLRYS	CAVSGTFFSDHMY-WFROAPGKGWVCFIRKNGGT	78
Db	1	EVQLVESGGGLVPGGSLRUS	CAVSGYSITSGYSWNIRQAPKGLEWASIK---YSGE	57
Qy	79	TEYAASVKDRFTISRDDSK	STAYLQMSLKIEDTAVYVCTTSVISHCRGGVCVG-GVFEF	137
Db	58	TKYNPVKGRITISRDDSK	NTFYLQMSLRAEDTAVYIC-----ARGSHYEGHHFAV	110
Qy	138	WGQALVTVSSASTGKPSVP	PLAPSSKTSGGTAALGCLVKDYFPEPVTVMNSGALTSG	197
Db	111	WGQGLTVTSASTGKPSVP	PLAPSSKTSGGTAALGCLVKDYFPEPVTVMNSGALTSG	170
Qy	198	VHTPFAVLQSSGLYSLSV	VTVPSSSLGTQTYICNVNHKPSNTKVDKAPKSCDKTHTC	257
Db	171	VHTPFAVLQSSGLYSLSV	VTVPSSSLGTQTYICNVNHKPSNTKVDKVPKSCDKTHTC	230
Qy	258	PPCPAPELLGPGSVFLPP	PKPDTMLISRPETVTCVVVDVSHEDPEVKFNWYVDGVEVHN	317
Db	231	PPCPAPELLGPGSVFLPP	PKPDTMLISRPETVTCVVVDVSHEDPEVKFNWYVDGVEVHN	290
Qy	318	AKTPREEQYNSTYRVVSV	LTVLHQDMLNGKEYCKVSNKALPAPIEKTI	377
Db	291	AKTPREEQYNSTYRVVSV	LTVLHQDMLNGKEYCKVSNKALPAPIEKTI	350
Qy	378	QVYTLPSRDELTKNQVSL	TCLVKGFYPSDIAVEWESNGQPENNYKTT	437
Db	351	QVYTLPSRDEMTKNQVSL	TCLVKGFYPSDIAVEWESNGQPENNYKTT	410
Qy	438	YSKLTVDKSRWQQGNVFS	CSMHEALHNHYTQKSLSLSPGK	478
Db	411	YSKLTVDKSRWQQGNVFS	CSMHEALHNHYTQKSLSLSPGK	451

```

RESULT 12
US-09-054-255-2
; Sequence 2, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody heavy chain
US-09-054-255-2

```

Qy	198	VHTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKABPKSCDKTHTC	257
Db	171	VHTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVBPKSCDKTHTC	230
Qy	258	PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	317
Db	231	PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	290
Qy	318	AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP	377
Db	291	AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP	350
Qy	378	QVYTLPPSRBELTKNOYSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFL	437
Db	351	QVYTLPPSRBELTKNOYSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFL	410
Qy	438	YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPCK	478
Db	411	YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPCK	451

RESULT 13
US-09-296-005-18
; Sequence 18, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: F1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-18

OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-18

```
Db 351 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSDGSFFL 410
Qy 438 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
Db 411 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 14
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-14
Query Match 83.2%; Score 2132; DB 2; Length 451;
Best Local Similarity 88.5%; Pred. No. 3.7e-164;
Matches 408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

Qy 20 EVQLVESGGGLVQPGGSLRVSQAVSGTFTSDHYMY-WFROAPGKGPWVGFIKPKNGGT 78
Db 1 EVQLVESGGGLVQPGGSLRVSQAVSGTFTSDHYMY-WFROAPGKGPWVGFIKPKNGGT 78
Qy 79 TEYAASVKDRFTISRDDSKSTAYLQMSLSKIEDTAVYCTTSYISHCRGVCYG-GYFEF 137
Db 58 TNYNPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYVC-----ARGSHYFGHWHFAV 110
Qy 138 WQOGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYKPKVNTKDKKAEPKSCDKTHTC 197
Db 111 WQOGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYKPKVNTKDKKAEPKSCDKTHTC 170
Qy 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 230
Qy 258 PPCPAPELLGGPSVFLFPPKPKDITLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
Db 231 PPCPAPELLGGPSVFLFPPKPKDITLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
Qy 318 AKTQPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
```

```
Db 291 AKTQPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
Qy 378 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSDGSFFL 437
Db 351 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSDGSFFL 410
Qy 438 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
Db 411 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 15
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-16
Query Match 83.2%; Score 2132; DB 2; Length 451;
Best Local Similarity 88.5%; Pred. No. 3.7e-164;
Matches 408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

Qy 20 EVQLVESGGGLVQPGGSLRVSQAVSGTFTSDHYMY-WFROAPGKGPWVGFIKPKNGGT 78
Db 1 EVQLVESGGGLVQPGGSLRVSQAVSGTFTSDHYMY-WFROAPGKGPWVGFIKPKNGGT 78
Qy 79 TEYAASVKDRFTISRDDSKSTAYLQMSLSKIEDTAVYCTTSYISHCRGVCYG-GYFEF 137
Db 58 TNYNPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYVC-----ARGSHYFGHWHFAV 110
Qy 138 WQOGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYKPKVNTKDKKAEPKSCDKTHTC 197
Db 111 WQOGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYKPKVNTKDKKAEPKSCDKTHTC 170
Qy 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 230
Qy 258 PPCPAPELLGGPSVFLFPPKPKDITLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
Db 231 PPCPAPELLGGPSVFLFPPKPKDITLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
```


Qy 318 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
Db 291 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
Qy 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
Db 351 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410
Qy 438 YSKLTVDKSRWQOGNVPFSCSVMHREALHNNHYTKSLSLSPGK 478
Db 411 YSKLTVDKSRWQOGNVPFSCSVMHREALHNNHYTKSLSLSPGK 451

Search completed: March 29, 2003, 09:17:43
Job time : 18.9836 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 18.3244 Seconds
(without alignments)
1531.829 Million cell updates/sec

Title: US-09-758-173-8

Perfect score: 2561

Sequence: 1 MGSLLLLFLVAVATRVQCE.....MHEALHHYTKSLSLSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2561	100.0	478	9	US-09-124-905-8
2	2561	100.0	478	9	US-09-948-429B-8
3	2184.5	85.3	452	9	US-09-726-258-71
4	2160	84.3	451	10	US-09-822-698A-26
5	2154	84.1	449	10	US-09-736-371B-21
6	2149.5	83.9	731	10	US-09-825-012-46
7	2149.5	83.9	741	10	US-09-825-012-55
8	2144.5	83.7	729	10	US-09-825-012-52
9	2144.5	83.7	739	10	US-09-825-012-61
10	2138.5	83.5	730	10	US-09-825-012-49
11	2138.5	83.5	740	10	US-09-825-012-58
12	2135	83.4	451	9	US-09-920-171-18
13	2132	83.2	451	9	US-09-925-179-65
14	2132	83.2	451	10	US-09-920-171-14
15	2132	83.2	451	10	US-09-920-171-16
16	2132	83.2	453	9	US-09-925-179-8
17	2132	83.2	453	10	US-09-802-077-8
18	2132	83.2	453	10	US-09-802-096-8
19	2129	83.1	451	9	US-09-925-179-66

Sequence 68, Appl
Sequence 3, Appl
Sequence 25, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 27, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 4, Appl
Sequence 36, Appl
Sequence 32, Appl
Sequence 230, App
Sequence 220, App
Sequence 37, Appl
Sequence 216, App
Sequence 218, App
Sequence 250, App
Sequence 43, Appl
Sequence 49, Appl
Sequence 222, App
Sequence 224, App
Sequence 248, App
Sequence 39, Appl
Sequence 41, Appl
Sequence 228, App
Sequence 47, Appl

20 2122 82.9 451 9 US-09-925-179-68
21 2091 81.6 476 10 US-09-747-669-3
22 2073.5 81.0 475 10 US-09-740-002-25
23 2073 80.9 476 9 US-10-124-905-4
24 2073 80.9 476 9 US-09-948-429B-4
25 2071.5 80.9 475 10 US-09-740-002-27
26 2053 80.2 476 9 US-10-124-905-12
27 2053 80.2 476 9 US-09-948-429B-12
28 2004 78.3 443 10 US-09-917-410-4
29 1997 78.0 470 10 US-09-859-053-36
30 1996 77.9 470 10 US-09-859-053-32
31 1992 77.8 451 9 US-09-996-288-230
32 1989.5 77.7 450 9 US-09-996-288-220
33 1989.5 77.7 450 10 US-09-796-848A-37
34 1988.5 77.6 450 9 US-09-996-288-216
35 1988.5 77.6 450 9 US-09-996-288-218
36 1988.5 77.6 450 9 US-09-996-288-250
37 1988.5 77.6 450 10 US-09-796-848A-43
38 1988.5 77.6 450 10 US-09-796-848A-49
39 1987.5 77.6 450 9 US-09-996-288-222
40 1987.5 77.6 450 9 US-09-996-288-224
41 1987.5 77.6 450 9 US-09-996-288-248
42 1987.5 77.6 450 10 US-09-796-848A-39
43 1987.5 77.6 450 10 US-09-796-848A-41
44 1984.5 77.5 450 9 US-09-996-288-228
45 1984.5 77.5 450 10 US-09-796-848A-47

ALIGNMENTS

RESULT 1
US-10-124-905-8
; Sequence 8, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS: 12
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-124-905-8

Query Match 100.0%; Score 2561; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.4e-129; Indels 0; Gaps 0;
Matches 478; Conservative 0; Mismatches 0;

QY 1 MGWSLILFLVAVATRVQCEVQLVSGGGLVQPGSLRVSCAVSGGFTFSDHYMYWFRQAP 60
DB 1 MGWSLILFLVAVATRVQCEVQLVSGGGLVQPGSLRVSCAVSGGFTFSDHYMYWFRQAP 60
QY 61 GKGPWVGFIKPKNGGTTTEYAASVKDRFTISRDDSKSIAYLQWSSLKIEDTAVYYCTTS 120
DB 61 GKGPWVGFIKPKNGGTTTEYAASVKDRFTISRDDSKSIAYLQWSSLKIEDTAVYYCTTS 120
QY 121 YISHCRGGVCGYGFYFQPGALVTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDY 180
DB 121 YISHCRGGVCGYGFYFQPGALVTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDY 180
QY 181 FPEPVTVSNWNSGALTSVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNT 240
DB 181 FPEPVTVSNWNSGALTSVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNT 240
QY 241 KVDKKAEPKSCDKTHTCPAPPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSH 300
DB 241 KVDKKAEPKSCDKTHTCPAPPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSH 300
QY 301 DPEVKFNWVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQDLMLNGKEYCKVSNKALP 360
DB 301 DPEVKFNWVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQDLMLNGKEYCKVSNKALP 360
QY 361 APIEKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
DB 361 APIEKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
QY 421 NYKTTTPVLDSDGSGFLLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
DB 421 NYKTTTPVLDSDGSGFLLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478

RESULT 2

US-09-948-429B-8
Sequence 8, Application US/09948429B
Patent No. US2002017689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948.429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-429B-8

Query Match 100.0%; Score 2561; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSLILFLVAVATRVQCEVQLVSGGGLVQPGSLRVSCAVSGGFTFSDHYMYWFRQAP 60
DB 1 MGWSLILFLVAVATRVQCEVQLVSGGGLVQPGSLRVSCAVSGGFTFSDHYMYWFRQAP 60
QY 61 GKGPWVGFIKPKNGGTTTEYAASVKDRFTISRDDSKSIAYLQWSSLKIEDTAVYYCTTS 120
DB 61 GKGPWVGFIKPKNGGTTTEYAASVKDRFTISRDDSKSIAYLQWSSLKIEDTAVYYCTTS 120
QY 121 YISHCRGGVCGYGFYFQPGALVTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDY 180
DB 121 YISHCRGGVCGYGFYFQPGALVTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDY 180
QY 181 FPEPVTVSNWNSGALTSVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNT 240
DB 181 FPEPVTVSNWNSGALTSVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNT 240
QY 241 KVDKKAEPKSCDKTHTCPAPPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSH 300
DB 241 KVDKKAEPKSCDKTHTCPAPPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSH 300
QY 301 DPEVKFNWVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQDLMLNGKEYCKVSNKALP 360
DB 301 DPEVKFNWVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQDLMLNGKEYCKVSNKALP 360
QY 361 APIEKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
DB 361 APIEKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
QY 421 NYKTTTPVLDSDGSGFLLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
DB 421 NYKTTTPVLDSDGSGFLLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478

RESULT 3

US-09-726-258-71
Sequence 71, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Kounenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA


```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-371B-21

Query Match      84.1%; Score 2154; DB 10; Length 449;
Best Local Similarity 89.5%; Pred. No. 6.1e-108;
Matches 411; Conservative 9; Mismatches 29; Indels 10; Gaps 2;

QY 20 EVQLVSGGGLVPGGSLRVSCHAVSGFTSDHVMYWFRAAPGKPEWVGFI RNKNGGTT 79
DB 1 EVQLVSGGGLVPGGSLRVSCHAVSGFTSDHVMYWFRAAPGKPEWVGFI RNKNGGTT 58
QY 80 EYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYICTTSYISHCRGVCYGGYFEFWG 139
DB 59 YRDSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYICAKFR-----QYSGGFDYWG 110
QY 140 QGALVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTVSWNSGALTSGVH 199
DB 111 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTVSWNSGALTSGVH 170
QY 200 TFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKDKAEKPSCKDKTHTCPP 259
DB 171 TFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKDKAEKPSCKDKTHTCPP 230
QY 260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAK 319
DB 231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAK 290
QY 320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOV 379
DB 291 TKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOV 350
QY 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS 439
DB 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS 410
QY 440 KLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSPGK 478
DB 411 KLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSPGK 449

RESULT 6
US-09-825-012-46
; Sequence 46, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMF1 heavy chain - DNase I fusion
US-09-825-012-46

Query Match      83.9%; Score 2149.5; DB 10; Length 731;
Best Local Similarity 84.9%; Pred. No. 1.7e-107;
Matches 406; Conservative 21; Mismatches 40; Indels 11; Gaps 2;

QY 1 MGWSLILFLVAVATRVQCEVOLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
DB 1 MGWSCILFLVATATGVHSQVLVQSGAEVKFGASVKVSKASGYTFSAIWIEWVRQAP 60
QY 61 GKGPEWVGFI RNKNGGTTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYICTTS 120
DB 61 GKGLEWVGFI--LPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSSLRSED TAVYICARS 118
QY 121 YISHCRGVCYGGYFEFWGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDY 180
DB 119 YDF-----ANFAYWGQGTLLTVTSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDY 169
QY 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNT 240
DB 170 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNT 229
QY 241 KVDKAEKPSCKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 300
DB 230 KVDKAEKPSCKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 289
QY 301 DPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
DB 290 DPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349
QY 361 APIEKTISKAKGQPREPOVTVLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
DB 350 APIEKTISKAKGQPREPOVTVLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 409
QY 421 NYKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSPGK 478
DB 410 NYKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSPGK 467

RESULT 7
US-09-825-012-55
; Sequence 55, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMF1 heavy chain - DNase I fusion
US-09-825-012-55

Query Match      83.9%; Score 2149.5; DB 10; Length 741;
Best Local Similarity 84.9%; Pred. No. 1.7e-107;
Matches 406; Conservative 21; Mismatches 40; Indels 11; Gaps 2;

QY 1 MGWSLILFLVAVATRVQCEVOLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
DB 1 MGWSCILFLVATATGVHSQVLVQSGAEVKFGASVKVSKASGYTFSAIWIEWVRQAP 60
QY 61 GKGPEWVGFI RNKNGGTTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYICTTS 120
DB 61 GKGLEWVGFI--LPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSSLRSED TAVYICARS 118
QY 121 YISHCRGVCYGGYFEFWGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDY 180
DB 119 YDF-----ANFAYWGQGTLLTVTSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDY 169
QY 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNT 240
DB 170 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNT 229
```

Qy 241 KYDKAEKPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHE 300
Db 230 KYDKAEKPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHE 289
Qy 301 DPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
Db 290 DPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349
Qy 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
Db 350 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 409
Qy 421 NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGK 478
Db 410 NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGK 467

RESULT 8
US-09-825-012-52
; Sequence 52, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-52

Query Match 83.7%; Score 2144.5; DB 10; Length 729;
Best Local Similarity 84.9%; Pred. No. 3.1e-107;
Matches 405; Conservative 21; Mismatches 40; Indels 11; Gaps 2;

Qy 1 MGWSLILFLVAVATRVQCEVOLVSGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAP 60
Db 1 MGWSLILFLVATATGVHSQVLQSGAEVKGPGASVKVSKASGYTFSAYWIEWRQAP 60
Qy 61 GKGPFWVGFI RNKPGGTTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
Db 61 GKGLEWVGEL--LPGSNNRYNEKFKGRVTVTRDTSTNTAYMELSLRSEDATAVYYCARS 118
Qy 121 YISHCRGGVCGYCYGFYFVQGGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDY 180
Db 119 YDF-----AWFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDY 169
Qy 181 FPEPVTVSNMNGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNT 240
Db 170 FPEPVTVSNMNGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNT 229
Qy 241 KYDKAEKPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHE 300
Db 230 KYDKAEKPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHE 289
Qy 301 DPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
Db 290 DPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349
Qy 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
Db 350 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 409

Qy 421 NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 477
Db 410 NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 466

RESULT 9
US-09-825-012-61
; Sequence 61, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-61

Query Match 83.7%; Score 2144.5; DB 10; Length 739;
Best Local Similarity 84.9%; Pred. No. 3.1e-107;
Matches 405; Conservative 21; Mismatches 40; Indels 11; Gaps 2;

Qy 1 MGWSLILFLVAVATRVQCEVOLVSGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAP 60
Db 1 MGWSLILFLVATATGVHSQVLQSGAEVKGPGASVKVSKASGYTFSAYWIEWRQAP 60
Qy 61 GKGPFWVGFI RNKPGGTTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
Db 61 GKGLEWVGEL--LPGSNNRYNEKFKGRVTVTRDTSTNTAYMELSLRSEDATAVYYCARS 118
Qy 121 YISHCRGGVCGYCYGFYFVQGGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDY 180
Db 119 YDF-----AWFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDY 169
Qy 181 FPEPVTVSNMNGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNT 240
Db 170 FPEPVTVSNMNGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNT 229
Qy 241 KYDKAEKPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHE 300
Db 230 KYDKAEKPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHE 289
Qy 301 DPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
Db 290 DPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349
Qy 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
Db 350 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 409
Qy 421 NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 477
Db 410 NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 466

RESULT 10
US-09-825-012-49
; Sequence 49, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting

```

; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIORITY APPLICATION NUMBER: US 60/237,159
; PRIORITY FILING DATE: 2000-10-02
; PRIORITY APPLICATION NUMBER: GB 0008049.9
; PRIORITY FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; - OTHER INFORMATION: Humanised HMFG1 heavy
US-09-825-012-49

```

Query Match 83.5%; Score 2138.5; DB 10; Length 730;
Best Local Similarity 84.9%; Pred. No. 6.4e-107;
Matches 404; Conservative 21; Mismatches 40; Indels 11;

Qy	1	MGWSLILFLVAVATRCQCEVOLVESGGGLVQPGSGSLRUSCAVSGFTPSDHYMYWRQAP	60
Db	1	MGWSLILFLVATATGVHSGVOLVQSGAEVYKFGASVKVSKASGYTFSAYIEWRQAP	60
Qy	61	GKGPBWGVFIRKNKGTTGYAASVKDRFTISRDSKSTAYLQWSSLKIEDTAVYVCWS	120
Db	61	GKGLFWGGEI--LPGSNNSRYNEKFGRVTVTRDTSTNTAYEWSLSRSEDTAVYICARS	118
Qy	121	YISHCRGGVCYGGYFEPWGGQALVTVSSASTKGPVSFPLAPSSKTSGGTAAAGCLVKDY	180
Db	119	YDF-----ANFAYWGGQTLTVSSASTKGPVSFPLAPSSKTSGGTAAAGCLVKDY	169
Qy	181	FPEPVTVSNSGALTSQVHHPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNT	240
Db	170	FPEPVTVSNSGALTSQVHHPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNT	229
Qy	241	KVDKKAEPKSKDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE	300
Db	230	KVDKKEPKSKDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE	289
Qy	301	DPEVKFNYYDGVVEVHNAKTKPREEQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALP	360
Db	290	DPEVKFNYYDGVVEVHNAKTKPREEQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALP	349
Qy	361	APIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVWESNGOPEN	420
Db	350	APIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVWESNGOPEN	409
Qy	421	NYKTTTPVLDSDGGFFLYSKLTVDKSRWQQGNVFCSVNMEALHNHYTQKSLSLSP	476
Db	410	NYKTTTPVLDSDGGFFLYSKLTVDKSRWQQGNVFCSVNMEALHNHYTQKSLSLSP	465

```

RESULT 11
US-09-825-012-58
; SEQ ID NO 58, Application US/09825012
; Patent No. US2002012798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 740
; TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised
US-09-825-012-58

```

Query Match 83.5%; Score 2138.5; DB 10; Length 740;
Best Local Similarity 84.9%; Pred. No. 6.5e-107;
Matches 404; Conservative 21; Mismatches 40; Indels 11;

Qy	1	MGWSLILLFLVAVATRVQCEVOLVPSGGGLVQPGSLSRVSCAVSGFTHSDHYMYWFRQAP	60
Db	1	MGWSCILFLVATATGVHSQVLVQSGAEVKKPGASVVKSCAKGYTFSAYWIEWFRQAP	60
Qy	61	GKGPEWVGIRKNKPGGTTEVAASVKDRFTTISRDDSKSIAYLOMSSLKIEDTAVYYCTTS	120
Db	61	GKGLEWVGII--LPGSNNSRYNEKFGRTVTTRTSTNTATMYELSSURSEDATVYYCARS	118
Qy	121	YISHCRGVCYGGYFEFGWQAGLVTVSSASATKGPSVFPFLAPSSKSTSGGTHAALGCLVKDY	180
Db	119	YDF-----AWFAYWQGQGLTVTVSSASATKGPSVFPFLAPSSKSTSGTAAALGCLVKDY	169
Qy	181	FPEPVTVSNNSGALTSGVHPTPAVLQSSGLYSLSASVTVTPSSSLIGTQTYICNVNHNKPSNT	240
Db	170	FPEPVTVSNNSGALTSGVHPTPAVLQSSGLYSLSASVTVTPSSSLIGTQTYICNVNHNKPSNT	229
Qy	241	KVDKKAEPKSCDKTHTCCPAPPELLGGPSVFLFPFKPKOTLMISRTPEVTCVVVDVSHS	300
Db	230	KVDKKVEPKSCDKTHTCCPAPPELLGGPSVFLFPFKPKOTLMISRTPEVTCVVVDVSHS	289
Qy	301	DBEVKNWTVVDGVEVHNNAKTKPRBQYQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP	360
Db	290	DPEVKENWTVVDGVEVHNNAKTKPRBQYQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP	349
Qy	361	APTEKTIKSAKQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPEN	420
Db	350	APIEKTIKSAKQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPEN	409
Qy	421	NYKTTPPVLDSGSPFLYSKLTVDKSRVQQGNVFSCSVMHEALNNHYTQKSLSLSP	476
Db	410	NYKTTPEVLDSGSPFLYSKLTVDKSRVQQGNVFSCSVMHEALNNHYTQKSLSLSP	465

```

RESULT 12
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

```

Query Match 83.4%; Score 2135; DB 10; Length 451;
Best Local Similarity 88.5%; Pred. No. 6.3e-107;

QY 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGP EWVGFIRNKPNGGT 78


```
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASIK---YSGE 57
      |||||
Qy 79 TEYAASVKDRFTISRDDSKSIAYLQWSSLIKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
      |||||
Db 58 TKNPNSVKGRITISRDDSKNTFYLQWNSLRADTAIVYC-----ARGSHYFGHWHFAV 110
      |||||
Qy 138 WGCGALVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 197
      |||||
Db 111 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170
      |||||
Qy 198 VHTFPAVLQSSGLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTC 257
      |||||
Db 171 VHTFPAVLQSSGLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTC 230
      |||||
Qy 258 PPCPAPELLGGPSVFLFPPPKDRLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
      |||||
Db 231 PPCPAPELLGGPSVFLFPPPKDRLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
      |||||
Qy 318 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
      |||||
Db 291 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
      |||||
Qy 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 437
      |||||
Db 351 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 410
      |||||
Qy 438 YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
      |||||
Db 411 YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
```

```
RESULT 13
US-09-925-179-65
; Sequence 65, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1CIUS
; CURRENT APPLICATION NUMBER: US/09/925.179
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Tabl
US-09-925-179-65
```

```
Query Match 83.2%; Score 2132; DB 9; Length 451;
Best Local Similarity 88.5%; Pred. No. 9.2e-107;
Matches 408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

Qy 20 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASIK---YSGE 57
      |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASIK---YSGE 57
      |||||
Qy 79 TEYAASVKDRFTISRDDSKSIAYLQWSSLIKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
      |||||
```

```
Db 58 TKNPNSVKGRITISRDDSKNTFYLQWNSLRADTAIVYC-----ARGSHYFGHWHFAV 110
      |||||
Qy 138 WGCGALVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 197
      |||||
Db 111 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170
      |||||
Qy 198 VHTFPAVLQSSGLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTC 257
      |||||
Db 171 VHTFPAVLQSSGLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTC 230
      |||||
Qy 258 PPCPAPELLGGPSVFLFPPPKDRLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
      |||||
Db 231 PPCPAPELLGGPSVFLFPPPKDRLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
      |||||
Qy 318 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
      |||||
Db 291 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
      |||||
Qy 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 437
      |||||
Db 351 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 410
      |||||
Qy 438 YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
      |||||
Db 411 YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
```

```
RESULT 14
US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920.171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/987,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match 83.2%; Score 2132; DB 10; Length 451;
Best Local Similarity 88.5%; Pred. No. 9.2e-107;
Matches 408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

Qy 20 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASIK---YSGE 57
      |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASIK---YSGE 57
      |||||
Qy 79 TEYAASVKDRFTISRDDSKSIAYLQWSSLIKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
      |||||
Db 58 TKNPNSVKGRITISRDDSKNTFYLQWNSLRADTAIVYC-----ARGSHYFGHWHFAV 110
      |||||
Qy 138 WGCGALVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 197
      |||||
Db 111 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170
      |||||
Qy 198 VHTFPAVLQSSGLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTC 257
      |||||
Db 171 VHTFPAVLQSSGLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTC 230
      |||||
```

QY 258 PPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 317
D 231 PPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 290
QY 318 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 377
D 291 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 350
QY 378 QVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL 437
D 351 QVYTLPPSRDEMTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL 410
QY 438 YSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 478
D 411 YSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 451

RESULT 15
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

Query Match 83.2%; Score 2132; DB 10; Length 451;
Best Local Similarity 88.5%; Pred. No. 9.2e-107;
Matches 408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

QY 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRAQPGKGPPEWVGFIRNKPNGGT 78
D 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSYGSWMNIRQAPGKLEWVASI---TYDGS 57
QY 79 TEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYCTTSYISHCRGVCYVGYREF 137
D 58 TYNPNSVKGRITISRDDSKNTFYLQMSLRAEDTAVYIC-----ARGSHYFGHWHFAV 110
QY 138 WGQALVTVSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
D 111 WGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170
QY 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNPKYDKKAEKPKSCDKTHTC 257
D 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNPKYDKKAEKPKSCDKTHTC 230
QY 258 PPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 317
D 231 PPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 290
QY 318 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 377
D 291 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 350
QY 378 QVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL 437

Db 351 QVYTLPPSRDEMTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL 410
QY 438 YSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 478
D 411 YSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 451

Search completed: March 29, 2003, 09:38:42
Job time : 21.3244 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 49.1632 Seconds
(without alignments)
1295.559 Million cell updates/sec

Title: US-09-758-173-8

Perfect score: 2561

Sequence: 1 MGWLLILFLVAVATRVQCE.....MHEALHNHYTKSLSPGK 478

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*
1: /SID82/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID82/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID82/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID82/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID82/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID82/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID82/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID82/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID82/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID82/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID82/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID82/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID82/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID82/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID82/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID82/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID82/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID82/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID82/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID82/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2561	100.0	478	19 AAW63763	Macaca primatized
2	2561	100.0	478	23 AAU11644	Protein sequence o
3	2555	99.8	478	18 AAW01820	Primatized anti-hu
4	2197	85.8	461	14 AAR42162	Anti-HIV-1 recombi
5	2184.5	85.3	452	20 AAY29458	Recombinant immuno
6	2184.5	85.3	452	21 AAB30322	Humanised anti-IL-
7	2184.5	85.3	452	21 AAY77766	Humanised anti-IL-
8	2183	85.2	474	23 AAO14065	Heavy chain protei
9	2177.5	85.0	477	22 AAU14288	Human novel protei
10	2175.5	84.9	452	19 AAW69316	Anti-IL-8 humanise

11	2172.5	84.8	475	13 AAR20057	Heavy chain of 3D6
12	2169.5	84.7	461	22 AAU07745	Humanised monoclon
13	2162	84.4	470	13 AAR22757	Reshaped CAMPATH-1
14	2161.5	84.4	444	21 AAY32263	Humanised anti-CD2
15	2160	84.3	451	22 AAE12715	Human recombinant
16	2156.5	84.2	481	13 AAR24442	Sequence of antibo
17	2154	84.1	449	21 AAY68810	A rat heavy chain
18	2151	84.0	477	15 AAR47453	chIT84.12 H3 heavy
19	2149.5	83.9	731	22 AAM52156	Humanised HMFg-1 h
20	2149.5	83.9	741	22 AAM52159	Humanised HMFg-1 h
21	2144.5	83.7	729	22 AAM52158	Humanised HMFg-1 h
22	2144.5	83.7	739	22 AAM52161	Humanised HMFg-1 h
23	2140	83.6	582	22 AAB81987	Ganglioside GD3 ep
24	2139	83.5	470	21 AAB08026	A dimeric anti-CD2
25	2138.5	83.5	459	14 AAR42066	Human anti-HBs hea
26	2138.5	83.5	730	22 AAM52157	Humanised HMFg-1 h
27	2138.5	83.5	740	22 AAM52160	Humanised HMFg-1 h
28	2137.5	83.5	465	22 AAB72228	Humanised 323/A3 (
29	2137	83.4	466	13 AAR24812	Sequence encoded b
30	2135	83.4	451	20 AAY50031	Human E27 anti-IgE
31	2135	83.4	451	20 AAW95663	Mus musculus anti-
32	2135	83.4	451	21 AAB07473	Amino acid sequenc
33	2135	83.4	451	22 AAB74212	E27 anti-IgE antib
34	2135	83.4	451	22 AAB76952	Full length heavy
35	2135	83.4	470	21 AAW90936	Humanised HFE7A de
36	2135	83.4	470	23 ABB74945	Humanised anti-Fas
37	2132.5	83.3	464	22 AAB72232	Humanised 323/A3 (
38	2132	83.2	451	20 AAW95659	Mus musculus anti-
39	2132	83.2	451	20 AAW95661	Mus musculus anti-
40	2132	83.2	451	21 AAY82021	Light chain amino
41	2132	83.2	451	22 AAB47088	Anti-IgE antibody,
42	2132	83.2	451	22 AAB76948	Full length heavy
43	2132	83.2	451	22 AAB76950	Full length heavy
44	2132	83.2	453	14 AAR33311	Humanised Ma211 Ve
45	2132	83.2	453	21 AAY85199	Heavy chain amino

ALIGNMENTS

RESULT 1
AAW63763
ID AAW63763 standard; Protein; 478 AA.
XX AAW63763;
XX AC
XX DT 29-SEP-1998 (first entry)
XX DE Macaque primatized 786 heavy chain protein.
XX KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation.
XX OS Macaca fascicularis.
XX PN WO9819706-A1.
XX PD 14-MAY-1998.
XX PF 29-OCT-1997; 97WO-US19906.
XX PR 08-NOV-1996; 96US-0746361.
XX PA (IDEC-) IDEC PHARM CORP.
XX PI Anderson DR, Brans P, Hanna N;
XX WFI; 1998-286601/25.
XX DR N-PSDB; AAV35487.
XX

PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PT cells, e.g. graft rejection or tumours
XX
PS Example 7; Fig 4b; 87pp; English.

XX This sequence represents a primatized form of the antibody 7B6 heavy
XX chain from macaque. This sequence is used in a method which studies new
XX monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
XX B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
XX Mab's are specific immunosuppressants for treatment of diseases involving
XX T cell/B cell interactions, particularly autoimmune disease, specifically
XX idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
XX I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
XX inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
XX host diseases, B cell lymphoma, infections (including by human immune
XX deficiency virus) or inflammatory disease and tumours. Optionally the
XX Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
XX also be used as imaging agents and as vaccines or immunogens to develop
XX anti-idiotype reagents. Mab's are optionally combined with other proteins
XX or small molecule immunosuppressants. Blocking B7/CD28 interactions
XX induces long-term, antigen-specific immunosuppression, i.e. it inhibits
XX production of interleukin-2 (IL-2), T cell proliferation and
XX antigen-specific immunoglobulin G (IgG) responses.

SQ Sequence 478 AA;

Query Match 100.0%; Score 2561; DB 19; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-152;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYWYFRAQP 60
DB 1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYWYFRAQP 60
QY 61 GKGPFWGFI RNKPNKPGTTEYAAVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
DB 61 GKGPFWGFI RNKPNKPGTTEYAAVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
QY 121 YISHCRGVCYGGYFEPFWGGALVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDY 180
DB 121 YISHCRGVCYGGYFEPFWGGALVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDY 180
QY 181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
DB 181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
QY 241 KVDKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVDVSH 300
DB 241 KVDKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVDVSH 300
QY 301 DPEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
DB 301 DPEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
QY 361 APTEKTSKAGQPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
DB 361 APTEKTSKAGQPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 420
QY 421 NYKTTPTPLDSDGSFFLYSKLTVDKSRWQOGNVFCSVMHEALHNHYTQKSLSLSPGK 478
DB 421 NYKTTPTPLDSDGSFFLYSKLTVDKSRWQOGNVFCSVMHEALHNHYTQKSLSLSPGK 478

RESULT 2
ID AAU11644
XX AAU11644 standard; Protein; 478 AA.
AC AAU11644;
XX

DT 12-MAR-2002 (first entry)

XX

DE Protein sequence of primatised form of the heavy chain of 7B6 antibody.
XX Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
XX neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW graft-vs-host disease; immunosuppression; organ rejection;
KW interleukin-2; IL-2; mutant; mutein.

XX Chimeric - Homo sapiens.
OS Chimeric - Macaca sp.
OS Synthetic.
PN WO2001189567-A1.
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16364.
XX
PR 22-MAY-2000; 2000US-0576424.
XX
PA (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Brama P;
DR WPI; 2002-089895/12.
XX N-PSDB; AAS17245.
DR

XX Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT treating cancer, graft-vs-host disease and autoimmune disease such as
PT allergy -
XX

XX Example 8; Fig 4b; 89pp; English.

XX The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host disease. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present protein
CC sequence represents the heavy chain of 7B6, a primatised antibody
CC used in the invention to induce apoptosis.

SQ Sequence 478 AA;

Query Match 100.0%; Score 2561; DB 23; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-152;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYWYFRAQP 60
DB 1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYWYFRAQP 60
QY 61 GKGPFWGFI RNKPNKPGTTEYAAVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
DB 61 GKGPFWGFI RNKPNKPGTTEYAAVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
QY 121 YISHCRGVCYGGYFEPFWGGALVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDY 180
DB 121 YISHCRGVCYGGYFEPFWGGALVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDY 180
QY 181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240

```

Db 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQYICNVNHPKPSNT 240
Qy 241 KVDKKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHE 300
Db 241 KVDKKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHE 300
Qy 301 DEVEKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 360
Db 301 DEVEKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 360
Qy 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQEN 420
Db 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQEN 420
Qy 421 NYKTTTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
Db 421 NYKTTTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478

RESULT 3
AAW01820
ID AAW01820 standard; Protein; 478 AA.
XX
AC AAW01820;
XX
DT 25-MAY-1997 (first entry)
XX
DE Primatised anti-human B7.1 antigen antibody 7B6 heavy chain.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 7B6;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR WPI; 1997-108638/10.
XX
DR N-PSDB; AAT13847.
XX
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
XX
PS Claim 8; Fig 9B; 81pp; English.
XX
CC 2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy
CC variable genes (see also AAT62511 and AAT13847) are inserted into
CC an expression vector (pref. NEOSPLA) which contains human light and
CC heavy chain constant region genes to allow prodn. of the primatised
CC antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
CC antibodies have also been produced (see also AAW01817-19 and
CC AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway,
CC making them useful immunosuppressants for the treatment of
CC autoimmune disorders and graft-versus-host disease.
XX
SQ Sequence 478-AA;

```

```

Query Match 99.8%; Score 2555; DB 18; Length 478;
Best Local Similarity 99.8%; Pred. No. 1.1e-151;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGWSLILLFLVAVATRVQCEVQLVSGGGLVQPGGSLRVSCAVSGTFTSDHYMYWFRQAP 60
Db 1 MGWSLILLFLVAVATRVQCEVQLVSGGGLVQPGGSLRVSCAVSGTFTSDHYMYWFRQAP 60
Qy 61 GKPEWVGFIRNPNNGTTEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
Db 61 GKPEWVGFIRNPNNGTTEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
Qy 121 YISHCRGGVCGYGFYFWGQCALVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDY 180
Db 121 YISHCRGGVCGYGFYFWGQCALVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDY 180
Qy 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQYICNVNHPKPSNT 240
Db 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQYICNVNHPKPSNT 240
Qy 241 KVDKKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHE 300
Db 241 KVDKKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHE 300
Qy 301 DEVEKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 360
Db 301 DEVEKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 360
Qy 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQEN 420
Db 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQEN 420
Qy 421 NYKTTTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
Db 421 NYKTTTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478

RESULT 4
AAR42162
ID AAR42162 standard; Protein; 461 AA.
XX
AC AAR42162;
XX
DT 27-APR-1994 (first entry)
XX
DE Anti-HIV-1 recombinant antibody 447-52D heavy chain.
XX
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW acquired immune deficiency syndrome; chimeric antibody;
KW surface glycoprotein gp120; V3 loop.
XX
OS Homo sapiens.
XX
PN WO9319785-A.
XX
PD 14-OCT-1993.
XX
PF 23-MAR-1993; 93WO-US02629.
XX
PR 01-APR-1992; 92US-0861701.
XX
PA (MERI ) MERCK & CO INC.
PA (JOHN/) JOHNSON L S.
PA (PFAR/) PFARR D S.
XX
PI Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;
XX
DR WPI; 1993-336600/42.
XX
DR N-PSDB; AAQ49834.
XX
PT New recombinant human antibody - with HIV neutralising activity

```

PT against at least two isolates, useful for preventing or treating
PT infection in diagnosis, etc.

XX Example 9; Fig 2A; 154pp; English.

PS BBV-transformed cell lines and mouse-human heterohybridomas
CC producing human MAb specific for the gp120 V3 loop of HIV-1 MN
CC isolate were obtained. MAb 447-52D was found to recognise the
CC tetrapeptide motif GGR, i.e. the Principal Neutralising
CC Determinant common to the V3 loop of different HIV isolates.
CC A recombinant Ab was produced in which the H chain V region was
CC derived from 447-52D and to which a signal sequence and a H chain
CC intronic sequence are appended, fused to a fragment contg. a short
CC intronic segment of the human gamma 1 C region and the human gamma
CC 1 encoding domain in its genomic form.

XX Sequence 461 AA;

Query Match 85.8%; Score 2197; DB 14; Length 461;
Best Local Similarity 90.2%; Pred. No. 2.4e-129;
Matches 416; Conservative 14; Mismatches 29; Indels 2; Gaps 1;

QY 20 EVQLVESGGGLVQPGGSLRVCASVGFSTSDHYMYWFRQAPGKPEWGFIRNKNPGGTT 79

Db 1 EVQLVESGGGLVQPGGSLRLTCAVSGFTSDVWMLNWVRQAPGKGLEWGRIRKSRDGGTT 60

QY 80 EYAASVKDRFTISRDDSKSTAYLQMSLKTEDTAVYCTTSYISHCRG--GVYGGYFEF 137

Db 61 DYAAASVKGRFTISRDDSKNTLYLQMSLKTEDTAVYCTTDFGIMRGVSEDIYYIMDV 120

QY 138 WGQALVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 197

Db 121 WGKGTITVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 180

QY 198 VHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKAEPKSCDKTHTC 257

Db 181 VHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKAEPKSCDKTHTC 240

QY 258 PPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 317

Db 241 PPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 300

QY 318 AKTAPREEQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 377

Db 301 AKTAPREEQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 360

QY 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL 437

Db 361 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL 420

QY 438 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478

Db 421 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 461

RESULT 5

AAV29458

ID AAV29458 standard; Protein; 452 AA.

XX AC AAV29458;

XX DT 05-OCT-1999 (first entry)

XX DE Recombinant immunoglobulin SEQ ID NO:71.

XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
XX diagnosis; inflammatory disorder; conjugate; immunoglobulin;
KW fusion protein.

XX OS Synthetic.

XX PN W0993779-A1.

XX

PD 29-JUL-1999.

XX 19-JAN-1999; 99WO-US01081.

XX 24-JUL-1998; 98US-012513.

PR 22-JAN-1998; 98US-0012116.

PR 24-FEB-1998; 98WO-US03337.

XX 24-JUL-1998; 98US-0121952.

PA (GETH) GENENTECH INC.

XX Haei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;

PI Zapata CA;

XX WPI; 1999-469134/39.

XX New conjugates of nonproteinaceous polymers with antibody fragments,
PT used for treating inflammatory disorders

XX Disclosure; Page 354-355; 360pp; English.

XX The present invention describes a novel conjugate having one or more
CC antibody fragments covalently attached to one or more nonproteinaceous
CC polymer molecules, where the apparent size of the conjugate is at least
CC about 500 kDa. Conjugates of antibody fragments which bind the human
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC treating inflammatory disorders e.g. acute lung injury, ischaemic
CC reperfusion disorder, and autoimmune diseases. They can also be used
CC for treating e.g. inflammatory skin diseases including psoriasis and
CC atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
CC diseases. The conjugates can also be used as reagents in an animal
CC model system for in vivo study of the biological functions of the
CC antigen recognised by the conjugate. The present sequence represents
CC a recombinant immunoglobulin protein from the present invention.

XX Sequence 452 AA;

Query Match 85.3%; Score 2184.5; DB 20; Length 452;
Best Local Similarity 89.2%; Pred. No. 1.4e-128;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;

QY 20 EVQLVESGGGLVQPGGSLRVCASVGFSTSDHYMYWFRQAPGKPEWGFIRNKNPGGTT 79

Db 1 EVQLVQSGGGLVQPGGSLRLCAASGYFSFHHYMWVRQAPGKLEWGVYI--DPSNGET 58

QY 80 EYAASVKDRFTISRDDSKSTAYLQMSLKTEDTAVYCTTSYISHCRGGVYCGG--YFEF 137

Db 59 TYNQKFKGRFTLSRDNSKNTAYLQMSLRADETAVYIC-----ARGDYRYNGDWFFDV 111

QY 138 WGQALVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 197

Db 112 WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 171

QY 198 VHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKAEPKSCDKTHTC 257

Db 172 VHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKAEPKSCDKTHTC 231

QY 258 PPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 317

Db 232 PPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 291

QY 318 AKTAPREEQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 377

Db 292 AKTAPREEQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 351

QY 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL 437

Db 352 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL 411

QY 438 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478

Db 412 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 6

AAAB30322
ID AAB30322 standard; Protein; 452 AA.
XX AC AAB30322;
XX DT 12-FEB-2001 (first entry)
XX DE Humanised anti-IL-8 antibody related protein SEQ ID NO: 71.
XX KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
KW adult respiratory distress syndrome; multiple organ failure;
KW bacterial pneumonia; inflammatory bowel disease.
XX OS Unidentified.
XX PN US6133426-A.
XX PD 17-OCT-2000.
XX PF 20-FEB-1998; 98US-0026985.
XX PR 21-FEB-1997; 97US-0038664.
XX PR 22-JAN-1998; 98US-0074330.
XX PA (GETH) GENENTECH INC.
XX PI Presta LG, Leong SR, Gonzalez TN;
XX WPI; 2000-686027/67.
XX Humanized anti-interleukin 8 monoclonal antibody variant useful for
PT treating inflammatory disorders, such as adult respiratory distress
PT syndrome, hypovolemic shock and ulcerative colitis -
PS Disclosure; Column 199-202; 240pp; English.
XX The present invention provides a number of humanised monoclonal anti-IL-8
CC antibodies which can be used in the diagnosis and treatment of
CC inflammatory disorders, including adult respiratory distress syndrome,
CC septic shock, multiple organ failure, bacterial pneumonia and
CC inflammatory bowel disease. The present sequence comprises one of the
CC antibodies of the invention.
XX SQ Sequence 452 AA;
Query Match 85.3%; Score 2184.5; DB 21; Length 452;
Best Local Similarity 89.2%; Pred. No. 1.4e-128;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;
Qy 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSQHYMYWFRQAPKGPWVGFTRNKGTT 79
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMYWFRQAPKGLWVGVI--DPSNGET 58
Qy 80 EYASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
Db 59 TYNQKFGKRFITLSDNSKNTAYLQNSLRAEDTAVYYC-----ARGDYRYNGWDFDV 111
Qy 138 WQOQALVTSSASTKGPVFLPAPSSKSTSGTAALCLVKDYFPEPVTVSWNSGALTSG 197
Db 112 WQOQTLVTSSASTKGPVFLPAPSSKSTSGTAALCLVKDYFPEPVTVSWNSGALTSG 171
Qy 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKKAPKSCDKTHTC 257
Db 172 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKKAPKSCDKTHTC 231
Qy 258 PPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 317
Db 232 PPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 291
Qy 318 AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
|||||

Db 292 AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351
Qy 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 352 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411
Qy 438 YSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSISPGK 478
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 412 YSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSISPGK 452
RESULT 7
AAAY77766
ID AAY77766 standard; Protein; 452 AA.
XX AC AAY77766;
XX DT 06-JUN-2000 (first entry)
XX DE Humanised anti-IL-8 antibody related protein seq ID No:71.
XX KW Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4V11N35A;
KW inflammatory disorder; adult respiratory distress syndrome;
XX affinity purification.
XX OS Homo sapiens.
XX PN US6025158-A.
XX PD 15-FEB-2000.
XX PF 20-FEB-1998; 98US-0027449.
XX PR 21-FEB-1997; 97US-0038664.
XX PR 22-JAN-1998; 98US-0074330.
XX PA (GETH) GENENTECH INC.
XX PI Presta LG, Leong SR, Gonzalez TN;
XX WPI; 2000-181809/16.
XX New nucleic acid molecule encodes a polypeptide which is an
PT anti-interleukin-8 monoclonal antibody or antibody fragment useful for
PT the production of anti-interleukin-8 monoclonal antibodies or fragments
XX
XX Examples; Columns 199-202; 188pp; English.
The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
CC (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs
CC (complementarity determining regions) of the humanized anti-IL-8
CC 6G4.2.5V11N35A light chain; and amino acids 24-253 of the humanized
CC anti-IL-8 6G4.2.5V11N35A heavy chain. The anti-IL-8 MAb and fragments
CC can be used in diagnosis, for affinity purification of IL-8 from
CC recombinant cell culture or natural sources and for the treatment of
CC inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic
CC acids encoding the anti-IL-8 MAb can be associated in a vector with
CC another gene encoding another protein or protein fragment to produce a
CC fusion protein which can make isolation and/or purification of the
CC protein an easier process.
XX SQ Sequence 452 AA;
Query Match 85.3%; Score 2184.5; DB 21; Length 452;
Best Local Similarity 89.2%; Pred. No. 1.4e-128;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;
Qy 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSQHYMYWFRQAPKGPWVGFTRNKGTT 79
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMYWFRQAPKGLWVGVI--DPSNGET 58
Qy 80 EYASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
|||||

Db 59 TYNQKFKGRFTLSRONSXNTAYLQMNLSRAEDTAVYYC-----ARGDYRYNGDWFFDV 111
Qy 138 WGGALVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSG 197
Db 112 WGGTLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSG 171
Qy 198 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKPAEPKSCDKTHTC 257
Db 172 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKPAEPKSCDKTHTC 231
Qy 258 PPCAPELGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHN 317
Db 232 PPCAPELGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHN 291
Qy 318 AKTKPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPEKTIISKAKGPREP 377
Db 292 AKTKPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPEKTIISKAKGPREP 351
Qy 378 QVTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFL 437
Db 352 QVTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFL 411
Qy 438 YSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPGK 478
Db 412 YSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPGK 452
RESULT 8
AAO14065
ID AAO14065 standard; Protein; 474 AA.
XX AAO14065;
XX
DT 07-MAY-2002 (first entry)
DE Heavy chain protein of the monoclonal antibody from clone JA.
XX
XX HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain;
KW human monoclonal rabies virus neutralising antibody; immunoglobulin;
KW light chain; central nervous system; CNS; prophylactic therapy; clone JA.
XX
OS Homo sapiens.
XX WO200188132-A2.
XX
XX 22-NOV-2001.
XX
XX 04-MAY-2001; 2001WO-US14468.
XX
XX 16-MAY-2000; 2000US-204518P.
XX
XX (UJJE-) UNIV JEFFERSON THOMAS.
XX
XX Hooper DC, Dietzschold B;
XX WPI; 2002-062381/08.
XX N-PSDB; AAK98701.
XX
XX Novel isolated human monoclonal rabies virus neutralising antibody
PT useful for treating individual exposed to rabies virus and for
PT preventing spread of rabies virus to central nervous system -
XX
XX Claim 4; Page 23-24; 25pp; English.
XX
XX This sequence represents the heavy chain protein of the monoclonal
CC antibody from clone JA. The invention relates to an isolated human
CC monoclonal rabies virus neutralising antibody (virucide) derived from
CC cDNA clones encoding the antibody heavy and light chains expressed in
CC heterologous expression systems and purified away from deleterious
CC contaminants. The invention provides a fused gene encoding a chimeric
CC immunoglobulin light chain and a fused gene encoding a chimeric
CC immunoglobulin heavy chain. The antibody of the invention is useful for

CC treating an individual exposed to a rabies virus by administering to the
CC individual a therapeutically effective amount of the antibody, and
CC preventing a spread of the rabies virus to the central nervous system
CC (CNS). The antibody of the invention provides a safe and efficacious post
CC -exposure prophylactic therapy for individuals exposed to a rabies virus.
XX
SQ Sequence 474 AA;
Query Match 85.2%; Score 2183; DB 23; Length 474;
Best Local Similarity 86.7%; Pred. No. 1.8e-128;
Matches 418; Conservative 18; Mismatches 34; Indels 12; Gaps 3;
Qy 1 MGSLILLLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSVCASGTFSDHYMYWEROAP 60
Db 1 MEFGSLWLFVAILKGVQCEVQLVESGGGLVQPGGSLRVSVCASGTFSDHYMYWEROAP 60
Qy 61 GKGPWVGFRNKPNGGTTTEYAAASVKDRFTISRDDSKSIAYLQMSLSKIEDTAVYYCT-- 118
Db 61 GKGLWWSAI--SASGHSTYLAADVSKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKD 118
Qy 119 --TSYISHCRGGCYGCGYFQGGALVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCL 176
Db 119 REVMTIVVLNGG-----FDYWGQGRVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCL 172
Qy 177 VKDYFPEPTVSNVNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNK 236
Db 173 VKDYFPEPTVSNVNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNK 232
Qy 237 PSNTKVDKKAEPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVD 296
Db 233 PSNTKVDKRVKPEKSCDKTHTCPPCAPPELLGGPSVFLFPPPKDITLMISRTPEVTCVVD 292
Qy 297 VSHEDPEVKFNWYDGVVHNNAKTKPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSN 356
Db 293 VSHEDPEVKFNWYDGVVHNNAKTKPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSN 352
Qy 357 KALPAPEKTIISKAKGPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG 416
Db 353 KALPAPEKTIISKAKGPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG 412
Qy 417 QPENNYKTTTPVLDSGSPFLYSLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSP 476
Db 413 QPENNYKTTTPVLDSGSPFLYSLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSP 472
Qy 477 GK 478
Db 473 GK 474
RESULT 9
AAU14288
ID AAU14288 standard; Protein; 477 AA.
XX AAU14288;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human novel protein #159.
XX
XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
XX Homo sapiens.
XX WO200155437-A2.
XX
XX 02-AUG-2001.
XX

PF 25-JAN-2001; 2001WO-US02623.
 PR 25-JAN-2000; 2000US-0491404.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-451939/48.
 DR N-PSDB; AAS22593.
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage -
 PS Example 4; Page 611-612; 894pp; English.
 XX The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicit an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.
 XX Sequence 477 AA;
 SQ
 Query Match 85.0%; Score 2177.5; DB 22; Length 477;
 Best Local Similarity 85.6%; Pred. No. 4e-128;
 Matches 416; Conservative 20; Mismatches 33; Indels 17; Gaps 3;
 QY 1 MCWSLILLFLVAVATRVQCEVLVESGGLVQPGSLRVSCAVSGFTFSDHYWYFRQAP 60
 Db 1 MEFGLSWFLVALLRGVQCQVLVESGGVVPGRSLRLSCAASGFTFSNYGMHWVRQAP 60
 QY 61 KGKPEWVGFIKPNKGGTTEAASVKDRFTLSRDDSKSIAYLQMSLKIETAVYCYTTS 120
 Db 61 KGKLEWVAALWY--DGSNKYVADSVKGRFTLSRDNKNTLQMNLSRAEDTAVYIC--- 115
 QY 121 YISHCRGG-----VCYGGYFFFWGQALVTVSSASTKGPSVFPLAPSSKTSGGTAA 172
 Db 116 ---AREGRWRYRTVTTRTIGYVFDWGQGLVTVSSASTKGPSVFPLAPSSKTSGGTAA 171
 QY 173 LGCLVKDYFPERVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQVINC 232
 Db 172 LGCLVKDYFPERVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQVINC 231
 QY 233 VNHKPSNTKVDKAEKPSCKDTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTC 292
 Db 232 VNHKPSNTKVDKRVPEKSCDTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVC 291
 QY 293 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNTSYRVSVLTVLHODWLNKGEYKC 352
 Db 292 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNTSYRVSVLTVLHODWLNKGEYKC 351
 QY 353 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 412

Db 352 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 411
 QY 413 ESGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNYTKSL 472
 Db 412 ESGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNYTKSL 471
 QY 473 SLSPGK 478
 Db 472 SLSPGK 477
 RESULT 10
 AAW69316
 ID AAW69316 standard; Protein; 452 AA.
 XX AAW69316;
 AC XX
 DT 15-FEB-1999 (first entry)
 XX XX
 DE Anti-IL-8 humanised antibody 6G4V11N35A.choSD.9.
 XX Humanised antibody; chimeric antibody; monoclonal antibody; mouse;
 KW human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW ischaemic reperfusion; adult respiratory distress syndrome;
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
 KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
 KW therapy; 6G4V11N35A.choSD.9.
 XX Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX WO9837200-A2.
 XX 27-AUG-1998.
 PD 20-FEB-1998; 98WO-US03337.
 XX 22-JAN-1998; 98US-0012116.
 PR 21-FEB-1997; 97US-080444.
 XX (GETH) GENENTECH INC.
 PA Hsei V, Koumenis I, Leong SR, Presta LR, Shahrokhi Z;
 PI Zapata GA;
 XX WPI; 1998-467563/40.
 DR N-PSDB; AAV44956.
 XX New conjugates of antibody fragments - having covalently attached
 PT non-proteinaceous polymer molecules, particularly polyethylene
 PT glycol, for improving the residence time in the circulation.
 XX Example P; Fig 48A-Z; 328pp; English.
 XX This polypeptide is encoded by vector plasmid p6G4V11N35A.choSD.9
 CC (see AAV44956). It comprises a humanised 6G4V11N35A IGG containing
 CC complementarity determining regions of murine anti-interleukin-8
 CC (IL-8) monoclonal antibody (Mab) 6G5.2.5 (see AAW69309-10) in a human
 CC template. Humanised anti-IL-8 Mabs (see AAW69301-04) are described
 CC for use in diagnostic applications and in the treatment of
 CC inflammatory disorders. The invention provides conjugates of an
 CC antibody fragment and a polymer, such as PEG, that have improved
 CC half-life, mean residence time, and/or clearance rate. The
 CC conjugates can be used for immune therapy of e.g. psoriasis,
 CC responses associated with inflammatory bowel disease (such as
 CC Crohn's disease and ulcerative colitis), ischemic reperfusion,
 CC adult respiratory distress syndrome, dermatitis, meningitis,
 CC encephalitis, uveitis, autoimmune diseases such as rheumatoid

```
CC arthritis, Sjorgen's syndrome, vasculitis, diseases involving
CC leukocyte diapedesis, central nervous system inflammatory disorder,
CC multiple organ injury, syndrome secondary to septicemia or trauma,
CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
CC mediated diseases, inflammations of the lung, including pleurisy,
CC alveolitis, vasculitis, pneumonia, chronic bronchitis,
CC bronchiectasis, and cystic fibrosis.
XX
SQ Sequence 452 AA;

Query Match 84.9%; Score 2175.5; DB 19; Length 452;
Best Local Similarity 88.7%; Pred. No. 5.1e-128;
Matches 409; Conservative 17; Mismatches 24; Indels 11; Gaps 3;

QY 20 EVQLVDSGGGLVPGGSLRVSICAVSGFTSDHYMYWFRQAPGKPEWVGFIENKNGGTT 79
DB 1 EVQLVDSGGGLVPGGSLRVSICAVSGFTSDHYMYWFRQAPGKPEWVGFIENKNGGTT 58
QY 80 EYAAVKDRFTISRDTSKSTAYLQMSLSLKIEDTAVYYCTTSYISHCRGVCYGG--YFEF 137
DB 59 TYNQKFGKFTLSRDNSKNTAYLQMSLSRAEDTAVYYC-----ARGDYRYNGWFFDV 111
QY 138 WQGGALVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALTSG 197
DB 112 WQGGTLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALTSA 171
QY 198 VHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKAEPKSCDKTHTC 257
DB 172 LHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTC 231
QY 258 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEHN 317
DB 232 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEHN 291
QY 318 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 377
DB 292 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 351
QY 378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL 437
DB 352 QVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPL 411
QY 438 YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
DB 412 YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 11
AAR20057
ID AAR20057 standard; Protein; 475 AA.
XX
AC AAR20057;
XX
DT 25-MAR-1992 (first entry)
XX
DE Heavy chain of 3D6 anti-HIV antibody.
XX
KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;
XX complementarity determining region.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal
FT Region 20..49
FT /label= Framework_1
FT Region 50..54
FT /label= CDR-1
FT Region 55..68
FT /label= Framework_2
FT Region 69..85
FT /label= CDR_2
```

```
FT Region 86..117
FT /label= Framework_3
FT Region 118..134
FT /label= CDR_3
FT Region 135..145
FT /label= Framework_4
FT Region 146..475
FT /label= Constant_region
XX
PN WO9118983-A.
XX
XX 12-DEC-1991.
XX
XX 28-MAY-1991; 91WO-1000067.
XX
XX 29-MAY-1990; 90AT-0001178.
XX (JUNG/) JUNGBAUER A.
XX
XX Felgenhauer M, Himmler G, Kohl J, Steindl F;
XX
XX WPI; 1992-007468/01.
XX N-PSDB; AAQ20066.
DR
XX Recombinant protein which binds to complex viral antigen and
FT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
XX
XX Claim 2; Page 24; 52pp; German.
XX
XX The variable region of the heavy chain is used in a recombinant
CC protein with the variable region from the kappa light chain of 306,
CC the two V regions being joined by a linker. The recombinant protein
CC binds to HIV gp160.
CC See also AAQ20067 and AAQ20068.
XX
SQ Sequence 475 AA;

Query Match 84.8%; Score 2172.5; DB 13; Length 475;
Best Local Similarity 86.2%; Pred. No. 8.3e-128;
Matches 417; Conservative 18; Mismatches 34; Indels 15; Gaps 4;

QY 1 MGWSLIILFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSICAVSGFTSDHYMYWFRQAP 60
DB 1 MELGLSWIFLLAILKGVQCEVQLVESGGGLVQPGGSLRVSICAVSGFTSDHYMYWFRQAP 60
QY 61 GKPEWVGFIENKNGGTTTAYAAVKDRFTISRDTSKSTAYLQMSLSLKIEDTAVYYCTTS 120
DB 61 GKLEWVSGI--SWDSSSIGYADSVKGRFTISRDNAKNSLYLQMSLSRAEDMALYYCV-- 116
QY 121 YISHCRGVCY--GGY----PEFWGQALVTSSASTKGPSVFPPLAPSSKSTSGGTAALG 174
DB 117 -----KGRDYYDSGGYFTVAFDIWGQGTMTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALG 171
QY 175 CLVKDYFPEPPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVN 234
DB 172 CLVKDYFPEPPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVN 231
QY 235 HKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 294
DB 232 HKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 291
QY 295 VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 354
DB 292 VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 351
QY 355 SNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 414
DB 352 SNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 411
QY 415 NGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSL 474
DB 412 NGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSL 471
```

QY 475 SPKG 478
|||||
Db 472 SPKG 475

RESULT 12
AAU07745
ID AAU07745 standard; Protein; 461 AA.
XX
AC AAU07745;
XX
DT 04-DEC-2001 (first entry)
XX
DE Humanised monoclonal antibody Hu266, heavy chain.
XX
KW Monoclonal antibody; Hu266; nontropic; neuroprotective; Abeta peptide;
KW Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
KW gene therapy.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= Signal_peptide
FT Protein 20..461 /label= Mature_Hu266_heavy_chain
FT /note= "This sequence is specifically claimed in claim 17"
XX
PN WO200162801-A2.
XX
PD 30-AUG-2001.
XX
PF 26-FEB-2001; 2001WO-US06191.
XX
PR 24-FEB-2000; 2000US-0184601.
PR 08-DEC-2000; 2000US-0254465.
PR 08-DEC-2000; 2000US-0254498.
XX
XX (UNIW) UNIV WASHINGTON.
PA (ELIL) LILLY & CO ELI.
XX
PI Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
PI Vasquez M;
XX
DR WPI; 2001-550087/61.
XX
XX New humanised antibody for the treatment of Alzheimer's comprises the
PT inhibition and reduction of the formation of amyloid plaques -
XX
PS Example 13; Fig 5; 63pp; English.
XX
CC The invention relates a humanised antibody that specifically binds
CC an epitope contained within positions 13-28 of amyloid beta peptide,
CC Abeta. The antibody is useful to inhibit and reduce the formation of
CC amyloid plaques or the effects of toxic soluble Abeta species in humans
CC their fragments are used for the manufacture of a medicament. This includes
CC the prolonged expression of recombinant sequences of them in human
CC tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
CC Down's syndrome or pre clinical cerebral amyloid angiopathy.
CC Specifically, the antibody is used to sequester Abeta into plasma, brain
CC or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
CC peptide within the brain thereby improving cognition. The present
CC sequence is the heavy chain of a humanised monoclonal antibody, Hu266,
CC based on the mouse antibody 266.
XX
SQ Sequence 461 AA;

Query Match 84.7%; Score 2169.5; DB 22; Length 461;
Best Local Similarity 86.8%; Pred. No. 1.2e-127;

Matches 415; Conservative 15; Mismatches 31; Indels 17; Gaps 2;

QY 1 MGWSLILLFLVAVATRVQCEVOLVESGGGLVQPGGSLRVSCAVSGFTTFDHYVWFRQAP 60
Db 1 MNFGLSLIIFLVVLKGVLCVQLVESGGGLVQPGGSLRLSCAASGFTFRYSNSWVRQAP 60
QY 61 KGKPEWVGFIIRKPNKGGTTEYAAASVKDRFTIISRDSSKSIAYLQMSSLKIEDTAVVYCTTS 120
Db 61 KGKLELVAQINSV--GNSTVYPDTVKGRFTISRDNKNTLYLQMNSLRAEDTAVVYCAG 118
QY 121 YISHCRGGVCYGGYFEFWGCGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
Db 119 -----DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 163
QY 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPSNT 240
Db 164 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPSNT 223
QY 241 KVDKKAAPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHE 300
Db 224 KVDKKEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHE 283
QY 301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
Db 284 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 343
QY 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOPEN 420
Db 344 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOPEN 403
QY 421 NYKTTTPVLDSGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPK 478
Db 404 NYKTTTPVLDSGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPK 461

RESULT 13
AAR22757
ID AAR22757 standard; Protein; 470 AA.
XX
AC AAR22757;
XX
DT 20-OCT-1992 (first entry)
XX
DE Reshaped CAMPATH-1 antibody heavy chain.
XX
KW Antigen; CDR; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT Region 50..54 "Complementarity determining region 1"
FT Region 69..87 "Complementarity determining region 2"
FT Region 101..110 "Complementarity determining region 3"
FT Peptide 1..19 "signal peptide"
FT Peptide 20..470 "mature peptide"
XX
PN WO9205274-A.
XX
PD 02-APR-1992.
XX
PF 16-SEP-1991; 91WO-GB01578.
XX
PR 17-SEP-1990; 90GB-0020282.
XX
XX (GORM/) GORMAN S D.
XX
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H;

```
XX WPI; 1992-132139/16.
DR N-PSDB; AAQ23570.
XX Humanisation of antibodies binding to human CD4 antigen - by
PT mutation of framework-encoding regions of DNA encoding variable
PT domain of rat or mouse antibody chain
XX
XX Disclosure; Fig 5; 74pp; English.
XX
CC The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.
CC Reshaped CD4 antibody can be used to induce tolerance against an
CC antigen. It can also be used to alleviate autoimmune diseases such
CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also AAR22754-R22763.
XX
SQ Sequence 470 AA;
Query Match 84.4%; Score 2162; DB 13; Length 470;
Best Local Similarity 86.0%; Pred. No. 3.7e-127;
Matches 411; Conservative 18; Mismatches 41; Indels 8; Gaps 2;
QY 1 MGWSLILFLVAVATRVQCEVLVESGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
DB 1 MGWSCILFLVATATCVHSQVQLVESGGLVLRPSQTLSTCTVSGFTTDFYMNVRQPP 60
QY 61 GKGPVWVGIRKPNKGTTEYAAVKDRFTISRDSKSIAYLQMSLKIEDTAVYYCTTS 120
DB 61 GRGLEWIGFIRDKAGYTTTEYNPSVKGRVTMLVDTSKQFSLRLSSVTAADTAVYYCARE 120
QY 121 YISHCGGVCYGGYRFFWGGALVTSSASTKGPSVFPLAPSSKTSVGTALGLCLVKDY 180
DB 121 --GHT-----AAPFDYWGQGLVTVSSASTKGPSVFPLAPSSKTSVGTALGLCLVKDY 172
QY 181 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTQYICNVNHPKSPNT 240
DB 173 FPEPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTQYICNVNHPKSPNT 232
QY 241 KVDKKAEPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTHMISRTPEVTCVVVDVSHSE 300
DB 233 KVDKKEPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTHMISRTPEVTCVVVDVSHSE 292
QY 301 DPEVKFNWYVDGVEHNATKPREQYNTYRVSVLTVLHODWLNKGEYKCKVSNKALP 360
DB 293 DPEVKFNWYVDGVEHNATKPREQYNTYRVSVLTVLHODWLNKGEYKCKVSNKALP 352
QY 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
DB 353 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 412
QY 421 NYKTTTPVLDSDGSFPLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478
DB 413 NYKTTTPVLDSDGSFPLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
RESULT 14
AAV32263
ID AAY32263 standard; Protein; 444 AA.
XX
AC AAY32263;
XX
DT 15-FEB-2000 (first entry)
XX
DE Humanised anti-CD23 Mab C11 heavy chain.
XX
KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
```

```
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PH Key
FT Region 1..30 Location/Qualifiers
FT /note= "framework region 1"
FT Region 31..35 /note= "CDR 1"
FT Region 36..49 /note= "framework region 2"
FT Region 50..68 /note= "CDR 2"
FT Region 69..100 /note= "framework region 3"
FT Region 101..103 /note= "CDR 3"
FT Region 104..111 /note= "framework region 4"
FT Region 112..444 /note= "constant region"
XX
PN WO9558679-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-GB01434.
XX
PR 09-MAY-1998; 98GB-0009839.
XX
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearlin J;
XX
WPI; 2000-053101/04.
XX N-PSDB; AA234748.
XX
CC Cell receptor specific antibodies useful for treating e.g. arthritis,
CC diabetes, multiple sclerosis and psoriasis -
CC Claim 9; Fig 4; 81pp; English.
CC
CC This amino acid sequence represents the heavy chain of humanised
CC anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
CC framework (HSIGKVII) and the heavy chain complementarity
CC determining regions (see AAY32257-59) of murine antibody C11. The
CC DNA was constructed by splice overlap PCR. The invention provides
CC altered antibodies, such as chimeric or humanised antibodies, which
CC comprise sufficient of the amino acid sequences of the C11 light
CC and heavy chain complementarity determining regions to render them
CC capable of binding to the CD23 type II molecule expressed on
CC haematopoietic cells. The antibodies are used to block soluble
CC CD23 formation in human therapy, for the treatment of arthritis,
CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
CC (particularly chronic bronchitis) or diabetes (particularly type 1
CC diabetes), and B-cell malignancies (clonated). They are also useful
CC for studying interactions between CD23 and various ligands and
CC determining the binding agents.
XX
SQ Sequence 444 AA;
```

```
Query Match 84.4%; Score 2161.5; DB 21; Length 444;
Best Local Similarity 89.8%; Pred. No. 3.7e-127;
Matches 412; Conservative 7; Mismatches 25; Indels 15; Gaps 1;
```

QY 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPWVGFIRNKPNGGTT 79
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFGVWMSWFRQAPGKGLEWAEIRLKSDNYAT 60
QY 80 EYAASVKDRFTISRDDSKSIAYLQWSSLIKIEDTAVYYCTTYSIHCRCGVCGYGFPEWG 139
Db 61 HYAESVKGKFTISRDDSKSRLLYQWNSLKTEDTAVYYCTD-----FIDWG 105
QY 140 QGALVTVSSASTKGPSVFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 199
Db 106 QGTLVTVSSASTKGPSVFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 165
QY 200 TFPAYVQSGLYSLSSVTVPSSTLGTQTYICNVNHPKSNKTKVDPKAPPKSCDKTHTCPP 259
Db 166 TFPAYVQSGLYSLSSVTVPSSTLGTQTYICNVNHPKSNKTKVDPKAPPKSCDKTHTCPP 225
QY 260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 319
Db 226 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 285
QY 320 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379
Db 286 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 345
QY 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS 439
Db 346 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS 405
QY 440 KLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 478
Db 406 KLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 444
RESULT 15
AAE12715
ID AAE12715 standard; Protein; 451 AA.
XX AC AAE12715;
XX DT 04-JAN-2002 (first entry)
XX DE Human recombinant immunoglobulin (Ig) heavy chain region.
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX KW heavy chain region; cancer; breast; ovary; lung; bladder;
XX KW cytostatic; therapy; immunoglobulin; Ig.
XX OS Homo sapiens.
XX PN WO200175110-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10589.
XX PR 30-MAR-2000; 2000US-0538913.
XX PA (DYAX-) DYAX CORP.
XX PI Hoogenboom HRJM, Henderikx MFG;
XX DR WPI; 2001-626437/72.
XX DR N-PSDB; AAD20745.
XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX PT its portion for binding to an epitope of the protein core of mucin-1 -
PS Claim 12; Page 106-108; 126pp; English.
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human recombinant immunoglobulin
CC (Ig) heavy chain region (variable VH and CH constant heavy chain).
XX SQ Sequence 451 AA;
Query Match 84.3%; Score 2160; DB 22; Length 451;
Best Local Similarity 89.8%; Pred. No. 4.7e-127;
Matches 412; Conservative 12; Mismatches 27; Indels 8; Gaps 3;
QY 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPWVGFIRNKPNGGTT 79
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVGISG--SGGST 58
QY 80 EYAASVKDRFTISRDDSKSIAYLQWSSLIKIEDTAVYYCTTYSIHCRCGVCGYGFPEWG 139
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCA----KHTGGGV--WDPIDYWG 112
QY 140 QGALVTVSSASTKGPSVFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 199
Db 113 QGTLVTVSSASTKGPSVFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 172
QY 200 TFPAYVQSGLYSLSSVTVPSSTLGTQTYICNVNHPKSNKTKVDPKAPPKSCDKTHTCPP 259
Db 173 TFPAYVQSGLYSLSSVTVPSSTLGTQTYICNVNHPKSNKTKVDPKAPPKSCDKTHTCPP 232
QY 260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 319
Db 233 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 292
QY 320 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379
Db 293 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 352
QY 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS 439
Db 353 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS 412
QY 440 KLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 478
Db 413 KLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

Search completed: March 29, 2003, 09:10:20
Job time : 51.1632 secs


```
Db 175 PEVTVSWNSGALTSVGHFFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNK 234
Qy 242 VDKKAEKPKCDKTHTCPPCPAPELLGGSPVFLFPKPKDMLISRTPEVTCVVVDVSHED 301
Db 235 VDKKAEKPKCDKTHTCPPCPAPELLGGSPVFLFPKPKDMLISRTPEVTCVVVDVSHED 294
Qy 302 PEVKFNWYVDGVEVHNNAKTPREEQYNSTRYVSVLTVLHODWLNKKEYCKKCVSNKALPA 361
Db 295 PEVKFNWYVDGVEVHNNAKTPREEQYNSTRYVSVLTVLHODWLNKKEYCKKCVSNKALPA 354
Qy 362 PIEKTIKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENN 421
Db 355 PIEKTIKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENN 414
Qy 422 YKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFPSCVMHEALHNNHYTKQSLSPGK 478
Db 415 YKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFPSCVMHEALHNNHYTKQSLSPGK 471

RESULT 2
Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
```

```
Query Match 71.8%; Score 1838; DB 4; Length 473;
Best Local Similarity 75.5%; Pred. No. 2.9e-151;
Matches 357; Conservative 33; Mismatches 67; Indels 16; Gaps 4;

Qy 8 LFLVAVATVQCEVQVGVESGGVLPQGGSLRVSCAVSG--FTFSDHYMYWPRQAPKGPKE 65
Db 15 LLLVAAPRWLRLQESGPGLLKPSVTLSTCTVSGDSVASSYWGWRQPPKRGLE 74

Qy 66 WVGFIKPNKGGTTEYAASVKDRFTISRDDSKSIAYLQMSLKIETDAVYYCTTSYISHC 125
Db 75 WIGTIN---FSGNMYYSPSLRSRVMTSADMSENSEFYLKLDSTVAADTAVYYCAAGHL--- 128

Qy 126 RGVCVCGYFEEFWGQALVTVSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPPPV 185
Db 129 -----VMGFGAHWGQGLKVSVPASTKGPSVFLPAPCSRSTSESTAAALGCLVKDYFPPV 183

Qy 186 TVSWNSGALTSVGHFFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTVKDK 245
Db 184 TVSWNSGALTSVGHFFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTVKDKR 243

Qy 246 AEPKSCDKTHTCPPCPAPELLGGSPVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVK 305
Db 244 VESK---YGPCCPCPAPEFLGGSPVFLFPKPKDMLISRTPEVTCVVVDVSDPEVQ 300

Qy 306 FNNYVDGVEVHNNAKTPREEQYNSTRYVSVLTVLHODWLNKKEYCKKCVSNKALPAPEK 365
Db 301 FNNYVDGVEVHNNAKTPREEQYNSTRYVSVLTVLHODWLNKKEYCKKCVSNKALPSSIEK 360

Qy 366 TISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTT 425
Db 361 TISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTT 420

Qy 426 PPVLDSDGSFFLYSKLTVDKSRWQGNVFPSCVMHEALHNNHYTKQSLSPGK 478
```

```
Db 421 PPVLDSDGSFFLYSKLTVDKSRWQGNVFPSCVMHEALHNNHYTKQSLSPGK 473

RESULT 3
Q8R3V9
ID Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024405; AAH24405.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 63.7%; Score 1632.5; DB 11; Length 469;
Best Local Similarity 63.0%; Pred. No. 2.1e-133;
Matches 303; Conservative 69; Mismatches 90; Indels 19; Gaps 7;

Qy 1 MWSLLILLFLVAVATRVQCEVQVGVESGGVLPQGGSLRVSCAVSGFTFSDHYMYWPRQAP 60
Db 5 LNW-----IFLVTLINGIQCEVNLVESGGVLPQGGSLRLSCAASGFTFTDYMYMSVWRQPP 60

Qy 61 GKGPBMWGFIRNKNPGTTEYAASVKDRFTISRDDSKSIAYLQMSLKIETDAVYYCTTS 120
Db 61 GKALEMLGFIKRNKANGYTTETYSASVKGRTTISRDNQSILYLQMNALRAEDSATYYCARD 120

Qy 121 YISHCRGGVCYGG-YFEFWGQALVTVSASTKGPSVFLPAPSSKSTSGGTAALGCLVKD 179
Db 121 R---RSSYYSGTSFAYWGQGLTVTVSAAKTTPPSVYPLAPGSAQAQNTSMVTLGCLVK 176

Qy 180 YFPEPVTVSWNSGALTSVGHFFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSN 239
Db 177 YFPEPVTVWNSGSLSGVHTFPVAVLQSD-LYTLSSSVTVPSSTWPSQVTCNVAPASS 235

Qy 240 TKVDKAEKPKCDKTHTCPP--CPAPELLGGSPVFLFPKPKDMLISRTPEVTCVVVDV 297
Db 236 TKVDKELVPRDCG----CRPCICTVPEV---SSVFIFFPKPKDVLITITLTPKVTCTVVVDI 288

Qy 298 SHEDPEVKFNWYVDGVEVHNNAKTPREEQYNSTRYVSVLTVLHODWLNKKEYCKKCVSNK 357
Db 289 SKDDPEVQFSMFVDDVEVHTAQTKPREEQFNSTFRSVSELPIMHQDNLNGKEFKCRVNSA 348

Qy 358 ALPAPIEKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQ 417
Db 349 AFPAPIEKTISKTKGRPKAPQVYTIPEPKQAKDKVSLTCTMTDFFPEDITVWQWNGQ 408

Qy 418 PENNYKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFPSCVMHEALHNNHYTKQSLSPG 477
Db 409 PAENYKNTQPMIDTDGSIYFVSKLVNQKNWEAGNTFTCSVLHGLHNNHTEKSLSHSPG 468

Qy 478 K 478
Db 469 K 469

RESULT 4
Q9D8L4
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1810060009Rik protein.
```


GN IGH-1 OR 1810060009RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehli Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK007918; BAB25349.1; -.
 DR HSP; P01842; 7FAB.
 DR MGB; MGI:96443; Igh-1.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig c1.
 DR InterPro; IPR003600; Ig like.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IgC1; 3.
 DR SMART; SM00406; IgV; 1.
 DR SMART; SM00410; Ig like; 1.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
 SQ SEQUENCE 473 AA; 51699 MW; 90ED57AS14475FBB CRC64;

Query Match 58.4%; Score 1495.5; DB 11; Length 473;
 Best Local Similarity 57.4%; Pred. No. 1.7e-121;
 Matches 278; Conservative 79; Mismatches 110; Indels 17; Gaps 5;

Qy 1 MWSLILFLVAVATRVQCEVQVLESGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAP 60
 Db 1 MEWSVFLFLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASYGTFDYINWVRP 60

Qy 61 GKGPEWVGFIKRNKPGGTTTEVAASVKDRFTISRDDSKSIAYLQMSLLKIEDTAVYCTTS 120
 Db 61 CQGLEWIKI--GPGSGTYNEKFGKATUTADKSSATYMLQSLTSDSAVYFC--- 115

Qy 121 YISHCRGVCGYGFPEFGQCALVTVSSASTKGPSVFLPAPSSKTSGGTAALGLVKDY 180
 Db 116 ----ARSGYDY-DWFAYWGQGTFLTVSAAKTAPSVVPLAPVCGGTGSSVTLGLVKGY 170

Qy 181 FPEVTVSWNSGALTSVGHVTPPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSN 240
 Db 171 FPEPVTLLTWNSSGSLSSVGHVTPPALQ--SGLYTLSSSVTVTNTWPSQITICNVAHPAS 229

Qy 241 KVDKAEPEK-----CDKTHTCPAPPELLGGPSVFLRPPKPKDTLMISRTPEVTCVV 294
 Db 230 KVDKIERVPIQTQPCPLKECPAPADLLGGPSVFIIPPKIKDVLMLSLSPWVTCVV 289

Qy 295 VDSHEDPEVKFNWYDGVVHNKTKPREEQYNSTRVVSVLTVLHQDLWNGKEYCKVK 354
 Db 290 VDSVEDDDVQISFWNNVEVHTAQTHREDYNSTRVVSALPIQHDWMSGKEFKCKV 349

Qy 355 SNKALPAPIEKTISKAKGQPRQPVVTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWES 414
 Db 350 NNRLSPSPIEKTIISKRGVPVRAQVYVLPAPAEEMTKKESFLTCMTGFLPAEIVDWT 409

Qy 415 NGOPENNYKTPPPVLSDSGSFFLYSKLTVDKSRWQOQGNVFCSSVMHEALHNHYTQKSLS 474
 Db 410 NGRTEQNYKNTATVLSDSGSYFMYSLRVQKSTWERSGLFACSVWHEGLHNLTKTISR 469

Qy 475 SPGK 478
 Db 470 SLGR 473

RESULT 5
 Q91205 PRELIMINARY; PRT; 473 AA.
 ID Q91205; Q91205; Q91205;
 AC 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-JUN-2002 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 51.9 kDa protein.
 GN AU044919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC010327; AAH10327.1; -.
 DR MGD; MGI:2144967; AU044919.
 DR InterPro; IPR000345; CytC heme_bind.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
 DR Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 57.8%; Score 1480.5; DB 11; Length 473;
 Best Local Similarity 59.2%; Pred. No. 3.5e-120;
 Matches 286; Conservative 69; Mismatches 105; Indels 23; Gaps 6;

Qy 5 LILFLVAVATRVQCEVQVLESGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAPGKGP 64
 Db 5 LNLVFLVLILKGVQCEVQVLESGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAPGKGL 64

Qy 65 EWGVFIRNKPNGGTTT--YAASVKDRFTISRDDSKSIAYLQMSLLKIEDTAVYCTTSYI 122
 Db 65 EWVAYI---NSGSTTYVADTVKGRFTISRDNKNTLFLQMTLSRSEDATMYCARE-- 118

Qy 123 SHCRGVCGYGFPEFGQCALVTVSSASTKGPSVFLPAPSSKTSGGTAALGLVKDYPP 182
 Db 119 -----LWLRLIDYWGQGTITTVSSAKTTPPSVYPLAPFCGDDTTGSSVTLGLVKGYFP 171

Qy 183 EPTVTVSWNSGALTSVGHVTPPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSN 242
 Db 172 ESVTVTVSWNSGSLSSVGHVTPPALQ--SGLYTVSSSVTVPSSTWPSQTVTCVAHPASSTTV 230

Qy 243 DKAEPKSCDKT-HTCPTP-----CPAPELLGGPSVFLRPPKPKDTLMISRTPEVTCVV 295
 Db 231 DKKLEPSGPISTINPCPCCKECHKCAPNLGGPSVFIIPPNIKDVLMLSLTPKVTCTVV 290

Qy 296 VDSHEDPEVKFNWYDGVVHNKTKPREEQYNSTRVVSVLTVLHQDLWNGKEYCKVK 355
 Db 291 VDSVEDDDVQISFWNNVEVHTAQTHREDYNSTRVVSALPIQHDWMSGKEFKCKVN 350

Qy 356 NKALPAPIEKTISKAKGQPRQPVVTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWES 415
 Db 351 NKDLSPSPERTISKIKGLVRAPQVILPAPAEQLSRKQVSLTCLVGFNPGDISEVWTSN 410

Qy 416 GOPENNYKTPPPVLSDSGSFFLYSKLTVDKSRWQOQGNVFCSSVMHEALHNHYTQKSLS 475


```

RESULT 10
Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL: BC025447; AAH25447.1; -.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 55.3%; Score 1415; DB 11; Length 474;
Best Local Similarity 55.9%; Pred. No. 1.7e-114;
Matches 271; Conservative 73; Mismatches 123; Indels 18; Gaps 5;

QY 1 MCHSLILLFVAVATVQCEVGVVQGGGLVQGGSLVSCAVSQTFSHDHMYWFRQAP 60
DB 1 MEWPCILFLLSVTEGSHVQVQLQSGPELVKPGASVKISCRASGYAFSKSMNWKRRP 60
QY 61 GKPEWVGFIKPNKPGGTTTEYAASVKDRPTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
DB 61 GKLEWIG--RIFPGDGDTHYSGKFGKAKLTADKSSVTAFILQTLSTSDSAVYFCARD 118
QY 121 YISHCGGVYCYGYFFWGGGALVTVSSASTKGPSVFFPLARSSKTSCTGAALGLVKDY 180
DB 119 -----SDYGDYFDWQGGATVTVSSAKTTPPSVYPLAFCGDTTSSVTGLCLVKGY 170
QY 181 FPEFVTVWNSGALTSVHTFPAVLQSSGLSVSVTVVPSSSLGTOFYICNVNHPKPSNT 240
DB 171 FPEFVTVWNSGSLSSVHTFPALQL-SGLYTMSSSVTVVPSSTPQSVTVCSVAHPASST 229
QY 241 KVDKAPKSCDKT-HTCP-----CPAPELLGGPSVFLPPPKDPTLMISRTPEVTCV 293
DB 230 TVDKLEPSPGISTINPCPFCKECHKCAPNLEGGPSVFLPPNKKVLMVLTSLPKVTCV 289
QY 294 VDVSHEDPEVFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 353
DB 290 VDVSEDDPDVQISWVFNWVEVHTAQTHREDYNTIRVVSALPIQHQDWMNGKEYKCK 349
QY 354 VSNKALPAIEKTIKAKQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWES 413
DB 350 VNNKDLFSPERTISKIGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFPNGDISVEWT 409
QY 414 SNGQPNNTKTPPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 473
DB 410 SNGHTEENYKOTAPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 473
QY 474 LSPGK 478
DB 470 RSPGK 474

RESULT 11
Q8R3H6 PRELIMINARY; PRT; 701 AA.
AC Q8R3H6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunofugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RL cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RE EMBL: AF272774; AAK58686.1; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA-.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla_1.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF_2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 49.5%; Score 1268; DB 4; Length 701;
Best Local Similarity 82.7%; Pred. No. 1.8e-101;
Matches 244; Conservative 4; Mismatches 29; Indels 18; Gaps 3;

QY 187 VSWNSGALTSVHTFPAVLQSSGLSVSVTVVPSSSLGTOFYICNVNHPKPS---NTKVD 243
DB 422 VSWGCGCATVG-----HFGVY-----TRVSQVIEWLQKLMESEPRPGVLLRAPFP 466
QY 244 KKAEPKSCDKTHTCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPE 303
DB 467 GSAEPKSCDKTHTCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPE 526
QY 304 VKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 363
DB 527 VKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 586
QY 364 EKTISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNQGPENNYK 423
DB 587 EKTISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNQGPENNYK 646
QY 424 TTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 478
DB 647 TTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 701

RESULT 12
Q8R3H6 PRELIMINARY; PRT; 337 AA.
AC Q8R3H6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region
DE (Fragment).
GN IGHC1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]

```


Search completed: March 29, 2003, 09:14:40
Job time : 45.353 secs

Search completed: March 29, 2003, 09:14:40
Job time : 45.353 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:54 ; Search time 2735.1 Seconds
(without alignments)
8508.978 Million cell updates/sec

Title: US-09-758-173-7
Perfect score: 1437
Sequence: 1 ATGGGTGGAGCCTCATCTT.....CCCTGCTCCGGTAAATGA 1437

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_esti:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	62.8	1020	14	BQ062878
2	864	60.1	947	14	BQ709771
3	850.4	59.2	958	14	BQ706140
4	842.4	58.6	926	12	BG755166
5	837.4	58.3	988	14	BQ708857
6	830.8	57.8	901	13	BM007892

7	824.4	57.4	1029	14	BQ063185
8	823.8	57.3	918	14	BQ708022
9	822.8	57.3	887	14	BQ711255
10	819	57.0	995	14	BM914540
11	808.8	56.3	881	14	BQ711291
12	800.2	55.7	1031	14	BQ064886
13	797.4	55.5	936	14	BQ711727
14	796	55.4	940	14	BQ705928
15	787.4	54.8	977	14	BQ710532
16	786.4	54.7	980	14	BM914504
17	785.2	54.6	843	13	BM007897
18	779.6	54.3	930	13	BM007597
19	778.8	54.2	991	14	BQ708936
20	777.2	54.1	973	14	BQ708204
21	770.6	53.6	981	14	BM914528
22	764.6	53.2	926	14	BQ710304
23	764.2	53.2	917	14	BQ708169
24	759.4	52.8	961	14	BQ710233
25	756.8	52.7	945	14	BQ712403
26	752.4	52.4	1012	14	BM914556
27	752.2	52.3	895	14	BQ708303
28	750.4	52.2	783	13	BM007838
29	749.4	52.2	1026	14	BM914288
30	741.4	51.6	914	14	BQ712363
31	740.2	51.5	913	14	BQ707472
32	739.6	51.5	906	14	BQ711709
33	733.8	51.1	855	13	BM007689
34	733.8	51.1	944	14	BQ712397
35	733.6	51.1	919	14	BQ709339
36	733.6	51.1	924	14	BQ710668
37	732.8	51.0	936	14	BQ707530
38	731.8	50.9	1014	14	BM914505
39	731	50.9	933	14	BQ710248
40	730.4	50.8	973	14	BQ708902
41	729.6	50.8	888	12	BG757604
42	729	50.7	936	14	BQ707915
43	728.8	50.7	941	14	BQ712021
44	728.6	50.7	925	14	BQ709853
45	728.4	50.7	991	14	BQ707621

ALIGNMENTS

RESULT 1
BQ062878
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ062878
AGENCY: 6826949 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420
5', mRNA sequence.
BQ062878
BQ062878.1 GI:19890085
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1020)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2094 row: h column: 21
High quality sequence start: 21
High quality sequence stop: 681.

FEATURES

source 1. 1020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5924420"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 239 a 344 c 269 g 166 t 2 others
ORIGIN

Query Match 62.8%; Score 902; DB 14; Length 1020;
Best Local Similarity 98.0%; Pred. No. 7.8e-211;
Matches 923; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

Qy 495 CACCTCTGGGGGACACGCGCCCTGGGCTCCCTGGTCAAGGACTCTCCCGCAACCGGT 554
Db 36 CACCTCTGGGGGACACGCGCCCTGGGCTCCCTGGTCAAGGACTCTCCCGCAACCGGT 95
Qy 555 GACGGTGTGGGAACTACGGCGCCCTGACGCGCGGTGCACACCTTCCCGGCTGTCT 614
Db 96 GACGGTGTGGGAACTCAAGCGCCCTGACGCGCGGTGCACACCTTCCCGGCTGTCT 155
Qy 615 ACAGTCTCAGGACTCTACTCTCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGG 674
Db 156 ACAGTCTCAGGACTCTACTCTCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGG 215
Qy 675 CACCAGACCTTACATCTGCAACGTGAATCAAGCCGACCAACACAGGTGGACAAAGAA 734
Db 216 CACCAGACCTTACATCTGCAACGTGAATCAAGCCGACCAACACAGGTGGACAAAGAA 275
Qy 735 AGCAGAGCCAAATCTTGTGCAAAACTCACATGCCACCGTGCACGACCTGAACT 794
Db 276 AGTTGAGCCCAATCTTGTGCAAAACTCACATGCCACCGTGCACGACCTGAACT 335
Qy 795 CCTGGGGGACCGTCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTC 854
Db 336 CCTGGGGGACCGTCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTC 395
Qy 855 CCGACCCCTCAGGTACATGCTGGTGGTGGAGCTGAGCCAGAGACCTGAGGTCAA 914
Db 396 CCGACCCCTCAGGTACATGCTGGTGGTGGAGCTGAGCCAGAGACCTGAGGTCAA 455
Qy 915 GTTCAACTGTTAGCTGACGCGCGTGGAGTGCATATGTCACAGACAAAGCCCGGGAGGA 974
Db 456 GTTCAACTGTTAGCTGACGCGCGTGGAGTGCATATGTCACAGACAAAGCCCGGGAGGA 515
Qy 975 GCAGTACAAAGACGCTACCGTGTGTGACGCTCTACCGTCTGACAGGACTGCT 1034
Db 516 GCAGTACAAAGACGCTACCGTGTGTGACGCTCTACCGTCTGACAGGACTGCT 575
Qy 1035 GAATGGCAAGGAGTACAAAGTGTCTCAACAAAGCCCTCCACGCCCCCATCGAGAA 1094
Db 576 GAATGGCAAGGAGTACAAAGTGTCTCAACAAAGCCCTCCACGCCCCCATCGAGAA 635
Qy 1095 AACCATCTCAAGACCAAGGGGACGCCCGAGAACACAGGTTGACACCTGCCCCCATC 1154
Db 636 AACCATCTCAAGACCAAGGGGACGCCCGAGAACACAGGTTGACACCTGCCCCCATC 695
Qy 1155 CCGGGATGAGCTGACCAAGAACACAGGTCAGCTGACCTGCTGGTCAAAAGGCTTCTATCC 1214
Db 696 CCGGGATGAGCTGACCAAGAACACAGGTCAGCTGACCTGCTGGTCAAAAGGCTTCTATCC 755
Qy 1215 CAGCGAATCTCCCGTGGAGTGGAGAGCAATGGGACCGCGGA - -GAACAATCTACAAGACC 1272

QY 686 ACATCTGCAACGTGATCACAAGCCCAAGCAACCAAGGTGGAACAAGAAAGCAGAGCCCA 745
Db 129 ACATCTGCAACGTGATCACAAGCCCAAGCAACCAAGGTGGAACAAGAAAGTGTAGGCCA 188
QY 746 AATCTTGTGACAAAACACTCACATACCCACCGTGCACAGCCTGAACCTCTGGGGGAC 805
Db 189 AATCTTGTGACAAAACACTCACATACCCACCGTGCACAGCCTGAACCTCTGGGGGAC 248
QY 806 CGTACGTCTTCTCTTCCGCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTG 865
Db 249 CGTACGTCTTCTCTTCCGCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTG 308
QY 866 AGGTACACATCGTGTGTGTGACGTGACGTGACGACAGACACCCCTCATGATCTCCCGGACCCCTG 925
Db 309 AGGTACACATCGTGTGTGTGACGTGACGTGACGACAGACACCCCTCATGATCTCCCGGACCCCTG 368
QY 926 ACGTGGACGGGTGAGGTGATTAATGCAAGCAACAAAGCCCGGAGAGCAGTACAAACA 985
Db 369 ACGTGGACGGGTGAGGTGATTAATGCAAGCAACAAAGCCCGGAGAGCAGTACAAACA 428
QY 986 GCACGTACCGTGTGTGACGTCTCACCGTCTCGACAGGACTGGCTGAATGGCAAGG 1045
Db 429 GCACGTACCGTGTGTGACGTCTCACCGTCTCGACAGGACTGGCTGAATGGCAAGG 488
QY 1046 AGTACAAGTGAAGGTCTCCAAAGACCCCTCCAGGCCCCCATCGAGAAACCATCTCCA 1105
Db 489 AGTACAAGTGAAGGTCTCCAAAGACCCCTCCAGGCCCCCATCGAGAAACCATCTCCA 548
QY 1106 AAGCAAAGGGACGCCCGGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGATGAGC 1165
Db 549 AAGCAAAGGGACGCCCGGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGATGAGC 608
QY 1166 TGACCAAGAACCAAGTCAAGCTGACCTGTGTGTCATTAAGGCTTATCCAGGACATCG 1225
Db 609 TGACCAAGAACCAAGTCAAGCTGACCTGTGTGTCATTAAGGCTTATCCAGGACATCG 668
QY 1226 CCGTGGAGTGGGAGCAATGGGAGCCGAGACAACTACAGCCACCAAGCCCTCCCGTGC 1285
Db 669 CCGTGGAGTGGGAGCAATGGGAGCCGAGACAACTACAGCCACCAAGCCCTCCCGTGC 728
QY 1286 TGGACTCCGACGGCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 1345
Db 729 TGGACTCCGACGGCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 788
QY 1346 AGCAGGGAGAGCTTCTCATGCTCCGTGTATGATAGGCTCTGCACAACTACACGC 1405
Db 789 AGCAGGGAGAGCTTCTCATGCTCCGTGTATGATAGGCTCTGCACCACTACACGC 848
QY 1406 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
Db 849 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 880

RESULT 3
BQ706140
LOCUS BQ706140 958 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8352177 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277512
5', mRNA sequence.
ACCESSION BQ706140
VERSION BQ706140.1 GI:21845039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 958)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2464 row: a column: 01
High quality sequence stop: 705.
Location/Qualifiers
1..958
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277512"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene),
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

FEATURES
Source

BASE COUNT 229 a 319 c 256 g 150 t 4 others
ORIGIN
Query Match 59.2%; Score 850.4; DB 14; Length 958;
Best Local Similarity 99.2%; Pred. No. 3.6e-198;
Matches 865; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 564 GTGGAACTCAGCGGCCCTGACCAAGCGGGGTGCACACCTTCCCGGCTGTCTACAGTCTCTC 623
Db 11 GTGGAACTCAGCGGCCCTGACCAAGCGGGGTGCACACCTTCCCGGCTGTCTACAGTCTCTC 70
QY 624 AGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTTCCAGCAGCTTTGGGACCCAGAC 683
Db 71 AGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTTCCAGCAGCTTTGGGACCCAGAC 130
QY 684 CTACATCTGCAACGTGAATCAACGCCCAAGCAACCAAGGTGGACAAGAAAGTGTAGGCC 743
Db 131 CTACATCTGCAACGTGAATCAACGCCCAAGCAACCAAGGTGGACAAGAAAGTGTAGGCC 190
QY 744 CAAATCTTGTGACAAAACCTCACATGCCACCGTGCACGACCTGAACTCTCTGGGGGG 803
Db 191 CAAATCTTGTGACAAAACCTCACATGCCACCGTGCACGACCTGAACTCTCTGGGGGG 250
QY 804 ACCGTCAAGTCTTCTCTTCCCGCCAAACCCCAAGCACCCTCATGATCTCCCGGACCCC 863
Db 251 ACCGTCAAGTCTTCTCTTCCCGCCAAACCCCAAGCACCCTCATGATCTCCCGGACCCC 310
QY 864 TGAGGTCAATCGCTGTGTGTGGAGCTGAGCCAGCAAGACCTTGAGGTCAAGTTCAACTG 923
Db 311 TGAGGTCAATCGCTGTGTGTGGAGCTGAGCCAGCAAGACCTTGAGGTCAAGTTCAACTG 370
QY 924 GTACGTGACCGGTGGAGGTGCATATGCAAGCAAGCCCGGGAGGAGAGTACAA 983
Db 371 GTACGTGACCGGTGGAGGTGCATATGCAAGCAAGCCCGGGAGGAGAGTACAA 430
QY 984 CAGCAGTACCGTGTGTGTGACCGTCTTCCCGCCAAACCCCAAGCACCCTCATGATCTCCCGGACCC 1043
Db 431 CAGCAGTACCGTGTGTGTGACCGTCTTCCCGCCAAACCCCAAGCACCCTCATGATCTCCCGGACCC 490
QY 1044 GGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGGCCCCCATCGAGAAACCATCTC 1103
Db 491 GGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGGCCCCCATCGAGAAACCATCTC 550
QY 1104 CAAAGCCAAAGGGCAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGA 1163
Db 551 CAAAGCCAAAGGGCAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGA 610
QY 1164 GCTGACCAAGAACCAAGGTTCAGCCTGACCTGCTGCTGCTCAAGAGGCTTCTATCCACGACAT 1223
Db 611 GCTGACCAAGAACCAAGGTTCAGCCTGACCTGCTGCTGCTCAAGAGGCTTCTATCCACGACAT 670

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2464 row: c column: 02
 High quality sequence stop: 716.
 Location/Qualifiers
 1..988
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6277561"
 /clone_lib="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAGGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

source

BASE COUNT 230 a 338 c 258 g 162 t

Query Match 58.3%; Score 837.4; DB 14; Length 988;
 Best Local Similarity 95.1%; Pred. No. 5.7e-195;
 Matches 908; Conservative 0; Mismatches 41; Indels 6; Gaps 4;

QY 400 TACTTCGAAATTCGGGGCCAGGGCCCTGGTTCACCGTCTCCTCAGTAGCAACAGGGC 459
 DB 6 TACTTTGACTAGTGGGCCAGGAGCGTGTTCACCGTCTCCTCGGCTCCACAGGGC 65
 QY 460 CCATCGGTCTTCCCTCGACACCTCTCCAGAGACCTCTGGGGGCAAGCGGCCCTG 519
 DB 66 CCATCGGTCTTCCCTCGACACCTCTCCAGAGACCTCTGGGGGCAAGCGGCCCTG 125
 QY 520 GGCTGCTGTCAAGGACTACTTCCCGAACCGGTGAGCGGTGCTGGAACTCAGGGCC 579
 DB 126 GGCTGCTGTCAAGGACTACTTCCCGAACCGGTGAGCGGTGCTGGAACTCAGGGCC 185
 QY 580 CTGACAGCGGGGTGACACCTTCCCGGCTGTCTACAGTCTCCTCAGACTCTACTCCCTC 639
 DB 186 CTGACAGCGGGGTGACACCTTCCCGGCTGTCTACAGTCTCCTCAGGACTCTACTCCCTC 245
 QY 640 AGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGSCACCCAGACCTACATCTGCAAGCTG 699
 DB 246 AGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGSCACCCAGACCTACATCTGCAAGCTG 305
 QY 700 AATCAAGCCAGCAACACCAAGGTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
 DB 306 AATCAAGCCAGCAACACCAAGGTGACAAAGGTGAGAGAGAGAGAGAGAGAGAGAGAG 365
 QY 760 ACTCACATGCCCCCGGCCCGCCAGCAGCTGAACTCTCCGGGGGACCGTCAAGTCTTCTC 819
 DB 366 ACTCACATGCCCCCGGCCCGCCAGCAGCTGAACTCTCTGGGGGACCGTCAAGTCTTCTC 425
 QY 820 TTCCCCCCCCAACCCAGGACACCTCTATGATCTCTCCGGACCCCTGAGGTCAATGCGTG 879
 DB 426 TTCCCCCCCCAACCCAGGACACCTCTATGATCTCTCCGGACCCCTGAGGTCAATGCGTG 485
 QY 880 GTGGTGGAGTGGAGCCAGCAACCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 939
 DB 486 GTGGTGGAGTGGAGCCAGCAACCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 545
 QY 940 GAGGTGCATAATGCCAAGCAAGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 999
 DB 546 GAGGTGCATAATGCCAAGCAAGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 605
 QY 1000 GTCAGCGTCTCACCGTCTCTGCACAGGACTGGCTGAATGCAAGGAGTCAAGTCAAG 1059

Db 606 GTCAGGCTCTCACCCTCTGCACAGGACTGGCTGAATGGCAAGGAGTCAAGTCAAG 665
 QY 1060 GTCTCCAAAGAGCCCTCCACGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAG 1119
 Db 666 GTCTCCAAAGAGCCCTCCACGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAG 725
 QY 1120 CCGGAGAAACACAGGTGTACACCTTGGCCCCCATCCCGGATGAGCTGACCAAGAACCG 1179
 Db 726 CCGGAGAAACACAGGTGTACACCTTGGCCCCCATCCCGGATGAGCTGACCAAGAA-CAG 784
 QY 1180 GTCAGCTGACCTGCTGTCAAGGCTTCTATCCAGCAGCATCGCGTGGAGTGGGAG 1239
 Db 785 GTCAGCTGACCTGCTGTCAAGGCTTCTATCCAGCAGCATCGCGTGGAGTGGGAG 844
 QY 1240 AGCAATGGGCGAG-CCGGAGAAACAACTACAAGACCAACGCTCCCGT---CTGGACTCCGA 1295
 Db 845 AGCAATGGGCGAGCCGGAGAAACAACTACCAGACCAACGCTCCCGTGGTGTGAACTCCGA 904
 QY 1296 CGGC-TCCTTCTCTCTACAGCAAGCTCACCGTGGAGCAAGCAGGTGGCGACA 1349
 Db 905 CGGCTCTCTTCTCTCTACAGAAAGCTCCCGGGGGAGCAAAAGCAGGCGTGGCA 959

RESULT 6
 BM007892 901 bp mRNA linear EST 30-OCT-2001
 LOCUS 603617577F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450611 5',
 DEFINITION mRNA sequence.
 ACCESSION BM007892
 VERSION BM007892.1 GI:16522233
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 901)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1939 row: j column: 20
 High quality sequence stop: 834.
 Location/Qualifiers
 1..901
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5450611"
 /clone_lib="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAGGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

source

BASE COUNT 209 a 315 c 234 g 143 t

ORIGIN

Query Match 57.8%; Score 830.8; DB 13; Length 901;
 Best Local Similarity 97.3%; Pred. No. 2.3e-193;
 Matches 866; Conservative 0; Mismatches 22; Indels 2; Gaps 2;

RESULT 7
BQ063185
LOCUS
DEFINITION
BQ063185 1029 bp mRNA linear EST 02-APR-2002
AGENCOUT 6876667 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924769
5', mRNA sequence.
ACCESSION BQ063185
VERSION BQ063185.1
KEYWORDS GI:19850681
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Query Match	57.4%	Score 824.4	DB 14	Length 1029
Best Local Similarity	99.0%	Pred. No. 9.1e-192		
Matches 861	Conservative 0	Mismatches 6	Indels 3	Gaps 3
QY 489	CAAGAGCCTCTGGGGGCACAGCGCCCTGGCGCTCCCTGGTCAAGGACTACTTCCCGGA	548		
DB				
DB 4	CMAGAGCCTCTGGGGGCACAGCGCCCTGGCGCTCCCTGGTCAAGGACTACTTCCCGGA	63		
QY 549	ACCGGTGACGGTGTCTGGGAACCTCAGCGCGCCTGACACGCGCGTGCACACCTTCCCGGC	608		
DB				
DB 64	ACCGGTGACGGTGTCTGGGAACCTCAGCGCGCCTGACACGCGCGTGCACACCTTCCCGGC	123		
QY 609	TGTCCTACAGTCTCAGAGACTCTACTCCCTCAGCAGGTGGTGCAGTCCCTCCAGCAG	668		
DB				
DB 124	TGTCCTACAGTCTCAGAGACTCTACTCCCTCAGCAGGTGGTGCAGTCCCTCCAGCAG	183		
QY 669	CTTGGGCACCCAGACCTACATCTGCACAGTGAATCAAGACCCAGCAACACCAAGGTGGA	728		
DB				
DB 184	CTTGGGCACCCAGACCTACATCTGCACAGTGAATCAAGACCCAGCAACACCAAGGTGGA	243		
QY 729	CAAGAAGCAGAGCCCAATCTTGTGCAAAACTCAACATGCCACCGTGCCCGAGCAC	788		
DB				
DB 244	CAAGAAGTTGAGCCCAATCTTGTGCAAAACTCAACATGCCACCGTGCCCGAGCAC	303		
QY 789	TGAATCTCTGGGGGACCGTCAGTCTCTCTTCCCTCCCAAAACCCAGGACACCCCTCAT	848		
DB				
DB 304	TGAACTCTCTGGGGGACCGTCAGTCTCTCTTCCCTCCCAAAACCCAGGACACCCCTCAT	363		
QY 849	GATCTCCCGGACCCCTGAGGTCAACATCGGTGGTGGAGCGTGAACCAAGACCCCTGA	908		
DB				
DB 364	GATCTCCCGGACCCCTGAGGTCAACATCGGTGGTGGAGCGTGAACCAAGACCCCTGA	423		
QY 909	GGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGGTGCATATGCCAGACAAAGCCGCG	968		
DB				
DB 424	GGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGGTGCATATGCCAGACAAAGCCGCG	483		
QY 969	GGAGGAGCAGTACAAACAGCAGCTACCGTGGTGGTGCAGCGTCTCACCGTCTGSCACCGGA	1028		

[illegible]

QY 1038 TGGCAAGGAGTACAAAGTGAAGTCTTCAACAAAGCCCTCCAGCCCTCCATCGAGAAAC 1097
 Db 421 TGGCAAGGAGTACAAAGTGAAGTCTTCAACAAAGCCCTCCAGCCCTCCATCGAGAAAC 480
 QY 1098 CATCTCCAAAGCCAAAGGAGCCCGGAGAGACCAAGTGTACACCTCGCCCTCCATCCG 1157
 Db 481 CATCTCCAAAGCCAAAGGAGCCCGGAGAGACCAAGTGTACACCTCGCCCTCCATCCG 540
 QY 1158 GGATGAGTGAACCAAGAACCAAGTGAAGTGTACCTGCTGCTCAAGAGTCTTATCCAG 1217
 Db 541 GGATGAGTGAACCAAGAACCAAGTGAAGTGTACCTGCTGCTCAAGAGTCTTATCCAG 600
 QY 1218 CGACATCCCGTGGAGTGGAGAGCAATGGGAGCCGAGGAGAACTACAAGACCAAGCC 1277
 Db 601 CGACATCCCGTGGAGTGGAGAGCAATGGGAGCCGAGGAGAACTACAAGACCAAGCC 660
 QY 1278 TCCGTGTGAGTCCGAGCGCTCTTCTTCTTCTACAGCAAGCTCACCGTGAGCAAG 1337
 Db 661 TCCGTGTGAGTCCGAGCGCTCTTCTTCTTCTACAGCAAGCTCACCGTGAGCAAG 720
 QY 1338 CAGGTGGCAGCAGGAGGAGCTTCTCATGCTCCGTGATCATGAGCTCTGCACAAAC 1397
 Db 721 CAGGTGGCAGCAGGAGGAGCTTCTCATGCTCCGTGATCATGAGCTCTGCACAAAC 780
 QY 1398 CTACAGCAGAGAGCCTCTCCCTGTCTCCG 1429
 Db 781 CTACAGCAGAGAGCCTCTCCCTGTCTCCG 812

RESULT 12
 LOCUS B0064886 1031 bp mRNA linear EST 02-APR-2002
 DEFINITION AGENCOURT 6887080 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929343
 5', mRNA sequence.

ACCESSION B0064886
 VERSION B0064886.1 GI:19893932
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1031)

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2107 row: e column: 24
 High quality sequence stop: 573.

FEATURES
 source
 1..1031
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5929343"
 /clone_lib="NIH MGC 99"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Size-selected >500bp for average insert size
 of 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 248 a 349 c 271 g 162 t 1 others
 ORIGIN
 Query Match 55.7%; Score 800.2; DB 14; Length 1031;
 Best Local Similarity 94.4%; Pred. No. 8.1e-186;
 Matches 840; Conservative 0; Mismatches 49; Indels 1; Gaps 1;
 QY 497 CCTCTGGGGGACACAGCGGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCCGGTGA 556
 Db 11 CCTCTGGGGGACACAGCGGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCCGGTGA 70
 QY 557 CGGTGCTGTGGAACTCAGCGCCCTGACAGCGGCTGCACACCTTCCCGGCTGTCTAC 616
 Db 71 CGGTGCTGTGGAACTCAGCGCCCTGACAGCGGCTGCACACCTTCCCGGCTGTCTAC 130
 QY 617 AGTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGGCA 676
 Db 131 AGTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGGCA 190
 QY 677 CCAGACCTTACATCTGCAACCTGAAATCACAGCCAGCAACACCAAGGTGGACAAAG 736
 Db 191 CCAGACCTTACATCTGCAACCTGAAATCACAGCCAGCAACACCAAGGTGGACAAAG 250
 QY 737 CAGAGCCCAATCTTTCACAAACTCACATGCTCCACCGTGCAGCAGCTGAACTCC 796
 Db 251 TTGAGCCCAATCTTTCGACAAACTCACATGCTCCACCGTGCAGCAGCTGAACTCC 310
 QY 797 TGGGGGACCGTCACTTCTTCTTCCCAAAACCAAGGACACCTCATGATCTCCC 856
 Db 311 TGGGGGACCGTCACTTCTTCTTCCCAAAACCAAGGACACCTCATGATCTCCC 370
 QY 857 GGACCCCTGAGGTACATGCTGCTGCTGAGCGTGCAGCGAGCCCTGAGGTCAAGT 916
 Db 371 GGACCCCTGAGGTACATGCTGCTGCTGAGCGTGCAGCGAGCCCTGAGGTCAAGT 430
 QY 917 TCAACTGTGTACGTGGACCGCTGGAGGTGCATTAATGCCAAGACAAAGCCCGGAGGAGC 976
 Db 431 TCAACTGTGTACGTGGACCGCTGGAGGTGCATTAATGCCAAGACAAAGCCCGGAGGAGC 490
 QY 977 AGTACAACAGCAGTACCGTGTGCTGCTGAGCGTCTCACCCTGCGACCGAGCTTGGCTGA 1036
 Db 491 AGTACAACAGCAGTACCGTGTGCTGCTGAGCGTCTCACCCTGCGACCGAGCTTGGCTGA 550
 QY 1037 ATGGCAAGGAGTACAAAGTGAAGTCTTCCAAAGCCCTCCAGCGCCCATCGAGAAA 1096
 Db 551 ATGGCAAGGAGTACAAAGTGAAGTCTTCCAAAGCCCTCCAGCGCCCATCGAGAAA 610
 QY 1097 CCATCTCCAAAGCCAAAGGAGCGCCGAGAACCAAGGTGTACACCTGCCCCCATCCC 1156
 Db 611 CCATCTCCAAAGCCAAAGGAGCGCCGAGAACCAAGGTGTACACCTGCCCCCATCCC 670
 QY 1157 GGGATGAGTGAACCAAGAACCAAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1216
 Db 671 GGGATGAGTGAACCAAGAACCAAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
 QY 1217 GGGATGAGTGAACCAAGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1275
 Db 731 GGGATGAGTGAACCAAGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 790
 QY 1276 CCTCCCGTGTGAGTCCGAGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1335
 Db 791 CCTCCCGTGTGAGTCCGAGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 850
 QY 1336 AGCAGGTGTCAGCAGGGGAAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1385
 Db 851 AAAGCAGGGGGCAACCGGGGGAACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900

RESULT 13
 LOCUS B0711727
 DEFINITION AGENCOURT 8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961
 5', mRNA sequence.

Db	430	TCACACAGAGCTGGCTGAATGGCAAGAGGTACAAAGTGCAGGTCTCCAAACAAAGCCCTCC	489
QY	1079	CAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAAACACAGGTGT	1138
Db	490	CAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAAACACAGGTGT	549
QY	1139	ACACCTCGCCCATCCCGGGATGAGCTGACCAAGAACACAGGTGAGCTGACCTGACCTGCCTGG	1198
Db	550	ACACCTCGCCCATCCCGGGATGAGCTGACCAAGAACACAGGTGAGCTGACCTGACCTGCCTGG	609
QY	1199	TCAAAGGCTTCTATCCAGCGACATCCCGTGAGATGGAGAGCAATGGCAGCCGGAGA	1258
Db	610	TCAAAGGCTTCTATCCAGCGACATCCCGTGAGATGGAGAGCAATGGCAGCCGGAGA	669
QY	1259	ACAACTACAAGACCA-CGCTCCCGTGTGGATCTCCGAGCGGTCTCTTCTCTCTACAGC	1317
Db	670	ACAACTACNAGAACACGGCTTCCCGTGTGGATCTCCGAGCGGTCTCTTCTCTCTACAGC	729
QY	1318	AAGCTACCGTGGACAAAGACAGGTGGACAGAGGGAACGTCTTCTCATGCTCCGTGATG	1377
Db	730	AAGCTACCGTGGACAAAGACAGGTGGACAGAGGGAACGTCTTCTCATGCTCCGGATG	789
QY	1378	CATGAGGCTCTGCACAAACCACTACAGCGAGAGAGCGCTCTCCCTGTCTCCGGTAAATGA	1437
Db	790	CATGAGGCTCTGGAC-ACCACCTAACCGAGAGAGCGCTCTCTCTCTCCCGGGAATGA	848

RESULT 14

BQ705928

LOCUS

DEFINITION

AGENCOURT 7976186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214795 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ705928
 1 (bases 1 to 940)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLCM2382 row: k column: 20
 High quality sequence stop: 619.

Location/Qualifiers
 1..940
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6214795"
 /clone_lib="NIH_MGC_113"
 /lab_host="PH108 (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G) Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

235 a 318 c 240 g 147 t

BASE COUNT
 ORIGIN

Search completed: April 6, 2003, 06:20:36
Job time : 2744.1 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 18:12:24 ; Search time 394.366 Seconds
(without alignments)
8205.894 Million cell updates/sec

Title: US-09-758-173-7

Perfect score: 1437

Sequence: 1 ATGGGTTGGACCTCACTT.....CCCTGTCTCCGGTAAATGA 1437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1437	100.0	1437	19 AAV35487	Macaque primatized
2	1437	100.0	1437	24 AAS17245	DNA sequence of a
3	1435.4	99.9	1437	18 AAT13847	Primate-derived anti-hu
4	1219	84.8	7521	22 AAF30315	Bicistronic chimer
5	1216	84.6	1616	24 AAS62785	cDNA sequence #572
6	1199.2	83.5	1386	14 AAQ49834	Anti-HIV-1 recombi
7	1186	82.5	1798	21 AAC98220	Human colon cancer
8	1185	82.5	1430	24 AAK98701	cDNA of the heavy
9	1184	82.4	1644	22 AAS22593	Human cDNA encodin

10	1183	82.3	1549	13 AAQ20066	Encodes heavy chai
11	1182.2	82.3	19035	19 AAV61794	Traget plasmid Man
12	1171.4	81.5	1427	19 AAV41431	Plasmid Hu19HCPcd
13	1171.4	81.5	1427	19 AAV41431	Plasmid Hu19HCPcd
14	1169.8	81.4	1427	19 AAV41429	Plasmid Hu19HCPcd
15	1169.4	81.4	1442	22 AAC84208	Plasmid Glambda-1B
16	1166.2	81.2	6281	22 AAC84206	Plasmid Glambda-1A
17	1165.4	81.1	1615	24 ABK34973	Human cDNA encodin
18	1163	80.9	1617	24 AAS62784	cDNA sequence #571
19	1158.4	80.6	6284	19 AAV41427	Plasmid Hu19HCPcd
20	1155.8	80.4	1576	14 AAQ49944	Human anti-HBs hea
21	1155.4	80.4	1641	15 AAH54655	chIT84.12 H3 heavy
22	1153.4	80.3	2974	22 AAH98397	Synthetic EST-deri
23	1147.2	79.8	1335	21 AAZ34748	Humanized anti-CD2
24	1142.8	79.5	1598	24 ABK34965	Human cDNA encodin
25	1142.8	79.5	1634	24 AAS62516	cDNA sequence #303
26	1141.4	79.4	1356	22 AAD20745	Human recombinant
27	1139.4	79.3	1412	13 AAQ25692	Sequence of the ch
28	1138.6	79.2	1347	21 AAZ60599	cDNA encoding a ra
29	1138.6	79.2	1590	24 ABK34976	Human cDNA encodin
30	1138.6	79.2	1640	24 ABK35183	Human cDNA encodin
31	1133.4	78.9	1599	24 ABK64550	Human benign prost
32	1133.4	78.9	1599	24 ABL62673	Colon adenocarcino
33	1133.4	78.9	1599	24 ABL65479	Lung cancer relate
34	1133.4	78.9	1599	24 ABL66294	Lung cancer relate
35	1131.8	78.8	1617	14 AAQ35099	Antibody D heavy c
36	1130.2	78.6	1449	20 AAX08951	Monoclonal antibod
37	1130.2	78.6	1449	20 AAX08952	Monoclonal antibod
38	1129.2	78.6	9182	24 ABK10574	Baculovirus expres
39	1127.8	78.5	1467	13 AAQ23570	Reshaped CAMPAT-1
40	1127.6	78.5	9182	24 ABL55051	Plasmid pTRABac/9F
41	1127	78.4	1428	22 AAH74680	Nucleotide sequenc
42	1125.8	78.3	9208	15 AAQ56629	Vector contg. rCAE
43	1125.8	78.3	13001	19 AAV61793	Traget plasmid Mol
44	1122.6	78.1	1413	21 AAA63531	DNA encoding a dim
45	1121	78.0	2912	22 AAS22718	Human cDNA encodin

ALIGNMENTS

RESULT 1
AAV35487
ID AAV35487 standard; DNA; 1437 Bp.
XX
AC AAV35487;

DT 29-SEP-1998 (first entry)

DE Macaque primatized 7B6 heavy chain DNA.

XX Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation; ss.

OS Macaca fascicularis.

XX Key Location/Qualifiers

FT CDS 1..1437

FT /*tag= a

FT /product= 7B6 heavy chain

XX WO9819706-A1.

XX 14-MAY-1998.

XX 29-OCT-1997; 97WO-US19906.

XX 08-NOV-1996; 96US-0746361.

XX (IDEC-) IDEC PHARM CORP.

XX	Anderson DR, Brams P, Hanna N; WPI; 1998-286601/25. P-PSDB; AAW63763.	XX	541	TTCCCCGAAACCGGTGACGGTGTCTGTGGAATCTAGGCGCCCTCTGACAGCGCGCTGCACACC	600
XX		XX	541	TTCCCCGAAACCGGTGACGGTGTCTGTGGAATCTAGGCGCCCTCTGACAGCGCGCTGCACACC	600
XX		XX	601	TTCCCGGCTGCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGTACCGCTGCCC	660
XX	New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours	XX	601	TTCCCGGCTGCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGTACCGCTGCCC	660
XX		XX	661	TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACC	720
XX	Example 7; Fig 4b; 87pp; English.	XX	661	TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACC	720
XX		XX	721	AAGTGTGACAAAGAGAGAGCCCAATCTTGTGACAAACTCACAATGCCCACCGTGC	780
XX	This sequence encodes a primatized form of the antibody 7B6 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.	XX	721	AAGTGTGACAAAGAGAGAGCCCAATCTTGTGACAAACTCACAATGCCCACCGTGC	780
XX		XX	781	CCAGCAGCTGAATCTCTGGGGGACCGTCTCAGTCTTCTTCCCCCAAAACCCCAAGGAC	840
XX		XX	781	CCAGCAGCTGAATCTCTGGGGGACCGTCTCAGTCTTCTTCCCCCAAAACCCCAAGGAC	840
XX		XX	841	ACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGTGACGTGAGCCACAGAA	900
XX		XX	841	ACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGTGACGTGAGCCACAGAA	900
XX		XX	901	GACCTCAGGTCAAGTTCAACTGTGTGACGGGTGTGAGTGCATTAATGCCAAGACA	960
XX		XX	901	GACCTCAGGTCAAGTTCAACTGTGTGACGGGTGTGAGTGCATTAATGCCAAGACA	960
XX		XX	961	AAGCGCGGGAGGAGACAGTACAAACAGCAGTACCCGTGTGTGAGGTCTCTACCGTCTGT	1020
XX		XX	961	AAGCGCGGGAGGAGACAGTACAAACAGCAGTACCCGTGTGTGAGGTCTCTACCGTCTGT	1020
XX		XX	1021	CACGAGACTGGCTGAATGCAAGGAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCCA	1080
XX		XX	1021	CACGAGACTGGCTGAATGCAAGGAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCCA	1080
XX		XX	1081	GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAAC	1140
XX		XX	1081	GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAAC	1140
XX		XX	1141	ACCTGTGCCCCATCCCGGATGAGTGCACNAGAACAGGTGAGCTGACCTGCTGCTGTC	1200
XX		XX	1141	ACCTGTGCCCCATCCCGGATGAGTGCACNAGAACAGGTGAGCTGACCTGCTGCTGTC	1200
XX		XX	1201	AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGCGAGCGAGAAC	1260
XX		XX	1201	AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGCGAGCGAGAAC	1260
XX		XX	1261	AACATAAGACACGCTCCCGTGTGGAGTCCGAGCGGTCTTCTTCTCTACAGCAAG	1320
XX		XX	1261	AACATAAGACACGCTCCCGTGTGGAGTCCGAGCGGTCTTCTTCTCTACAGCAAG	1320
XX		XX	1321	CTACCCGTGGACAAGAGCAGGTGGCAGAGGGGAGAGTCTTCTCATGTCTCCGTGATGAT	1380
XX		XX	1321	CTACCCGTGGACAAGAGCAGGTGGCAGAGGGGAGAGTCTTCTCATGTCTCCGTGATGAT	1380
XX		XX	1381	GAGGCTCTGCACAACTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAATGA	1437
XX		XX	1381	GAGGCTCTGCACAACTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAATGA	1437
XX		XX	RESULT 2		
XX		XX	AAS17245		
XX		XX	ID AAS17245 standard; DNA; 1437 BP.		
XX		XX	AC AAS17245;		
XX		XX	DT 12-MAR-2002 (first entry)		
XX		XX	DE DNA sequence of a primatized form of the heavy chain of 7B6 antibody.		
XX		XX	Human; macaque monkey; light chain; primatized antibody; 7B6 antibody		
XX		XX			


```

XX 23-MAR-1993; 93WO-US02629.
XX PF
XX PR
XX PR 01-APR-1992; 92US-0861701.
XX (MERI ) MERCK & CO INC.
XX PA (JOHN/) JOHNSON L S.
XX PA (PFARR/) PFARR D S.
XX PI
XX Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;
XX WPI; 1993-336600/42.
XX P-PSDB; AAR42162.
XX PR
XX PR
XX PR New recombinant human antibody - with HIV neutralising activity
XX PT against at least two isolates, useful for preventing or treating
XX PT infection in diagnosis, etc.
XX PT
XX Example 9; Fig 2A; 154pp; English.
XX PS
XX PS EBV-transformed cell lines and mouse-human heterohybridomas
XX CC producing human MAbS specific for the gp120 V3 loop of HIV-1 MN
XX CC isolate were obtained. MAb 447-52D was found to recognise the
XX CC tetrapeptide motif GPGR, i.e. the Principal Neutralising
XX CC Determinant common to the V3 loop of different HIV isolates.
XX CC A recombinant AB was produced in which the H chain V region was
XX CC derived from 447-52D and to which a signal sequence and a H chain
XX CC intronic sequence are appended, fused to a fragment contg. a short
XX CC intronic segment of the human gamma 1 C region and the human gamma
XX CC 1 encoding domain in its genomic form.
XX SQ
XX Sequence 1386 BP; 333 A; 429 C; 377 G; 247 T; 0 other;

Query Match 83.5%; Score 1199.2; DB 14; Length 1386;
Best Local Similarity 92.1%; Pred. NO. 3.5e-230;
Matches 1277; Conservative 0; Mismatches 103; Indels 6; Gaps

```

Db	121	CCAGGGAAGGGGCTGGAGTGGGTGGCGCGGTATTAAGAGCAGAACTGATGGTGGGCAACA	180
Qy	238	GAATACGGCGGCTGTGTAAGACAGATTCCACATCTCCAGAGATGATTCCAAAGCATC	297
Db	181	GACTACGTGATCCGTGAAGCGAGATTCACATCTCAAGAGATGACTCAAANAACAG	240
Qy	298	GCGTATCTGCAAAATGACAGCGCTGAAAAATCGAGGACACGGCCGTCTATTACTGTACTACA	357
Db	241	CTATATCTGCAAAATAGACTGCTGAAAAACAGAGGACACAGCCGTTTATTCTCGCACACA	300
Qy	358	TCCTACATTTACATCTGTCGGGG-----TGGTGTCTCTATGGAGGTACTTTCGAATTTC	411
Db	301	GATGGTTTTATTGATTCGGGAGGTCTCCGAGGACTACTACTACTACATGAGAGTT	360
Qy	412	TGGGCCAAGGCGCCCTGGTGTACCGGTCTCTCAGCTAGCACCAAGGCCCATCGGTCTTC	471
Db	361	TGGGGCAAGGGGACACGGGTACCGGTAGCTCAGCCCTCCACCAAGGGCCCATCGGTCTTC	420
Qy	472	CCCTCTGGCACCCCTCCTCCAGAGACACTCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTTC	531
Db	421	CCCTCTGGCACCCCTCCTCAAGAGCACTCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTTC	480
Qy	532	AAGGACTACTTTCGCCGAACCGGTGACGGTGTCTGTGGAACTCAGGCGGCCCTGACCAACGGCG	591
Db	481	AAGGACTACTTTCGCCGAACCGGTGACGGTGTCTGTGGAACTCAGGCGGCCCTGACCAACGGCG	540

Db 293 DYSEDDPQVSWFNNVNVLTQTHREDYNTSTIRVVSALPIQHDWMSGKFKCKVN 352
QY 354 NKALPAPTEKTSKAKGQPEPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESN 413
Db 353 NKDLAPARTISKIKGIVRAPQVYILSPPEQLSRKDVSLTCLAVGSPEDISVETSIN 412
QY 414 GOPENNYKTTPEVLDSDGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLS 473
Db 413 GHTENYKDTAPVLDSDGSFYISKLNMTKSKWEKTDSPFCNVRHEGLKNYLYLKTISRS 472
QY 474 PKG 476
Db 473 PKG 475

RESULT 14

Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacekovic, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994.
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IGG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 48.9%; Score 1259; DB 2; Length 328;
Best Local Similarity 69.3%; Pred. No. 2.2e-67;
Matches 230; Conservative 43; Mismatches 53; Indels 6; Gaps 2;

QY 147 ASTKGPSVFPLAPSKSTSGTAAAGCLVKDYFPEPTVWMSNGALTSGVHTFPAVLQSS 206
Db 1 APKTAPSVVPLAPCSRDTSGPNVALGCLASSYFPEPTVTWNSGALSSGVHTFPAVLQPS 60
QY 207 GLYSLSSVTVPSLSLGTQYICNVNKKPSNTKVDKAEKPCDKTHTCCPCAPPELLGG 266
Db 61 GLYSLSSVTVPSLSLSSKSTCNVNHPPATTKVDKRGVTKTKPCPCPCACESP---G 116
QY 267 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
Db 117 PSVFIFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFN 176
QY 327 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRPOVYTLPPSRDE 386
Db 177 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRPOVYTLPPHAE 236
QY 387 LTKNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSFFLYSKLTVDKS 444
Db 237 LSRKSVSTICLVIGFYPPDIDVEHQNRQDPEPEGNVYRTTPQQQVDGTVFLYKFSVDKA 296
QY 445 RMQOQNVFCSCVMHEALHNHYTKSLSLSPGK 476
Db 297 SWQGGGIFQCAVMHEALHNHYTKSISKTPECK 328

RESULT 15

S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filpula, D.

submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
C:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 48.7%; Score 1256; DB 4; Length 255;
Best Local Similarity 97.1%; Pred. No. 2.5e-67;
Matches 232; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 238 TKVDKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSH 297
Db 17 TVAQADVESKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSH 76
QY 298 EDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 357
Db 77 EDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136
QY 358 PAPIEKTISKAKGQPRPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPE 417
Db 137 PAPIEKTISKAKGQPRPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPE 196
QY 418 NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSLSPGK 476
Db 197 NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSLSPGK 255

Search completed: March 29, 2003, 09:16:17
Job time : 23.3633 secs

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from mouse
 A:Reference number: A02157; MUID:80120716; PMID:6766534
 A:Contents: a allele
 A:Accession: A02157
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'P', 193-474 <YAM>
 A:Cross-references: GB:J00461
 A:Note: the sequence was determined from the germline gene
 R:Ucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979
 A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain
 A:Reference number: A26235; MUID:80081501; PMID:117548
 A:Contents: MPC 11
 A:Accession: A26235
 A:Molecule type: mRNA
 A:Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU1>
 A:Note: Lys-474 is probably removed posttranslationally
 R:Ucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin
 A:Reference number: A26232; MUID:80081502; PMID:117549
 A:Accession: A26232
 A:Molecule type: DNA
 A:Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU2>
 R:Ollio, R.; Rougeon, F.
 Nature 296, 761-763, 1982
 A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b
 A:Reference number: A26233; MUID:82173203; PMID:6803173
 A:Contents: b allele
 A:Accession: A26233
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'P', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
 A:Cross-references: GB:J00461
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.
 J. Biol. Chem. 269, 12345-12350, 1994
 A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A:Reference number: A53598; MUID:94216359; PMID:7512967
 A:Accession: A53598
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 234-251 <KIM>
 C:Comment: The a allele sequence is shown.
 C:Genetics:
 A:Introns: 138/1; 236/1; 258/1; 368/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger multimers.
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
 F:157-222/Domain: immunoglobulin homology <IM1>
 F:236-257/Region: hinge
 F:281-350/Domain: immunoglobulin homology <IM2>
 F:387-454/Domain: immunoglobulin homology <IM3>
 F:152/Disulfide bonds: interchain (to light chain) #status predicted
 F:164-220,288-348,394-432/Disulfide bonds: #status predicted
 F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
 F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 52.0%; Score 1341; DB 1; Length 474;
 Best Local Similarity 53.4%; Pred. No. 4.9e-72;
 Matches 258; Conservative 71; Mismatches 138; Indels 16; Gaps 4;
 QY 1 MKHLWFFLLVAAAPRWLSQVLOQWCEGLLOPSETLRTCVVSGSISGYIYWTWIROT 60
 DB 1 MEWSIFLUSGTAGVHSEVQLOQSGELVNPFGASVRKSCASGYTFI-TYVMHWVKQK 59
 QY 61 PGRLEWIGHYNGATTNNPSLKSRTISKTSKQNFLLNLSVTDADTAVVYCARGP 120
 DB 60 PQGLEWIGYINPNKDGTFKNEFKGKATLTSDKSNATYMLSLTSBDSAVVYCARDY 119
 QY 121 RPDCTTICVGVWDVWVGPDILVTVSSASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFP 180

DB 120 DYD-----WFAWYGOGLTVTSAAKTTPSPVYPLAPCGDITGSSVTSGCLVKGYFP 171
 QY 181 EPTVWNSGALTGVHTFPVAVLSSGLYSLSVTVVPPSSSLGTQTYICNNHKPNSTKV 240
 DB 172 ESVTVWNSGSLSSSVHLSQALLQSLGYTMSSSVTVPSSTWPSQTVTCVAHPASTTV 231
 QY 241 DKKABPKSCDKT-HTPCPP-----CPAPELGGPSVFLFPKPKDLMISRTPEVTCVVV 293
 DB 232 DKKLSPSGPISTINPCPKCKECHKCPAPNLEGGPSVIFPPNIKDVLMISLTPEVTCVVV 291
 QY 294 DVSHEDPEVKFNWYVDGVEVNAKTKPREQYNSYTVVSVLTVLHODWLNGLNGEYKCKVS 353
 DB 292 DYSDDPDVQISWFWNNYVHTAQTHREDYNSGTIRVSTLPIQHDMMGSKFEKCKVN 351
 QY 354 NKALPAPIEKTSKAKGQPREPQVYVTLPPSPDELTKNQVSLTCLVKGFYPSDIAVEWESN 413
 DB 352 NKDLSPSPTISIKGLVRAQVYVILPPPAEQLSRKQVSLTCLVWGFNPGDISVEMTSN 411
 QY 414 GQENNYKTTPVLDSDGSPFLYSKLTVDKSRWQGNVFCVSVHSEALHNNHYTKSLSL 473
 DB 412 GHTENYKDTAPVLDSDGSPFYISKLNKTKSWKTDTSFCNVRHEGLKNYLLKTKISRS 471
 QY 474 PGK 476
 DB 472 PGK 474
 RESULT 13
 S01321
 Ig gamma-2b chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
 C:Accession: S01321
 R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
 Eur. J. Biochem. 176, 287-295, 1988
 A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed as
 A:Reference number: S01320; MUID:88329081; PMID:3138116
 A:Accession: S01321
 A:Molecule type: mRNA
 A:Residues: 1-475 <DEI>
 A:Cross-references: EMBL:X13188; NID:951780; PID:CA31580.1; PID:951781
 A:Note: this sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F:159-223/Domain: immunoglobulin homology <IMM>
 Query Match 51.6%; Score 1329.5; DB 2; Length 475;
 Best Local Similarity 53.4%; Pred. No. 2.3e-71;
 Matches 258; Conservative 79; Mismatches 131; Indels 15; Gaps 7;
 QY 1 MKHLWFFLLVAAAPRWLSQVLOQWCEGLLOPSETLRTCVVSGSISGYIYWTWIROT 60
 DB 1 MEWSIFLUSGTAGVHSEVQLOQSGAEALAPGASVLSKASGYTLTSYGI-SVWKQR 59
 QY 61 PGRLEWIGHYNGATTNNPSLKSRTISKTSKQNFLLNLSVTDADTAVVYCARGP 120
 DB 60 PQGLEWIGYIYPGSGNSYFNEFKGKATLTVDKSSSTAYLHLSLTSBDSAVYFCA-GP 118
 QY 121 RPDCTTICVGVWDVWVGPDILVTVSSASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFP 180
 DB 119 R-QVGLLPFG---YWGQGLTVTASAAKTTPSPVYPLAPCGDITGSSVTGLCLVKGYFP 173
 QY 181 EPTVWNSGALTGVHTFPVAVLSSGLYSLSVTVVPPSSSLGTQTYICNNHKPNSTKV 240
 DB 174 ESVTVWNSGSLSSSVHHTFPALLO-SGLYTMSSSVTVPSSTWPSQTVTCVAHPASTTV 232
 QY 241 DKKABPKSCDKT-HTPCPP-----CPAPELGGPSVFLFPKPKDLMISRTPEVTCVVV 293
 DB 233 DKKLSPSGPTSTINPCPKCKECHKCPAPNLEGGPSVIFPPNIKDVLMISLTPEVTCVVV 292
 QY 294 DVSHEDPEVKFNWYVDGVEVNAKTKPREQYNSYTVVSVLTVLHODWLNGLNGEYKCKVS 353

Db 356 RTISKPKGSRAPQVYVLPPEEEMTKQVTLTCMTDFMPEDIVVETWNGKTELNYKN 415
QY 423 TPVVLSDGSGFFLYSKLTVDKSRWQGNVFCSCVMEALHNYHTOKSLSLSPGK 476
Db 416 TEPVLSDGSGFFLYSKLTVDKSRWQGNVFCSCVMEALHNYHTOKSLSLSPGK 469

RESULT 10
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akaishi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JCS810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
F:251-320/Domain: immunoglobulin C region; immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 53.4%; Score 1376.5; DB 2; Length 444;
Best Local Similarity 55.6%; Pred. No. 3.6e-74;
Matches 260; Conservative 73; Mismatches 100; Indels 35; Gaps 9;

QY 20 QVKLQWGGELGLOPSETLRTCTVVGSGISGYYYTWIOTPGRGLEWIGHIYNGATTN 79
Db 1 EQVQVETGGGLVRPGNSLKLCLTSGFTFSN-YRMHLRQPPGKLEWIAVITVKSDNYG 59

QY 74 NGATTNPNLSKSRVTISKDTSKNOPFLNLSVTDADTAVYVCARGPRDCTTICYGWV 133
Db 60 ----AKYAESVRGRFTISRDDSKSVILQMNRLRDEDTATYCCRTP-----WV 104

QY 134 ---DVMPGDLTVSSASTKGSVPFLAPSSKSTSGTAAALGCLVKDYPPEVTVSNMSG 190
Db 105 YAMDCWGGQTSVIVSSAKTTPPSVYPLAPGSAATNSMYTLGCLVKGYFPPEVTVSNMSG 164

QY 191 ALTSGVHTPAVLOSGLYSLSVTVPPSSSLGTQTYICNVNHPKSNTKVDKABPKSCD 250
Db 165 SUSSGVHTPAVLQSD-LYTLSSSVTPSPSTFETVCNVAHPASSTKVDKKIYPRDCG 223

QY 251 KTHTCPP--CPAPELGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYV 308
Db 224 ----CKPCICTVPEV---SSVFIFFPKPKDVTITLTPKVTCCVVVDISKDDPEVQFSWFV 276

QY 309 DGVEVHNATKPREQNSTYRVSVLTVLHODWLNKGEYCKVKNKALPAPIEKTISKA 368
Db 277 DQVEVHTAQTPREEQNFSTRFSBELPIHQDWLNKGEYCKVKNKALPAPIEKTISKT 336

QY 369 KQGPPEQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLD 428
Db 337 KGRPKAPQVYITPPPKQMAKDKVSLTCTMTDFFPEDIVFQWNGQPAENYKNTQPTMD 396

QY 429 SDGSFFLYSKLTVDKSRWQGNVFCSCVMEALHNYHTOKSLSLSPGK 476
Db 397 TDGSYFVSKLVNQRKSNWAGNFTTCSVLHEGLHNNHTEKSLSHSPGK 444

RESULT 11
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bilsch
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295

A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: Pyroglutamic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 53.2%; Score 1370; DB 2; Length 446;
Best Local Similarity 57.0%; Pred. No. 8.8e-74;
Matches 261; Conservative 66; Mismatches 117; Indels 14; Gaps 5;

QY 20 QVKLQWGGELGLOPSETLRTCTVVGSGISGYYYTWIOTPGRGLEWIGHIYNGATTN 79
Db 1 QIQLOQSGPELVRPGASVKLSCKASGYTFDYIY-HWKQRPGELEWIGHIYPGSGNTK 59

QY 80 YNPILSKSRVTISKDTSKNOPFLNLSVTDADTAVYVCARGPRDCTTICYGWVDVWGP 139
Db 60 YNEKFKGKATLTVDTSSTAYMQLSSLTSDSAVYFCARGK-----FAMDYWGQG 110

QY 140 DLTVSSASTKGSVPFLAPSSKSTSGTAAALGCLVKDYPPEVTVSNMSGALTSGVHTF 199
Db 111 TSVTVSSAKTTPPSVYPLAPGSAATNSMYTLGCLVKGYFPPEVTVSNMSGVHTF 170

QY 200 PAVLQSSGLYSLSVTVPPSSSLGTQTYICNVNHPKSNTKVDKABPKSCDKTHTCPP-- 257
Db 171 PAVLQSD-LYTLSSSVTVSTWPSQITCNVAHPASSTKVDKKIEPRG-PTIKPDPCK 228

QY 258 CPAPELGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNK 317
Db 229 CPAPNLGGPSVFIFFPKIKDVLMISSLSPMVTCCVVVDVSEDDPDVQISWPNVNVLTQA 288

QY 318 TKPREQNSTYRVSVLTVLHODWLNKGEYCKVKNKALPAPIEKTISKAKQGPPEQV 377
Db 289 TQTHREDYNSTLRVVSALPIQHQDWMGSKFEKCKVNNKOLPAPIERTISKPKGSRAPQV 348

QY 378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLY 437
Db 349 YVLPPPEEEMTKQVTLTCMTDFMPEDIVVETWNGKTELNYKNTPEVLDSGSPFMS 408

QY 438 KLTVDKSRWQGNVFCSCVMEALHNYHTOKSLSLSPG 475
Db 409 KLRVEKKNWYERNYSYCSVHVEGLHNNHTTKSFSPTPG 446

RESULT 12
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
R:Accession: S25057; A02157; A26235; A26232; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A:Reference number: S25057
A:Accession: S25057
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827

Best Local Similarity 61.6%; Pred. No. 6.6e-83;
Matches 294; Conservative 61; Mismatches 112; Indels 10; Gaps 6;

QY 4 LWFLLVAAPRWLSQVQLQWGGELLPQSTLRTCTVVGSGISGYVYTWIRQTPEGR 63
DB 2 LMTLLFVLSAPRGVLSQVRLQSGGSLATLLQTLSTCTISGFSLNNGV-DWVRQAFGK 60
QY 64 GLEWIGHIYGNG--ATTNNPNSLSKRVITISKDTSKNQFFLNLSVTDADTAVYYCARGPR 121
DB 61 ALEWLG--GSGYDEIDIDNPVLSKSLITKDTSKQVSLTSLTSTTTEDTAVYYCARVDY 117
QY 122 PDCTTTCYGGWVDVWGPDLVTVSSASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPE 181
DB 118 DSHAFAYASY-DFWGPGLLISVLSASTPPKVPYPLTSCCGDTSSIVTLGLCLVSSYME 176
QY 182 PVTVSNWNSGALTSVGHVTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVD 241
DB 177 PVTVWNSGALTSVGHVTFPAVLQSSGLYSLSVTVTPASTSGAQTFCINVAHPASTTKVD 236
QY 242 KKAEPKCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 301
DB 237 KRVEPCPDPEKHC-RCPPPELLGGPSVFLFPPKPKDTLTISGTPEVTCVVVDVGDQDPE 295
QY 302 VKPNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPI 361
DB 296 VQSFVFNVDNVEVRTAKTPREEQFNSTFRVVSALPTIQHODWTGGKEFKCKVHNEALPAPI 355
QY 362 EKTISKAKGQPREPOVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENN 419
DB 356 VRTISRTKGQAREPQVYVLAAPQEEUSKSTLSVCLVTGTFYDYDAVEWQKNGQRESEDK 415
QY 420 YKTTPPVLDSDGFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 476
DB 416 YGTTTSLQDADGSYFLYSLRLVNDKSNQEGDTVACVMEALHNHYTQKSISKPPGK 472
RESULT 8
S69339
IG heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlichi, A.A.; Autourier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95362687; PMID:7744049
A:Accession: S69339
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Accession: S72664
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 57.7%; Score 1487; DB 2; Length 374;
Best Local Similarity 62.3%; Pred. No. 8.9e-81;
Matches 297; Conservative 24; Mismatches 38; Indels 118; Gaps 7;

QY 8 LLLVAAPRWLSQVQLQWGGELLPQSTLRTCTVVGSGIS-----GYVYTWIRQTP 61
DB 8 LLLTIFSWLSQITLSESGFTLVKPTQTTLTCTSGFSLSGVG-----WIRQPP 62
QY 62 GRGLEWIGHIYGNGATTNNPNSLSKRVITISKDTSKNQFFLNLSVTDADTAVYYCARGPR 121
DB 63 GOALEWIALIFWDD-DKRYFSLRSLRLTITKDTSKNQVLTWINDPADTATYYCYGSVE 121

QY 122 PDCTTTCYG-GW-VDWVGPDGLVTVSSASTKGPSVFPLAPSKSTSGTAAALGCLVKDYF 179
DB 122 G-----YGGYRPHSGWGQTLTVTVSS----- 142
QY 180 PEPVTVSNWNSGALTSVGHVTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTK 239
DB 143 ----- 142
QY 240 VDKAEPKCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
DB 143 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 197
QY 300 PEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPA 359
DB 198 PEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPA 257
QY 360 PIEKTIISKAKGQPREPOVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
DB 258 PIEKTIISKAKGQPREPOVYVTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 317
QY 420 YKTTPPVLDSDGFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 476
DB 318 YKTTPPVLDSDGFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 374
RESULT 9
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:9406252; PID:CAA49868.1; PID:9406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 54.7%; Score 1408.5; DB 2; Length 469;
Best Local Similarity 56.3%; Pred. No. 5e-76;
Matches 267; Conservative 70; Mismatches 126; Indels 11; Gaps 5;

QY 5 WFFLLVAAPRWLSQVQLQWGGELLPQSTLRTCTVVGSGISGYVYTWIRQTPEGR 64
DB 5 WIFLFLSGTAGVHCQIQLOQSGPELVKPGASVKISCKASGYTFDYI-NWVKQKPGQG 63
QY 65 LEWIGHIYGNGATTNNPNSLSKRVITISKDTSKNQFFLNLSVTDADTAVYYCARGPRPDC 124
DB 64 LKWIGWIYPASGNTKYNENPKGKATLTVDTSSTAYVQLSLSLTSSTEDTAVYFCARAMGATA 123
QY 125 TTCYGGWVDVWGPDLVTVSSASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPVT 184
DB 124 TLL-----DYWGQGTTLTVSSAKTTPAVVYPLAPVCGDITGSSVTLGCLVKGYFPEPVT 177
QY 185 VSNWNSGALTSVGHVTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKA 244
DB 178 LTNWNSGSLSSGVHVFPAVLQSD-IYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVDKI 236
QY 245 EPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 302
DB 237 EPRG-PTIKPCPPCKCPAPNLLGGPSVFLFPPKIKDVLMSLSPIVTCVVVDVSEDQPDV 295
QY 303 KFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPI 362
DB 296 QISWFNWVNHVHTAQTOQTHREDYNSTLRVVSALPIQHDMMSGKEFKCKVKNKDLPAPI 355
QY 363 KTIISKAKGQPREPOVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNKT 422

A:Accession: A90933
 A:Molecule type: DNA
 A:Residues: 1-327 <ELL>
 A>Note: the sequence was determined from the germline gene
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
 Biochem. J. 117, 33-47, 1970
 A:Title: Human immunoglobulin subclclasses. Partial amino acid sequence of the constant
 A:Reference number: A90249; MUID:70207560; PMID:4192699
 A:Accession: A90249
 A:Molecule type: protein
 A:Residues: 1-30; 81-326 <PIN>
 C:Genetics:
 A:Gene: GDB:IGHG4
 A:Cross-references: GDB:119340; OMIM:147130
 A:Map position: 14q32.33-14q32.33
 A:Introns: 99/1; 111/1; 221/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:99-110/Region: hinge
 F:134-203/Domain: immunoglobulin homology <IM2>
 F:240-307/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted
 F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.6%; Score 1586.5; DB 1; Length 327;
 Best Local Similarity 90.6%; Pred. No. 1e-86;
 Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

QY 147 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPPVTVSNWNGALTSQVHTFPAVLOSS 206
 DB 1 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPPVTVSNWNGALTSQVHTFPAVLOSS 60

QY 207 GLYSLSVVTVPSLSLGTQYICNVNHPKSNKVDKAEPSKCDKTHCPPCPAPELGG 266
 DB 61 GLYSLSVVTVPSLSLGTQYICNVNHPKSNKVDKAEPSKCDKTHCPPCPAPELGG 117

QY 267 PSVELPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYN 326
 DB 118 PSVELPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYN 177

QY 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKTIISKAKGQPREPQVYTLPPSRDE 386
 DB 178 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKTIISKAKGQPREPQVYTLPPSRDE 237

QY 387 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 446
 DB 238 MTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 297

QY 447 QCGNVFSCSVMEALHNNHYTKSLSPGK 476
 DB 298 QCGNVFSCSVMEALHNNHYTKSLSPGK 327

RESULT 6
 S22080
 IG heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
 N:Alternate names: IG gamma-1 chain C region (Clone 8.10)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Jul-1999
 A:Accession: S22080; S06610; A31303
 R:Sanders, P.G.
 submitted to the EMBL Data Library, November 1991
 A:Reference number: S22080
 A:Accession: S22080
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-470 <SAN>
 A:Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
 Mol. Immunol. 26, 841-850, 1989
 A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
 A:Reference number: S06610; MUID:90097956; PMID:2513487
 A:Accession: S06610
 A:Molecule type: DNA
 A:Residues: 142-470 <SYM>
 A:Cross-references: EMBL:X16701
 A>Note: the sequence was determined from the germline gene
 C:Genetics:
 A:Gene: IG CH gamma-1
 A:Introns: 98/1; 111/1; 221/1
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
 F:161-225/Domain: immunoglobulin homology <IMM>
 F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.6%; Score 1537; DB 2; Length 470;
 Best Local Similarity 62.6%; Pred. No. 1.3e-83;
 Matches 299; Conservative 60; Mismatches 109; Indels 10; Gaps 7;

QY 1 MKHLWFFLLVAAPRVLSOVKLOQMGEGLLQPSSETLSRTCTVSVSGSISGYVYWTWIRQT 60
 DB 1 MNPLWTLFLVLSAPIGVLSQVLRSGPSLVKPSQTLSTCTVSGFSLSSYAL-TWVROA 59

QY 61 PGRGLEWIGHIYNGGATTNYPNLSKSRVTISKDTKNQPFNLNSVTDADTAVVYCARGP 120
 DB 60 PGKALEWVGII-TSGGTTYNPALKRSLITKENSQVLSVSVTPEDTATYYCARST 118

QY 121 RPDCTTCYGVWDVMPGDLVTVSSASTKGPSVFFPLAPSSKSTSGTAAALGLVLDYFP 180
 DB 119 YGB--VGDCAIADANGQLLVTVSSASTTAPKYPLSSCCGDKSSSTVTLGLVSSYP 175

QY 181 EPTVSNWNGALTSQVHTFPAVLSGLYSLSVVTVPSLSLGTQYICNVNHPKSNKTV 240
 DB 176 EPTVTVSNWNGALTSQVHTFPAVLSGLYSLSVVTVPSLSLGTQYICNVNHPKSNKTV 234

QY 241 DKAEPSKCDKTHCPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
 DB 235 DKAVDP-TC-KPSPCCCPPELPPGPSVFIFFPKPKDTLTISGTPEVTCVVVDVSHEDP 292

QY 301 EVKFNWYVDGVEVNAKTKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
 DB 293 EVKFSFVDDDEVNTATTKPREQYFNSTYRVVSALRIHQDWTGGKEPKCKVHNEGLPAP 352

QY 361 IEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--EN 418
 DB 353 IVRTISRTKGPAREPQVYVLAAPPQELSKSTVSLTCTCMVTSFYPDYIAVEWQNGQPESED 412

QY 419 NYKTTTPVLDSDGSFFLYSLKLTVDKSRWQGVNFCVSNMHEALHNNHYTKSLSPGK 476
 DB 413 KYGTFPQLDADSSYFLYSLKLRVDRNSWQEGDTYTCVNMHEALHNNHYTKSLSPGK 470

RESULT 7
 S31459
 IG gamma-1 chain - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S31459
 R:Patel, S.; Nau, F.
 submitted to the EMBL Data Library, December 1992
 A:Reference number: S31459
 A:Accession: S31459
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-472 <PAT>
 A:Cross-references: EMBL:X69797
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 59.2%; Score 1525; DB 2; Length 472;

Query Match 63.0%; Score 1624.5; DB 2; Length 377;
Best Local Similarity 81.7%; Pred. No. 6.8e-89;
Matches 308; Conservative 10; Mismatches 12; Indels 47; Gaps 1;

Qy 147 ASTKGPSVFLPAPSSKSTSGTAAALCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 206
Db 1 ASTKGPSVFLPAPSSKSTSGTAAALCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60

Qy 207 GLYSLSVVTVSSSLGTQTYICNVNHPKSNKVDKKA----- 244
Db 61 GLYSLSVVTVSSSLGTQTYICNVNHPKSNKVDKRVELKTPGLDTHTCRCRCPKSC 120

Qy 245 -----EPKSCDTHTCPCPAPELLGGPSVFLFPPKPKDT 279
Db 121 DTPPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPAPELLGGPSVFLFPPKPKDT 180

Qy 280 LMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNSTYRVVSVLTVLH 339
Db 181 LMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNSTYRVVSVLTVLH 240

Qy 340 QDWLNKGVKCKVSNKALPAPTEKTSKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVK 399
Db 241 QDWLNKGVKCKVSNKALPAPTEKTSKAKGQPREPQVYTLPPSRDEMTKNOVSLTCLVK 300

Qy 400 GFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNFVSCSVNHE 459
Db 301 GFYPDSIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSLRSLTVDKSRWQGNFVSCSVNHE 360

Qy 460 ALHNHYTQKSLSLSPGK 476
Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 4
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132

A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la;
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:239-306/Domain: immunoglobulin homology <IM2>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:217-85,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.1%; Score 1600; DB 1; Length 326;
Best Local Similarity 90.9%; Pred. No. 1.6e-87;
Matches 300; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

Qy 147 ASTKGPSVFLPAPSSKSTSGTAAALCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 206
Db 1 ASTKGPSVFLPAPSSKSTSGTAAALCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60

Qy 207 GLYSLSVVTVSSSLGTQTYICNVNHPKSNKVDKKAEPKSCDKHTCCPCPAPELLGG 266
Db 61 GLYSLSVVTVSSSLGTQTYICNVNHPKSNKVDKVTVERKCCVE---CPPCPAPP-VAG 116

Qy 267 PSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREQYN 326
Db 117 PSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREQYN 176

Qy 327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 386
Db 177 STFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy 387 LTKNOVSLTCLVKGYFSDTAVERESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
Db 237 MTKNOVSLTCLVKGYFSDTAVERESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296

Qy 447 QQGNVFCSVNHEALHNHYTQKSLSLSPGK 476
Db 297 QQGNVFCSVNHEALHNHYTQKSLSLSPGK 326

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662

igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Content: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A>Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilechmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Content: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A>Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Content: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Content: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83.144-204.250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109.112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 68.4%; Score 1763; DB 1; Length 330;
Best Local Similarity 99.7%; Pred. No. 3.9e-97;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 147 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 206
Db 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 207 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTPCPAPPELLGG 266
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTPCPAPPELLGG 120
QY 267 PSVLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNKATKPREEOYN 326
Db 121 PSVLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNKATKPREEQYN 180
QY 327 STYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
Db 181 STYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 446
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 447 QGQNVFSCSWMHLEALHNHYTQKSLSLSPGK 476
Db 301 QGQNVFSCSWMHLEALHNHYTQKSLSLSPGK 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMW>
Query Match 63.1%; Score 1626.5; DB 2; Length 377;
Best Local Similarity 81.7%; Pred. No. 5.2e-89;
Matches 308; Conservative 10; Mismatches 12; Indels 47; Gaps 1;
QY 147 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 206
Db 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 207 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA----- 244
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVELKTLPLGDTTHTCPKCPKSC 120
QY 245 -----EPKSCDKTHTPCPAPPELLGGPSVFLPFPKPKDT 279
Db 121 DTPPPCPKCPKSCDTPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPEPKPKDT 180
QY 280 LMTSRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNKATKPREEQYNSTYRVVSVLTVLH 339
Db 181 LMTSRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNKATKPREEQYNSTYRVVSVLTVLH 240
QY 340 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 399
Db 241 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300
QY 400 GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQGNVFSCSWME 459
Db 301 GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQGNVFSCSWME 360
QY 460 ALHNHYTQKSLSLSPGK 476
Db 361 ALHNHYTQKSLSLSPGK 377
RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMW>

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 21.3633 Seconds
(without alignments)
2141.995 Million cell updates/sec

Title: US-09-758-173-4

Perfect score: 2577

Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHNYTKSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1763	68.4	330	1 GHU	Ig gamma-1 chain C
2	1626.5	63.1	377	2 A23511	Ig gamma-3 chain C
3	1624.5	63.0	377	2 A60764	Ig gamma-3 chain C
4	1600	62.1	326	1 G2HU	Ig gamma-2 chain C
5	1586.5	61.6	327	1 G4HU	Ig gamma-4 chain C
6	1537	59.6	470	2 S22080	Ig heavy chain pre
7	1525	59.2	472	2 S31459	Ig gamma-1 chain -
8	1487	57.7	374	2 S69339	Ig heavy chain V r
9	1408.5	54.7	469	2 S37483	Ig gamma-2a chain
10	1376.5	53.4	444	2 PC4436	monoclonal antibody
11	1370	53.2	446	2 S40295	Ig gamma-2a chain
12	1341	52.0	474	1 G2MS11	Ig gamma-2b chain
13	1329.5	51.6	475	2 S01321	Ig gamma-2b chain
14	1259	48.9	328	2 I47159	Ig gamma-2a chain
15	1256	48.7	255	4 S31866	Ig gamma-1 chain C
16	1253	48.6	328	2 I47160	Ig gamma 2b chain
17	1250	48.5	234	2 PT0207	Ig gamma chain C r
18	1227	47.6	328	2 I47158	Ig gamma 1 chain c
19	1226.5	47.6	323	1 GHRB	Ig gamma chain C r
20	1223	47.5	328	2 I47161	Ig gamma-3 chain c
21	1212.5	47.1	329	1 G2GP	Ig gamma-2 chain C
22	1157.5	44.9	308	2 C30554	Ig heavy chain C r
23	1152	44.7	289	1 G3HUW1	Ig gamma-3 heavy c
24	1148	44.5	326	2 PS0017	Ig gamma-1 chain C
25	1142.5	44.3	333	2 PS0018	Ig gamma-2b chain
26	1138	44.2	324	1 GLWS	Ig gamma-1 chain C
27	1137	44.1	329	1 G3MSC	Ig gamma-3 chain C
28	1133	44.0	393	1 G1WSM	Ig gamma-1 chain C
29	1126	43.7	398	1 G3WSM	Ig gamma-3 chain C

30	1122	43.5	330	1 G2MSA	Ig gamma-2a chain
31	1119.5	43.4	335	1 G2MSAB	Ig gamma-2a chain
32	1117	43.3	399	1 G2MSAM	Ig gamma-2a chain
33	1114.5	43.2	329	2 S00847	Ig gamma-2c chain
34	1108	43.0	322	2 PS0019	Ig gamma-2a chain
35	1088.5	42.2	327	2 S06611	Ig gamma-2 chain C
36	1080	41.9	405	1 G2MSBM	Ig gamma-2b chain C
37	1062	41.2	277	2 I47162	Ig gamma 4 chain c
38	908	35.2	548	2 S38864	Ig epsilon chain C
39	903	35.0	220	2 A49444	Ig gamma-1 heavy c
40	794.5	30.8	549	2 S04845	Ig heavy chain pre
41	771	29.9	592	2 S25705	Ig mu chain - shee
42	727.5	28.2	572	2 B45229	Ig Y heavy chain (
43	719	27.9	627	2 S14683	Ig mu chain precu
44	713.5	27.7	249	2 S69340	Ig heavy chain VHI
45	709.5	27.5	241	2 S69131	Ig heavy chain (DO

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C;Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Bersson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers;

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A;Reference number: A90563; MUID:71064024; PMID:5489771

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96,'R',98-135 <CUN>

A;Note: this sequence has the G1m(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A;Reference number: A90564; MUID:71064025; PMID:5530842

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,'

A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seayler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primarstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

QY 494 CTGGGGGACACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAAACGGGTGACGG 553
DB |||||||
DB 491 CTGGGGGACACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAAACGGGTGACGG 550
QY 554 TGTCTGTGGAACCTCAGCGCCCTGACGAGCGGCTGCACACACTTCCCGGCTGTCTTACAGT 613
DB |||||||
DB 551 TGTCTGTGGAACCTCAGCGCCCTGACGAGCGGCTGCACACACTTCCCGGCTGTCTTACAGT 610
QY 614 CCTCAGGACTTACTTCCCTCAGCAGCGGTGACCCGTGCTTCCAGCAGCTTGGGCACCC 673
DB |||||||
DB 611 CCTCAGGACTTACTTCCCTCAGCAGCGGTGACCCGTGCTTCCAGCAGCTTGGGCACCC 670
QY 674 AGACCTACATCTGCACGTAATCAACAGCCAGCAACCAAGGTGGACAGAAAGCAG 733
DB |||||||
DB 671 AGACCTACATCTGCACGTAATCAACAGCCAGCAACCAAGGTGGACAGAAAGCAG 730
QY 734 AGCCCAAAATCTTGTGACAAAACCTCACATGCCCCACCGTGCACGACCTGAACTCTCTGG 793
DB |||||||
DB 731 AGCCCAAAATCTTGTGACAAAACCTCACATGCCCCACCGTGCACGACCTGAACTCTCTGG 790
QY 794 GGGGACCGTCAAGTCTTCTCTTCCCCCCCCAAAACCCNAGGACACCTCATGATCTCCCCGA 853
DB |||||||
DB 791 GGGGACCGTCAAGTCTTCTCTTCCCCCCCCAAAACCCNAGGACACCTCATGATCTCCCCGA 850
QY 854 CCCCTGAGGTCAATGCTGCTGCTGGAGCTGAGCCAGCAAGACCTGAGGTCAAGTTCA 913
DB |||||||
DB 851 CCCCTGAGGTCAATGCTGCTGCTGGAGCTGAGCCAGCAAGACCTGAGGTCAAGTTCA 910
QY 914 ACTGTGACGTGAGCGGCTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGT 973
DB |||||||
DB 911 ACTGTGACGTGAGCGGCTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGT 970
QY 974 ACAACGACGTAACCGTGTGCTGAGGTCTCTCAACGCTCTGACACGAGTGGCTGAATG 1033
DB |||||||
DB 971 ACAACGACGTAACCGTGTGCTGAGGTCTCTCAACGCTCTGACACGAGTGGCTGAATG 1030
QY 1034 GCAGGAGTACAAAGTCAAGTCTCAACAAAGCCCTCCAGCCGCCATCGAGAAAACCA 1093
DB |||||||
DB 1031 GCAGGAGTACAAAGTCAAGTCTCAACAAAGCCCTCCAGCCGCCATCGAGAAAACCA 1090
QY 1094 TCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATCCCGGG 1153
DB |||||||
DB 1091 TCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATCCCGGG 1150
QY 1154 ATGAGCTGACCAAGAACCGGTGAGCTGACCTGACCTGCTGCTCAAGGCTTCTATCCAGCG 1213
DB |||||||
DB 1151 ATGAGCTGACCAAGAACCGGTGAGCTGACCTGACCTGCTGCTCAAGGCTTCTATCCAGCG 1210
QY 1214 ACATCGCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACCAACTACAAGACCAAGCCTC 1273
DB |||||||
DB 1211 ACATCGCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACCAACTACAAGACCAAGCCTC 1270
QY 1274 CCGTGTGGAATCCGACGGCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCA 1333
DB |||||||
DB 1271 CCGTGTGGAATCCGACGGCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCA 1330
QY 1334 GGTGGCAGCGGGGAAAGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACT 1393
DB |||||||
DB 1331 GGTGGCAGCGGGGAAAGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACT 1390
QY 1394 ACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1431
DB |||||||
DB 1391 ACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1428

Qy	1214	ACATCGCGTGGAGTGGAGAGCAATGGGAGCGGAGAGAAACAATCAAGACCAACGCTC	1273
Db	1211	ACATCGCGTGGAGTGGAGAGCAATGGGAGCGGAGAGAAACAATCAAGACCAACGCTC	1270
Qy	1274	CCGTGCTGGACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGCA	1333
Db	1271	CCGTGCTGGACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGCA	1330
Qy	1334	GGTGGCAGCGGGAAAGCTCTTCTCATGCTCCGTGATGATGATGAGGCTCTGCACAACCACT	1393
Db	1331	GGTGGCAGCGGGAAAGCTCTTCTCATGCTCCGTGATGATGATGAGGCTCTGCACAACCACT	1390
Qy	1394	ACACGCAAGAGAGCTCTCCCTGTCTCCGGTAAATGA	1431
Db	1391	ACACGCAAGAGAGCTCTCCCTGTCTCCGGTAAATGA	1428

RESULT 10
 US-08-634-224-17
 ; Sequence 17, Application US/08634224
 ; Patent No. 5866125
 ; GENERAL INFORMATION:
 ; APPLICANT: BRAMS, Peter
 ; APPLICANT: CHAWAT, Soulaïma Salim
 ; APPLICANT: PAN, Li-Zhen
 ; APPLICANT: WALSH, Edward E.
 ; APPLICANT: HEARD, Cheryl Janne
 ; APPLICANT: NEWMAN, Roland Anthony
 ; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
 ; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/634,224
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/488,376
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-150
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1428 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1428
 US-08-634-224-17

Query Match	78.5%	Score 1123.6	DB 2	Length 1428
Best Local Similarity	88.5%	Pred. No. 2.8e-265		
Matches 1255	Conservative	0	Mismatches 154	Indels 9
				Gaps 3

Qy	17	TCTTCTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCCAGGTGAAGCTGCAGCAGT	76
Db	17	TCTTGTCTTCTTCTGTGCGTGTGTGTACGCTGTCTGTGCCAGGTGCAGTTTGCAGGAGT	76
Qy	77	GGGGGAAGAGACTTCTGCAGCCTTCCGAGAACCTGTCCGCGACCTGCTGCTGTCTCTGGT	136
Db	77	CTGGTCTGTGGTGGTGAACCCACAGACAGCCTCACGCTGACCTGCACCGTCTCTGGGT	136
Qy	137	GCTC- --CATCAGCGGTACTACTACTGAGCCTTGGATCCGCGAGACCCCGAGGAGGGGAC	193
Db	137	TCTCAGCTCAGCAACCTTAGAATGGGTGTGACCTTGGATCCGTGAGCCCCCGGGAAGGCC	196
Qy	194	TGGAGTGGATTGGCCATATTTATGGTAATGGTGCACACCAACTACAATCCCTCCCTCA	253
Db	197	TAGAAATGGCTTGGAAACATTTTTCAGTGTGACGAGAAGTC- --CTTCAGTCTCTCTCGA	253
Qy	254	AGAGTCAGTCAACAATTTCAAAAGACAGCTCCAAGAACAGTCTTCTCTGAACTGGAATT	313
Db	254	AGAGCAGACTCAGCACCTCCAGGACACCTCCAGAAAGCCAGGTGGTCTTAAGCTTTGACCA	313
Qy	314	CTGTGACGAGCGGACAGCGCGCTATTACTGTGCGAGAGCGCCTCGCCCTGAATTGCA	373
Db	314	ACGTGGACCTGTGGACACAGCCACATATTACTGTGC- --ACGGGTAGGACTGTATGACA	370
Qy	374	CAACCAATTTGTATGGCGGTGGGTGCATGTCTTGGGGCCCGGAGACCTTGGTCAACCGTCT	433
Db	371	TCAATGCTTATTACCTATACTACTCTGGATATTGGGGGACGAGAACCTTGGTCAACCGTCT	430
Qy	434	CTCTCAGCTAGCACAAAGGGCCCATCGGTCTTCCCCTGTGCAACCTCTCTCCAAAGACACT	493
Db	431	CCTCAGCTAGCACAAAGGGCCCATCGGTCTTCCCCTGTGCAACCTCTCTCCAAAGACACT	490
Qy	494	CTGGGGCACAGCGGCCCTGGGCTGGTCAAGGACTACTTCCCAGAACCGGTGACGG	553
Db	491	CTGGGGGCAACAGCGGCCCTGGGCTGGTCAAGGACTACTTCCCAGAACCGGTGACGG	550
Qy	554	TGTCGTGGAACTCAGGCGCCCTGACCAGCGGGGTGCACACCTTCCCGGTGTCTCTACAGT	613
Db	551	TGTCGTGGAACTCAGGCGCCCTGACCAGCGGGGTGCACACCTTCCCGGTGTCTCTACAGT	610
Qy	614	CTCTCAGACTCTACTCTCTCAGCAGCGTGGTGACCGTGCCTCTCAGCAGCTTGGGACCC	673
Db	611	CCTCAGGACTCTACTCTCTCAGCAGCGTGGTGACCGTGCCTCTCAGCAGCTTGGGACCC	670
Qy	674	AGACCTACATCTGCAAGTGAATCACAAGCCAGCAACACCAAGGTGACAGAAAGCAG	733
Db	671	AGACCTACATCTGCAAGTGAATCACAAGCCAGCAACACCAAGGTGACAGAAAGCAG	730
Qy	734	AGCCCAATCTGTGACAAACTCACACATGCCACCGTCCCGACACTGAATCTCTGG	793
Db	731	AGCCCAATCTGTGACAAACTCACACATGCCACCGTCCCGACACTGAATCTCTGG	790
Qy	794	GGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGACACCTCATGATCTCCCCGA	853
Db	791	GGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGACACCTCATGATCTCCCCGA	850
Qy	854	CCCTGAGGTCAATCGGTGGTGGGACGTGAGCCAAGAAAGCCCTGAGGTCAAGTTCA	913
Db	851	CCCTGAGGTCAATCGGTGGTGGGACGTGAGCCAAGAAAGCCCTGAGGTCAAGTTCA	910
Qy	914	ACTGTGACGTGGAGCGGTGGAGTGCATAATGCCAAGCAAAAGCCGGGAGGAGCAGT	973
Db	911	ACTGTGACGTGGAGCGGTGGAGTGCATAATGCCAAGCAAAAGCCGGGAGGAGCAGT	970
Qy	974	ACAAAGCAGCTACCGTGGTTCAGCGTCTCACCGTCTCTGCAACAGGACTGGCTGAATG	1033
Db	971	ACAAAGCAGCTACCGTGGTTCAGCGTCTCACCGTCTCTGCAACAGGAGTGGCTGAATG	1033
Qy	1034	GCAAGGAGTCAAGTGCAGGTCTCMAACAAAGCCCTCCAGCCCCCATCGAGAAACCA	1093
Db	1031	GCAAGGAGTCAAGTGCAGGTCTCMAACAAAGCCCTCCAGCCCCCATCGAGAAACCA	1093

Query Match 78.5%; Score 1123.6; DB 2; Length 1428;
Best Local Similarity 88.5%; Pred. NO. 2.8e-265;
Matches 1255; Conservative 0; Mismatches 154; Indels 9;

QY 1334 GGTGGCAGCAGGGAACTCTTCTCATGCTCCGTGATGAGGCTCTGCACAACCACT 1393
|||||
Db 1331 GGTGGCAGCAGGGAACTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACT 1390
|||||
QY 1394 ACACGAGAAGAGCTCTCCCTGTCTCCGGGTAAATGA 1431
|||||
Db 1391 ACACGAGAAGAGCTCTCCCTGTCTCCGGGTAAATGA 1428
|||||

RESULT 9
US-08-634-223-17
; Sequence 17, Application US/08634223
; Patent No. 5840298
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Deane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
US-08-634-223-17

Query Match 78.5%; Score 1123.6; DB 2; Length 1428;
Best Local Similarity 88.5%; Pred. No. 2.8e-265;
Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;

QY 17 TCTTCTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCCAGGTGAAGCTGCAGCAGT 76
|||||
Db 17 TCTTGTCTCTCTGTGGTGTGTGTACCGTGTCTGTCCAGGTGCAGTTGCAGGAGT 76
|||||

QY 77 GGGGGAAGAGCTTCTGCAGCTTCGGAGACCTGTCCCGCACCTGCGTGTCTCTGTG 136
|||||
Db 77 CTGGTCTGTGGTGGTGAACCCACAGAGACCCTCAGCGTGACCTGCACCGTCTCTGGGT 136
|||||

QY 137 GCTC---CATCAGCGTWTACTACTAGCCTGGATCCGCCAGACCCCCAGGGAGGGAC 193
|||||
Db 137 TCTCACTCAGCAACCCCTAGAAATGGGTGTGACCTGGATCCGTGAGCCCCCGGGAAGGCC 196
|||||
QY 194 TGGAGTGGATTTGGCCATATTTATGGTAAATGGTGCAGCACCACTACAAATCCCTCCCTCA 253
|||||
Db 197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAATC---CTTCAGTCTCTCTCTGA 253
|||||
QY 254 AGAGTCGAGTCACCATTTTCAAAAGACAGTCCAAAGAACAGATTCTTCTTGAATTTGAATT 313
|||||
Db 254 AGAGCAGACTCACCATCTCCAGGACACCTCCAGAAGCCAGGTGGTCTTAAAGCTTGAACCA 313
|||||
QY 314 CTGTGACCGCAGCGGACACGGCGCTTATTACTGTGCGAGAGGSCCTCGCCCTGATTGA 373
|||||
Db 314 ACGTGACCCCTGTGGACACAGGCACACATATTACTGTGC---ACGGGTAGACTGTATGACA 370
|||||
QY 374 CAACCATTTTGTATGGCGCTGGGTGATGCTGTGGGGCCCGGGAGACCTTGGTCACTGCT 433
|||||
Db 371 TCAATGCTTATTACCTATATACCTGGATTATTGGGGCAGGGAACCCCTGGTCACTGCT 430
|||||
QY 434 CTTCACTAGCAGCAAGAGGCCCATCGGTCTTCCCTCTGSCACCTCTCTCCAAAGAGCACCT 493
|||||
Db 431 CTTCACTAGCAGCAAGAGGCCCATCGGTCTTCCCTCTGSCACCTCTCTCCAAAGAGCACCT 490
|||||
QY 494 CTGGGGGCACAGCGGCCCTGGGTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGG 553
|||||
Db 491 CTGGGGGCACAGCGGCCCTGGGTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGG 550
|||||
QY 554 TGTGCTGGAACTCAGCGGCCCTGACAGCGGGGTGCACACCTTCCCGGTGCTCTACAGT 613
|||||
Db 551 TGTGCTGGAACTCAGCGGCCCTGACAGCGGGGTGCACACCTTCCCGGTGCTCTACAGT 610
|||||
QY 614 CTTCACTAGTCTTACTCTCTCAGCAGCGTGTGACCGTGCCTCTCAGCAGCTTTGGGACCC 673
|||||
Db 611 CTTCACTAGTCTTACTCTCTCAGCAGCGTGTGACCGTGCCTCTCAGCAGCTTTGGGACCC 670
|||||
QY 674 AGACCTACATCTGCAACGTGAATCAACAAGCCAGCAACCAAGGTGGACAAGAAAGCAG 733
|||||
Db 671 AGACCTACATCTGCAACGTGAATCAACAAGCCAGCAACCAAGGTGGACAAGAAAGCAG 730
|||||
QY 734 AGCCCAAAATCTTGTGACAAAATCTACACATGCCCAACCGTGCAGCAGCTGAATCTCTGG 793
|||||
Db 731 AGCCCAAAATCTTGTGACAAAATCTACACATGCCCAACCGTGCAGCAGCTGAATCTCTGG 790
|||||
QY 794 GGGGACCGTCACTCTCTCTTCTTCCCGCAAAACCAAGGACACCTCATGATCTCTCCGGA 853
|||||
Db 791 GGGGACCGTCACTCTCTCTTCTTCCCGCAAAACCAAGGACACCTCATGATCTCTCCGGA 850
|||||
QY 854 CCCTTGAGGTTCACATCGGTGGTGGAGCTGAGCCACCAAGACCCCTGAGGTCAAGTTCA 913
|||||
Db 851 CCCTTGAGGTTCACATCGGTGGTGGAGCTGAGCCACCAAGACCCCTGAGGTCAAGTTCA 910
|||||
QY 914 ACTGTACGTGGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGT 973
|||||
Db 911 ACTGTACGTGGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGT 970
|||||
QY 974 ACAACAGCAGTACCGTGTGGTCAAGGTCTCTACCGTCTCTGACAGGACTGGCTGAATG 1033
|||||
Db 971 ACAACAGCAGTACCGTGTGGTCAAGGTCTCTACCGTCTCTGACAGGAGTGGCTGAATG 1030
|||||
QY 1034 GCAAGGAGTACAAGTCAAGGTCTCAACAAGAGCCCTCCAGCGCCCATCGAGAAAACCA 1093
|||||
Db 1031 GCAAGGAGTACAAGTCAAGGTCTCAACAAGAGCCCTCCAGCGCCCATCGAGAAAACCA 1090
|||||
QY 1094 TCTCCAAAGCAAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTTGCCTCCCTCCCTCCGGG 1153
|||||
Db 1091 TCTCCAAAGCAAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTTGCCTCCCTCCCTCCGGG 1150
|||||
QY 1154 ATGAGCTGACCAAGAACCGAGGTGAGCCTGACCTGGTCAAGGCTTCTATCCAGCG 1213
|||||
Db 1151 ATGAGCTGACCAAGAACCGAGGTGAGCCTGACCTGGTCAAGGCTTCTATCCAGCG 1210
|||||

Db 1354 CTGCACACCACTACACAGAGAGCCCTCTCCCTGTCTCTGGTAAATGA 1404

RESULT 8

```
US-08-488-376-17
; Sequence 17, Application US/08488376
; Patent No. 5811524
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV P-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22131-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
US-08-488-376-17

Query Match 78.5%; Score 1123.6; DB 1; Length 1428;
Best Local Similarity 88.5%; Pred. No. 2.8e-265;
Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;

Qy 17 TCTTCTCTCTCTGGTGGCAGCTCCAGATGGTCTGTCCAGGTGAAGTGCAGCAGT 76
Db 17 TCTTGTCTTCTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 76

Qy 77 GGGGCGAAGGACTTCTGACGCTTCGGAGACCTGTCCCGCACCTGCTGCTGTG 136
Db 77 CTGGTCTGTGGTGTGAACCCACAGACCTTACGCTGACCTGTGACCTGTCTGGT 136

Qy 137 GCTC---CATCAGCGGTACTACTACTGACCTGTGATCCGCGAGACCCCGAGGGGAC 193
Db 137 TCTCACTAGCAACCCCTAGAAATGGGTGTGACCTGGATCGGTGAGCCCGCGGAGGCC 196

Qy 194 TGGAGTGGATGGCCATATTTATGTTAATGGTGGACACCACTACATCTCTCCCTCA 253
Db 197 TAGAATGGCTTGGAAACATTTTTCAGATGACGAGAAGTC---CTTCACTCTCTGA 253
```

```

; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/523,894
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1404
; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: 1..1404
; US-08-523-894-9

```

Query Match 81.5%; Score 1166.6; DB 3; Length 1404;
Best Local Similarity 89.8%; Pred. No. 8.8e-276;
Matches 1285; Conservative 0; Mismatches 119; Indels 27; Gaps 2;

Qy	1	ATGAAACACCTGTGGTCTTCTCTCTCTGGTGGCAGCTCCAGATGGGTCTGTGCCAG	60
Db	1	ATGAAACACCTGTGGTCTTCTCTCTCTGGTGGCAGCCCCAGATGGGTCTGTGCCAG	60
Qy	61	GTGAAGCTGCAGCAGTGGGCGAAGGACTTCTGAGCCTTCGAGACCTGTGCCGAC	120
Db	61	GTGCAGCTGCAGNGTCGGGCCAGNCTGGTGAACCTTCGAGACCTGTCCCTCAC	120
Qy	121	TGCGTTCTCTGTGTGCTCCATCAGCGGTATCTACTCGACCTGGATCGGCCAGAC	180
Db	121	TGCAGTGTCTCTGTGTGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCGCCAGTCC	180
Qy	181	CCAGGGAGGGACCTGGAGTGGATTGGCCATATTTATGGTAACTGGTCGACCAACCACTAC	240
Db	181	CCAGGGAAAGGACCTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCACCAATTAC	240
Qy	241	ANTCCCTCCCTCAAGAGTCSAGTCAACATTTCAAAAACACACGTCCCAAGAACCCAGTTCTTTC	300
Db	241	AATCCCTCCCTCAACAATCSAGTCTCCATTTCAAATAGACACGTCCCAAGAACCTTCTCTCC	300


```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
CHROMOSOME/SEGMENT: 4
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
FEATURE:
NAME/KEY: mat peptide
LOCATION: 1..1404
US-08-523-894-7

```

[illegible]

Db	523		GAA	CCGGT	GAC	GGT	GT	CGT	GAA	CT	CAG	GGG	CCCT	GAC	CA	GGG	GGT	GCA	CAC	TTCCCG	582	
Qy	601		GCT	GT	CT	CTA	CAG	TCT	CAG	GA	CT	TA	CT	CCCT	CAG	AG	GGT	GT	GAC	CGT	CCCT	660
Db	583		GCT	GT	CT	CTA	CAG	TCT	CAG	GA	CT	TA	CT	CCCT	CAG	CA	GGT	GT	GAC	CGT	CCCT	642
Qy	661		AG	CT	TGG	CA	CC	CAG	AC	CT	TAC	AT	CT	GCA	AG	GT	AA	TCA	CA	AG	CC	720
Db	643		AG	CT	TGG	CA	CA	AG	AC	CT	TAC	CT	GCA	AG	GT	TA	GA	TCA	CA	AG	CC	702
Qy	721		GAC	AA	GA	AG	CAG	AG	CC	AA	AT	CT	T	GT	GCA	AA	AA	CT	CA	CA	TG	780
Db	703		GAC	AA	GA	AG	AT	T	GAG	T	CCA	AA	TAT	G	-----	T	CC	CC	AT	CA	TG	753
Qy	781		CT	TG	AA	CT	CT	GG	GG	AG	CG	T	CA	GT	CT	CT	CT	CT	CT	CT	CT	840
Db	754		CT	TG	AG	T	CT	GG	GG	AG	CA	CT	CA	GT	CT	CT	CT	CT	CT	CT	CT	813
Qy	841		AT	GA	T	CT	CC	GG	A	CC	CT	GAG	GT	CA	CA	TG	GT	GT	G	CA	GT	900
Db	814		AT	GA	T	CT	CC	GG	A	CC	CT	GAG	GT	CA	CA	TG	GT	GT	G	CA	GT	873
Qy	901		GAG	GT	CA	AG	T	T	CA	CT	GT	GA	CG	GT	GA	AG	GT	GC	ATA	T	GC	960
Db	874		GAG	GT	CC	AG	T	T	CA	CT	GT	GA	CG	GT	GA	AG	GT	GC	ATA	T	GC	933
Qy	961		CG	GA	GAG	CAG	TAC	AA	CAG	CA	GT	AC	CG	TG	TG	GT	CA	CG	GT	CT	CA	1020
Db	934		CG	GA	GAG	CAG	T	T	CA	CA	GT	AC	CG	TG	TG	GT	CA	CG	GT	CT	CA	993
Qy	1021		GAC	TG	CT	GA	AT	GG	CA	AG	GAT	TAC	AA	GT	GT	CT	CC	AA	AG	CC	CT	1080
Db	994		GAC	TG	CT	GA	AT	GG	CA	AG	GAT	TAC	AA	GT	GT	CT	CC	AA	AG	CC	CT	1053
Qy	1081		AT	CG	AA	AA	AC	CA	T	CT	CA	AA	CG	CA	GG	CA	CC	CG	AG	AA	CA	1140
Db	1054		AT	CG	AA	AA	AC	CA	T	CT	CA	AA	CG	CA	GG	CA	CC	CG	AG	AA	CA	1113
Qy	1141		CC	CC	CA	T	CC	GG	AT	GAC	TG	AC	CA	AG	AA	CAG	GT	CA	CG	CT	CA	1200
Db	1114		CC	CC	CA	T	CC	GG	AT	GAC	TG	AC	CA	AG	AA	CAG	GT	CA	CG	CT	CA	1173
Qy	1201		T	T	CT	AT	CT	CA	CG	CA	T	CG	GT	GA	GT	GG	AG	CA	AT	GG	CA	1260
Db	1174		T	T	CT	AT	CT	CA	CG	CA	T	CG	GT	GA	GT	GG	AG	CA	AT	GG	CA	1233
Qy	1261		A	GA	CA	CA	CG	CT	CC	GT	GAC	T	CG	CA	GG	CT	CT	CT	CT	CT	CA	1320
Db	1234		A	GA	CA	CA	CG	CT	CC	GT	GAC	T	CG	CA	GG	CT	CT	CT	CT	CT	CA	1293
Qy	1321		GT	GG	CA	AG	CAG	GT	TGG	CAG	CA	GGG	AA	CG	T	CT	CT	CA	TG	CT	CG	1380
Db	1294		GT	GG	CA	AG	CAG	GT	TGG	CAG	CA	GGG	AA	CG	T	CT	CT	CA	TG	CT	CG	1353
Qy	1381		CT	GC	CA	CA	CA	CT	CA	CG	CAG	AG	CC	T	CT	CC						

RESULT 6
US-08-523-894-11
; Sequence 11, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSER: RURNS, DOANE
; SWECKER & MATTHEWS

REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:

/	REGISTRATION NUMBER:	24,618
/	REFERENCE/DOCKET NUMBER:	660-118-0 PCT
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE:	703-413-3000
/	TELEFAX:	703-413-2220
/	INFORMATION FOR SEQ ID NO:	7:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	1418 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	linear
/	MOLECULE TYPE:	other nucleic acid
/	FEATURE:	
/	NAME/KEY:	CDS
/	LOCATION:	1..1418
/	FEATURE:	
/	NAME/KEY:	sig_peptide
/	LOCATION:	1..57
/	FEATURE:	
/	NAME/KEY:	mat_peptide
/	LOCATION:	58..1418
/	OTHER INFORMATION:	/product= "IMMUNOGLOBIN, HEAVY"
/	OTHER INFORMATION:	CHAIN"
/	US-08-793-450-7	
Query Match 84.6%; Score 1210.4; DB 4; Length 1418;		
Best Local Similarity 92.4%; Pred.No.1.8e-286;		
Matches 1310; Conservative 0; Mismatches 96; Indels 12; Gaps		
Qy	13	TGTTTCTTCCTCCTCGTGTCAGCTCCACAGATGGTCTCTGCCAGGTGAAGCTGCAG 72
Dd	13	TGRTATCATCTCTTCTTTGGTAGCAAGCTAAGGTGTCACTCCAGGTCCAATTGGAG 72
Qy	73	CAGTGGGGCAAGAAGACTTCTGCAGCCCTCGGAGACCCTTCGCGACCTTCGCGACTGTCTCT 132
Dd	73	CAGTGGGGCGCAGGACTGTTTGAAGCCTTCGGAGACCCTTCGCTCACCTGCACCTGTCTAT 132
Qy	133	GTTGGCTTCATCAGCGGTACTACTATCGAACCTTGATCGGCAGACCCGAGGGAGGGA 192
Dd	133	GGTGGGTCTCTTCAGTGGT---TACTACTGGAGTGGATCGCGACGCCCCGAGGAAGGG 189
Qy	193	CTGGAGTGGAAITGGCCNATTTTATGGTAATGGTGCACCAACAATCTACAATCCCTCCCTC 252
Dd	190	CTGGAGTGGAAITGGGNAATCAA---TCATAGTGGAAAGCACCAACTACAACCGCTCCCTC 246
Qy	253	AAGAGTCAGTACCAATTTCAAAGACACGTCCAAGAAACAGTTCTTCCTGAAC TTGAAT 312
Dd	247	AAGAGTCAGTACCAATATCAGTAGACACGTCCAAGAAACAGTTCTTCCTCTGAAC TGAAC 306
Qy	313	TCTGTGACGACGGGACAGGCGCTATTACTGTGCGAGAGGCCCTCGCCCTGATTGC 372
Dd	307	TCTGTGACCGCGCGGACAGGCTGTGTATTCTGTGCGAGGG-----CCCAGAGTAT 360
Qy	373	ACAACCAATTTGTATGCGCGCTGGGTGCAATGTCTGGGGGCCGCGGAGACCTGTACCGCTC 432
Dd	361	AAATGGAAAGTATCATGGGACTGGTTGACCCCTGGGGCCAAAGTACCAC TGTCACCGTC 420
Qy	433	TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCAACCTTCTCCAAAGACACC 492
Dd	421	TCCTCAGCCTCCACAAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAGAGACCC 480
Qy	493	TCTGGGGGCA CAGCGGCCCTGGGTGCTCGTCAAGACTACTTTCGCCGAACGGTGAAG 552
Dd	481	TCTGGGGGCA CAGCGGCCCTGGGTGCTCGTCAAGACTACTTTCGCCGNACGGTGAAG 540
Qy	553	GTGTCTGTGGAACTCAGGCGCCCTGACCAAGCGGGGTGCACACCTTCCCGGTGTCCTACAG 612
Dd	541	GTGTCTGTGGAACTCAGGCGCCCTGACCAAGCGGGGTGCACACCTTCCCGGTGTCCTACAG 600
Qy	613	TCCTCAGACTCTACTCCCTCAGCAGCGTGGTGNACCGTGCCCTCCAGCAGCTTGGGCACC 672
Dd	601	TCCTCAGACTCTACTCCCTCAGCAGCGTGGTGNACCGTGCCCTCCAGCAGCTTGGGCACC 660

Qy	673	GAGACCTCATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGGACAAAGAAGCA	732
Db	661	CAGACCTCATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGGACAAAGAAGCA	720
Qy	733	GAGCCCAAAATCTTGTGACAAAACTCACATGCCCAACGGTGCCAGACACCTGAACCTCGT	792
Db	721	GAGCCCAAAATCTTGTGACAAAACTCAGACATGCCCAACGGTGCCAGACACCTGAACCTCGT	780
Qy	793	GGGGGACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCCCTCATGATCTCCCGG	852
Db	781	GGGGGACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCCCTCATGATCTCCCGG	840
Qy	853	ACCCCTGAGGTACATGCGTGTGTGGACGTGAGCCACGAAAGACCCCTGAGGTCAAGTTC	912
Db	841	ACCCCTGAGGTACATGCGTGTGTGGACGTGAGCCACGAAAGACCCCTGAGGTCAAGTTC	900
Qy	913	AACCTGTACGTGGACGGCGTGGAGGTGATTAATGCCAAGACAAAGCCGCGGAGGAGCAG	972
Db	901	AACCTGTACGTGGACGGCGTGGAGGTGATTAATGCCAAGACAAAGCCGCGGAGGAGCAG	960
Qy	973	TACAACAGCACGTACCGTGTGTGTCAGCGTCTCACCGTCTGTGACAGGACTGCTGAAT	1032
Db	961	TACAACAGCACTTTACCGGTGTGTGAGCGTCTTCAAGTCTCTGCACAGGACTGCTGAAT	1020
Qy	1033	GGCAAGGAGTACAAGTGTGAAGTCTTCCAACAAAGCCCTCCAGAGCCCATCGCAAAAACC	1092
Db	1021	GGCAAGGAGTACAAGTGTGAAGTCTTCCAACAAAGCCCTCCAGAGCCCATCGCAAAAACC	1080
Qy	1093	ATCTCCAAAGCCAAAGGGCAGCCCGAGAAACACAGGTGTACACCTGCCCCCACTCCCGG	1152
Db	1081	ATCTCCAAAGCCAAAGGGCAGCCCGAGAAACACAGGTGTACACCTGCCCCCACTCCCGG	1140
Qy	1153	GATGAGCTGACCAAGAACCAGGTTCAGCTGCCTGCTGGTCAAAGGTTCTATCCGACG	1212
Db	1141	GATGAGCTGACCAAGAACCAGGTTCAGCTGCCTGCTCAAAGGTTCTATCCCTAGC	1200
Qy	1213	GACATCCCGTGGAGTGGGAGAGCAATGGCGAGCCGGAGAACCACTACAAGACCAACGCT	1272
Db	1201	GACATCCCGTGGAGTGGGAGAGCAATGGCGAGCCGGAGAACCACTACAAGACCAACGCT	1260
Qy	1273	CCCGTGTGACCTCCGACGGCTCTTCTTCCTATACAGACGCTCACCGTGGACAAGAGC	1332
Db	1261	CCCGTGTGACCTCCGACGGCTCTTCTTCCTATACAGACGCTCACCGTGGACAAGAGC	1320
Qy	1333	AGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACAC	1392
Db	1321	AGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACAC	1380
Qy	1393	TACACGAGAAAGCCCTCTCCCTGTCTCCGGGTAATG	1430
Db	1381	TACACGAGAAAGCCCTCTCCCTGTCTCCGGGTAATG	1418

RESULT 5
US-08-523-894-7
; Sequence 7, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

LOCATION: 1..1431

US-08-487-550-11

Query Match 91.9%; Score 1315.8; DB 3; Length 1431;

Query Match
Best Local Similarity
95.0%; Pred. No. 3.3e-312;

Matches 1359;	Conservative	0;	Mismatches	72;	Indels	0;	Gaps	0;
---------------	--------------	----	------------	-----	--------	----	------	----

Qy	1	ATGAAACACCTGTGGTTCCTCTCTCTGTGTGGAGCTCCAGATGGGTCTGTCCGAG	60
Db	1	ATGAAACACCTGTGGTTCCTCTCTCTGTGTGGAGCTCCAGATGGGTCTGTCCGAG	60
Qy	61	GTCAAGCTGCAGCAGTGGGGCAAGACCTTCGTGAGCCTTCGGAGACCTGTCCCGACCC	120
Db	61	GTGAGCTGCAGAGTCTGGGCGCCAGACTGTGTGAACCTTCGGAGACCTGTCCCTCACC	120
Qy	121	TGCGTTGTCTCTGTGGTTCCTCATCATGACGGTTACTACTGTGGACCTGGATCCGCGACCC	180
Db	121	TGCGTGTCTCTGTGGTTCCTCATCATGACGGTGTATGCTGGGCTGGATCCGCGACGCC	180
Qy	181	CCAGGAGGGGACTGAGTGGATTCGCCCATATTTATGTAATGTTGTGCGACACCAACTAC	240
Db	181	CCAGGAGAGGGCTGAGTGGATTTGGAGTTCTATAGTAGTAGTGGGAACA CTTACTAC	240
Qy	241	AATCCCTCCCTCAAGAGTCCAGTCCACATTTCAAAGACACGTC CAAAGAACCAAGTTCTTC	300
Db	241	AACCCCTCCCTCAAGAGTCAAGTCCACATTTCAACAGACACGTC CAAAGAACCAAGTTCTTC	300
Qy	301	CTGAACCTTGAAATCTGTGACCGACGGGACACGGCCGCTATTACTGTGGAGAGGCCCT	360
Db	301	CTGAAGCTGAACCTCTATGACCGCCGGACACGGCCGCTATTACTGTGTGAGAGATCGT	360
Qy	361	CGCCCTGATTGCAACACCATTTGTTATGCGGCTGGGTGCGATGTCTGGGGCCGGGAGAC	420
Db	361	CTTTTTTCAGTTGTTGGAATGGTTTACAACACACTGGTTCGATGCTCTGGGCGCCGGGAGTC	420
Qy	421	CTGTGTACCGTCTCTCAGCTAGACCAAGGGCCCATCGTCTTCCTCCCTGTGGACCTCC	480
Db	421	CTGTGTACCGTCTCTCAGCTAGACCAAGGGCCCATCGTCTTCCTCCCTGTGGACCTCC	480
Qy	481	TCCAAGAGCACCTCTGGGGCACAGGGGCCCTGGGCTGCTGTTCAAGGACTACTTCCCC	540
Db	481	TCCNAGAGCACCTCTGGGGGCA CAGGGGCCCTGGGCTGCTTGGTCAAGGACTACTTCCCC	540
Qy	541	GAACCGGTGACGGTGTCTGTGGAACTCAGCGGCCCTTGACAGCGGGGTGCACACCTTCCCG	600
Db	541	GAACCGGTGACGGTGTCTGTGGAACTCAGCGGCCCTTGACAGCGGGGTGCACACCTTCCCG	600
Qy	601	GCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGACGGTGGTGACCGTCCCTCCAGC	660
Db	601	GCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGACGGTGGTGACCGTCCCTCCAGC	660
Qy	661	AGCTTGGGCAACCCAGACCTACATCTGCAACGTTGAATCAAGGCCAGCAACCAAGGTG	720
Db	661	AGCTTGGGCAACCCAGACCTACATCTGCAACGTTGAATCAAGGCCAGCAACCAAGGTG	720
Qy	721	GACAGAAAGACAGGCCCAATCTTGTGCAAAACTCACACATGCCACCGTGGCCACGCA	780
Db	721	GACAGAAAGACAGGCCCAATCTTGTGCAAAACTCACACATGCCACCGTGGCCACGCA	780
Qy	781	CCTCAACTCTCTGGGGGACCGTCACTCTTCTTCTCCCCCAAAACCAAGGACACCCCTC	840
Db	781	CCTGAACTCTCTGGGGGACCGTCACTCTTCTTCTCCCCCAAAACCAAGGACACCCCTC	840
Qy	841	ATGATCTCCGGACCCCTGAGGTCA CATGTGGTGGTGGAGCTGAGCGACGAGACCCCT	900
Db	841	ATGATCTCCGGACCCCTGAGGTCA CATGTGGTGGTGGAGCTGAGCGACGAGACCCCT	900
Qy	901	GAGTCTAAGTTCAACTGTGTGAGCGGGCTGGAGGTGCATAATGCCAAGACAAAGCCG	960
Db	901	GAGTCTAAGTTCAACTGTGTGAGCGGGCTGGAGGTGCATAATGCCAAGACAAAGCCG	960
Qy	961	CGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCGTCTCTCACCGTCTGACCCAG	1020

Best Local Similarity 100.0%; Pred. No. 0;				Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	ATGAACACCTGTTGGTCTTCTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCCAG	60				
Db	1	ATGAACACCTGTTGGTCTTCTCTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCCAG	60				
Qy	61	GTGAAGCTGCAGCAGTGGGGGGAAGGACTTCTGCAGGCTTCGGAGACCTGTCCCGACCC	120				
Db	61	GTGAAGCTGCAGCAGTGGGGGGAAGGACTTCTGCAGGCTTCGGAGACCTGTCCCGACCC	120				
Qy	121	TGCGTGTCTGTGGTTCCTCATCAGCGGTTACTACTTGGACTTGGATCCGCGACAC	180				
Db	121	TGCGTGTCTGTGGTTCCTCATCAGCGGTTACTACTTGGACTTGGATCCGCGACAC	180				
Qy	181	CCAGGAGGAGCTGGAGTGGATTTGGCCATATTTATGGTAATGTGTGCACCAACTAC	240				
Db	181	CCAGGAGGAGCTGGAGTGGATTTGGCCATATTTATGGTAATGTGTGCACCAACTAC	240				
Qy	241	AATCCCTCCCTCAAGAGTCGAGTCACCAATTTCAAAGACACGTCCTCAAGAACCACTTCTTC	300				
Db	241	AATCCCTCCCTCAAGAGTCGAGTCACCAATTTCAAAGACACGTCCTCAAGAACCACTTCTTC	300				
Qy	301	CTGAATCTTGAATTTCTGACCGACCGGACACGCGCGTCTATTACTGTGGAGAGGCGCT	360				
Db	301	CTGAATCTTGAATTTCTGACCGACCGGACACGCGCGTCTATTACTGTGGAGAGGCGCT	360				
Qy	361	CGCCCTGATTGCACACCAATTTGTTATGGCGGCTGGGTGATGTCTGGGGCCCGGAGAC	420				
Db	361	CGCCCTGATTGCACACCAATTTGTTATGGCGGCTGGGTGATGTCTGGGGCCCGGAGAC	420				
Qy	421	CTGTGCACCGTCTCTCAGCTAGACACCAAGGCGCCATCGGTCTTCCCTCGGCACCCCTCC	480				
Db	421	CTGTGCACCGTCTCTCAGCTAGACACCAAGGCGCCATCGGTCTTCCCTCGGCACCCCTCC	480				
Qy	481	TCCAAAGACACCTCTGGGGGACACGCGCCCTGGGCTGCTTGGTCAAGGACTTCTCCC	540				
Db	481	TCCAAAGACACCTCTGGGGGACACGCGCCCTGGGCTGCTTGGTCAAGGACTTCTCCC	540				
Qy	541	GAACCGGTGACGGTGTCTGGAACCTCAGTCCCTCAGCAGCGTGGTACCGTCCCTCCAGC	600				
Db	541	GAACCGGTGACGGTGTCTGGAACCTCAGTCCCTCAGCAGCGTGGTACCGTCCCTCCAGC	600				
Qy	601	GCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCCAGC	660				
Db	601	GCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCCAGC	660				
Qy	661	AGTTTGGGACCCAGACCTTACATCTGCAACGTTGAATCAAGCCCGACCAACCAAGGTG	720				
Db	661	AGTTTGGGACCCAGACCTTACATCTGCAACGTTGAATCAAGCCCGACCAACCAAGGTG	720				
Qy	721	GACAAAGAGCAGAGCCCAATTTGTGACAAAATCAACATGCGCCACCGTGCACAGCA	780				
Db	721	GACAAAGAGCAGAGCCCAATTTGTGACAAAATCAACATGCGCCACCGTGCACAGCA	780				
Qy	781	CTGAACCTCTGGGGGACCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	840				
Db	781	CTGAACCTCTGGGGGACCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	840				
Qy	841	ATGATCTCTCCCGACCCCTGAGTGCATGCGTGGTGGAGCGTGGAGCCAGCAAGACCCCT	900				
Db	841	ATGATCTCTCCCGACCCCTGAGTGCATGCGTGGTGGAGCGTGGAGCCAGCAAGACCCCT	900				
Qy	901	GAGGTCAAGTTCACTGGTACCTGAGCGCGGTGGAGGTGCATTAATGCCAAGCAAGCGG	960				
Db	901	GAGGTCAAGTTCACTGGTACCTGAGCGCGGTGGAGGTGCATTAATGCCAAGCAAGCGG	960				
Qy	961	CGGAGGAGCAGTACAAAGCAGCTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1020				
Db	961	CGGAGGAGCAGTACAAAGCAGCTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1020				
Qy	1021	GACTGGCTGAATGGCAAGGATGCAAGGTCTCCAAAGAGGCTCTCCAGAGCCCTCCAGCCCC	1080				

RESULT 2
US-08-487-550-11
; Sequence 11, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 65.1566 Seconds
(without alignments)
6735.375 Million cell updates/sec

Title: US-09-758-173-3

Perfect score: 1431

Sequence: 1 ATGAACACCTGCTGCTT.....CCCTGCTCCGGTAAATGA 1431

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A-COMB.seq:*

2: /cgn2_6/prodata/1/ina/5B-COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A-COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B-COMB.seq:*

5: /cgn2_6/prodata/1/ina/PCTUS-COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	3	US-08-487-550-3
2	1315.8	91.9	1431	3	US-08-487-550-11
3	1234.8	86.3	1567	3	US-09-049-672A-17
4	1210.4	84.6	1418	4	US-08-793-450-7
5	1171.4	81.9	1404	3	US-08-523-894-7
6	1168.2	81.6	1404	3	US-08-523-894-11
7	1166.6	81.5	1404	3	US-08-523-894-9
8	1123.6	78.5	1428	1	US-08-488-376-17
9	1123.6	78.5	1428	2	US-08-634-223-17
10	1123.6	78.5	1428	2	US-08-634-224-17
11	1123.6	78.5	1428	2	US-08-634-400-17
12	1123.6	78.5	1428	2	US-08-635-878-17
13	1123.6	78.5	1428	2	US-08-770-057-17
14	1123.6	78.5	1428	2	US-09-335-697B-17
15	1123.6	78.5	1428	4	US-09-335-697B-17
16	1117.2	78.1	1437	3	US-08-487-550-7
17	1117.2	77.7	1428	1	US-08-488-376-19
18	1112.4	77.7	1428	2	US-08-634-223-19
19	1112.4	77.7	1428	2	US-08-634-224-19
20	1112.4	77.7	1428	2	US-08-634-400-19
21	1112.4	77.7	1428	2	US-08-635-878-19
22	1112.4	77.7	1428	2	US-08-770-057-19
23	1112.4	77.7	1428	4	US-09-335-697B-19
24	1112.4	77.7	1428	4	US-09-335-697B-19
25	1111.6	77.1	19040	2	US-09-343-485A-3
26	1103.6	77.1	1617	2	US-08-378-939-9
27	1092.6	76.4	6557	1	US-08-286-740-3

Query Match

100.0%; Score 1431; DB 3; Length 1431;

28	1092.6	76.4	6557	5	PCT-US95-09576-3	Sequence 3, Appli
29	1090.6	76.2	8120	3	US-09-027-449-68	Sequence 68, Appl
30	1090.6	76.2	8120	3	US-09-026-985-68	Sequence 68, Appl
31	1090.6	76.2	8120	4	US-09-121-952A-68	Sequence 68, Appl
32	1090.6	76.2	8120	4	US-09-234-340A-68	Sequence 68, Appl
33	1090.2	76.2	1576	1	US-08-157-101A-6	Sequence 6, Appli
34	1087	76.0	9209	1	US-08-149-099C-3	Sequence 3, Appli
35	1087	76.0	9209	1	US-08-476-275-2	Sequence 2, Appli
36	1087	76.0	9209	2	US-08-478-967A-3	Sequence 3, Appli
37	1087	76.0	9209	4	US-08-475-815B-3	Sequence 3, Appli
38	1087	76.0	18986	2	US-08-819-866-2	Sequence 2, Appli
39	1087	76.0	18986	2	US-09-023-715-2	Sequence 2, Appli
40	1087	76.0	18986	4	US-09-343-485A-2	Sequence 2, Appli
41	1080.2	75.5	1350	1	US-08-157-101A-9	Sequence 9, Appli
42	1049.8	73.4	1655	3	US-09-049-672A-21	Sequence 21, Appl
43	1044.6	73.0	1135	1	US-08-236-311-8	Sequence 8, Appli
44	1044.6	73.0	1135	3	US-08-457-918-8	Sequence 8, Appli
45	1040	72.7	6285	1	US-08-467-420A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-3
; Sequence 3, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF INVENTIONS: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; LENGTH: 1431 base pairs
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
; US-08-487-550-3

Db 180 HREDYNSTRVVSALPIQHQDMSGKFKCKVNNRALPSPIEKTIKSPRGVPVAPQVYL 239
Qy 381 PPSRDLTKQVSLTCLVKGYPSPDI AVEWESNGQPNYKTPPVLDSDSGSPFLYSKLT 440
Db 240 PPPAEEMTKESFLTCMTIGLPAEIAVDWTSNGRTQNYKNTATVLDSDSGSPFMYSKLR 299
Qy 441 VDKSRWQGNVFCSCVMHEALHNYTKSLSPGK 476
Db 300 VQSTWEGSLFACSVVHEVLHNNHTTKTISRLGK 335

RESULT 15

GCAM_MOUSE
ID GCAM_MOUSE STANDARD; PRT: 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
THE A ALLELE.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch).

EMBL: J00471; AAB59661.1; ALT_INIT.
PIR: A02154; G2MSAM.
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; Igc1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT DISULFID 346 363
FT TRANSMEM 364 399
FT DOMAIN 364 399
FT CARBOHYD 180 180 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;
Query Match 43.3%; Score 1117; DB 1; Length 399;
Best Local Similarity 63.4%; Pred. No. 1.1e-71; Indels 4; Gaps 3;
Matches 210; Conservative 43; Mismatches 74;
Qy 147 ASTKGPSVFPPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSD 206
Db 1 AKTTAPSVVPLAPVCGDITGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 60
Qy 207 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKYDKKAEKPKSCDKHTHTCPP--CPAPELL 264
Db 61 -LYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 118
Qy 265 GGPSVFLRPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324
Db 119 GGPSVFIFFPKIKDVLMIISLSPITVCVVVDVSEDDPDVQISFVNNVEVHTAQTQTHRED 178
Qy 325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSR 384
Db 179 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSRAPQVYVLPPE 238
Qy 385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDSGSFYLYSKLTVDKS 444
Db 239 EEMTKQVTLTLCVTDFTMPEDYIWEVTNNGKTELYNKTEPVLDSDSGSYFMYSKLRVEKK 298
Qy 445 RMOQGNVFCSCVMHEALHNYTKSLSPG 475
Db 299 NWVERNSYSCSVVHEGLHNNHTTKSFSRTPG 329

Search completed: March 29, 2003, 09:11:13
Job time : 13.3492 secs

```

RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the FC fragment. Implications
RL for the evolution of immunoglobulin structure and function.";
RN Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RN Eur. J. Biochem. 30:452-462(1972).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; Ig like; 1.
DR SMART; SM00407; IGG1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN) .
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN) .
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN) .
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN) .
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
FT SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;
Query Match 43.5%; Score 1122; DB 1; Length 330;
Best Local Similarity 63.8%; Pred. No. 4e-72;
Matches 211; Conservative 43; Mismatches 74; Indels 4; Gaps 3;
QY 147 ASTKGPSVFPFLAPSSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
Db 1 AKTAPSVPLVPVCGDGTGSSVTLGCLVKGYFPEPVTLTWSGSLSSGVHTFPAVLQSD 60
QY 207 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKAEPKCDKTHTCPP--CPAPELL 264
Db 61 -LYTLSSSVTVTSSTWPSQSTICNVNHPASSTKVDKKIEPRG-PTIKCPCKCPAPNLL 118
QY 265 GGPSVFLFPKPKDGLMIKSTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQ 324
Db 119 GGPSVFLFPKPKDGLMIKSTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQ 178
QY 325 YNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
Db 179 YNSTLWVSALPIQHDWMSGKEFKCKVNNKDLPAPIEKTISKPGSVRAPQVYVLPPE 238
QY 385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLTVDSK 444
Db 239 EEMTKKQVTLTCMTVDMPEDIVVENTNNGKTELNKNTEPVLDSGDSYFMYSKLRVEKK 298
QY 445 RWQGNVFCSSVMHEALHNHYTQKSLSLSPGK 476

```

```

Db 299 NWVERNSYSCSVVHGLNHHHTTKSFSTRPGK 330
RESULT 14
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2aa and IgG2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Stroberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain FC regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00479; -, NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig like; 1.
DR SMART; SM00407; IGG1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW Immunoglobulin C region.
FT NON_TER 1
FT SEQUENCE 335 AA; 36596 MW; FA3382792CB813C6 CRC64;
Query Match 43.4%; Score 1119.5; DB 1; Length 335;
Best Local Similarity 61.3%; Pred. No. 6.1e-72;
Matches 206; Conservative 52; Mismatches 71; Indels 7; Gaps 2;
QY 147 ASTKGPSVFPFLAPSSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
Db 1 AKTAPSVPLVPVCGDGTGSSVTLGCLVKGYFPEPVTLTWSGSLSSGVHTFPAVLQ-S 59
QY 207 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKAEPK-----SCDKTHTCPCPA 260
Db 60 GLYTLSSSVTVTSNWSQSTICNVNHPASSTKVDKKIEPRVPIITQNPCPPHORVPPCA 119
QY 261 PELLGGPSVFLFPKPKDGLMIKSTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNATKPK 320
Db 120 PDLGGPSVFLFPKPKDGLMIKSTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNATKPK 179
QY 321 REEQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 380

```



```
Db 1 AKTTPSVVPLAPGSAQAQTNSMVTGLCLVKGYFPEPVTVTVWNSGSLSSGVTHTPAVLQSD 60
Qy 207 GLYSLSVVTVPSLSSLTGTQTYICNVNHPKSTKYDKKAEKPKSCDKTHTCP--CPAPELL 264
Db 61 -LYTSSSVTVPSRPSETVTCNVAHPASSTKYDKKIVPRDCG---CKPCICTVPEV- 114
Qy 265 GGPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 324
Db 115 --SSVFIFFPKPKDVLITLTPKVTVCVVDVSKDDPEVQFSWFVDDVEVHTAQTPREEQ 172
Qy 325 YNSTYRVVSVLTVLHQDLNGKEYCKVSKNKPAPIEKTIKAKGQRPFPQVYTLPPSR 384
Db 173 FNSPTRSVSELPIMHQDLNGKEFKRVNSAFAPIEKTISTKGRPKAPQVYTIPEPK 232
Qy 385 DELTKNQVSLTCLVKGYFSPVDIAVWEWSNGQPENNYKTTTPVLDSDSGSFYLSKLTVDKS 444
Db 233 EQMAKDKVSLTCLMTIDFPEDITVEWQNGQPAENYKNTQPIINTNGSYFYLSKLVQKS 292
Qy 445 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPG 475
Db 293 NWEAGNTFTCSVLHLEGLNHHHTKSLSPG 323

RESULT 12
GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00451; AAB59655.1; .
DR EMBL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A02155; G3MSM.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER . 1 1
```

```
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 43.7%; Score 1126; DB 1; Length 398;
Best Local Similarity 63.8%; Pred. No. 2.6e-72;
Matches 210; Conservative 46; Mismatches 69; Indels 4; Gaps 3;

Qy 148 STKGSVFPLPSSSXTSGTAAALGCLVKDYFPEPVTVWNSGSLSSGVTHTPAVLQSG 207
Db 1 TTTAPSVVPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVWNSGSLSSGVTHTPAVLQSG 59
Qy 208 LYSLSVTVTPSSSLGTQTYICNVNHPKSTKYDKKAEKPKSCDKTHTCP--PCPAPELLG 265
Db 60 FYSLSLVTVPSSTWPSQTVICNVAHPASKTELKRIEPR-IPKSTPPGSSCPGNIIG 118
Qy 266 GPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 325
Db 119 GPSVFIFFPKPKDALMISLTLPKVTVCVVDVSEDDPDVHVSFVDNKEVHTAWTQPREAQY 178
Qy 326 NSTYRVVSVLTVLHQDLNGKEYCKVSKNKPAPIEKTIKAKGQRPFPQVYTLPPSRD 385
Db 179 NSTFRVYSALPIQHQQDMRGEKFKCKVNNKALPAPIERTISPKGRAQTPQYTIPTPPRE 238
Qy 386 ELTKNOVSLTCLVKGYFSPVDIAVWEWSNGQPENNYKTTTPVLDSDSGSFYLSKLTVDKSR 445
Db 239 QMSKKVSLTCLVTNFFSEALISVEWERNGELEQDYKNTPEILDSDGTLYSLKLTVDTS 298
Qy 446 WQGNVFCSCVMHEALHNHYTQKSLSLSP 474
Db 299 WLQGEFTCSVHLEGLNHHHTQKNLSRSP 327

RESULT 13
GCAA_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollio R., Auffray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
suggests that exons can be exchanged between genes in a multigenic
```



```

RESULT 9
GCL_MOUSE
ID GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RN SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RN SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RN SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RN DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00795; CAA24176.1; -
DR PIR; A02159; GIMS.
DR HSP; P01842; 7FAB.
DR GlycoSuiteDB; P01868; -
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00407; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS00290; Ig MHC; 1.
KW Immunoglobulin domain; immunoglobulin C region; Glycoprotein;
Alternative splicing.
KW NON_TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .).
FT DISULFID 244 302 /FTID-CAR_000055.
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812P3D1F2C93 CRC64;
Query Match 44.2%; Score 1138; DB 1; Length 324;
Best Local Similarity 62.0%; Pred. NO. 2.9e-73;
Matches 206; Conservative 55; Mismatches 61; Indels 10; Gaps 4;
QY 147 ASTKGPVVFPLAPSSKSTSGCTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
Db 1 AKTTPSVVYFLAPGSAQAQNSMTLGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 60
QY 207 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKDKAEKPKCDKTHCTCPP--CPAPELL 264
Db 61 -LYTLSSSVTPSPSPSEVTVCNVAHPASSTKVDKIVPRDCG----CKPCICTVPEV- 114
QY 265 GGSVYFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 324
Db 115 --SSVFIFFPKPKDKVLTITLTTPKVTCTVVDISKDDPEQSFVDFVDDVEVHTAQTQPREEQ 172
QY 325 YNSTYRVVSVLTVLHODWLNKGKVKCVSNKALPAPEKTIKSKAKOPREPQVYVTLPPSR 384
Db 173 FNSFTRSVSELPIMHQDWLNGKEFKCVNSAAPAPAEKTIKTKGRPKAPQVYVTLPPPK 232
QY 385 DELTKNOVSUTCLVKGYFPSDIAVEWESNGQPENNYKTTTPVPLDSDGSPFLYSLKLVKDS 444
Db 233 EQAKDKVSLTCTMTIDFPFEDITVEWQWNGQPAENYKNTQPIINMTNGSYFVYSKLVNPKS 292
QY 445 RWQGNVFSQSVNHEALHNHYTOKSLSLSPGK 476
Db 293 NWEAGNTFTCSVLHLEGLHNHHHTKSLSHSPGK 324
RESULT 10
GCL_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```
QY 371- QPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD 430
Db 185 QPREPOVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVEWESGQPENNYKTPPVLDSD 244
QY 431 GSFYLYSKLTVDSKRWQGNVFCSCVMHEALHNHYTKQSLSPGK 476
Db 245 GSFYLYSKLTVDSKRWQGNVFCSCVMHEALHNRYTKQSLSPGK 290

RESULT 7
GCL_RAT ID_GCL_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RL "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 92
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 44.5%; Score 1148; DB 1; Length 326;
Best Local Similarity 63.1%; Pred. No. 5.7e-74;
Matches 210; Conservative 52; Mismatches 61; Indels 10; Gaps 4;

QY 147 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 206
Db 1 AETAPSVYPLAPGALTKNSMTVTLGCLVKGYFPEPTVWNSGALSSGVHTFPAVLQ-S 59

QY 207 GLYSLSVTVTPSSSLGTQYICNVNHNKSPNTKVDKKAEPKSCDKTHTCPPELPGG 266
Db 60 GLYTLTSSVTPSSSTPQSVTCNVNHNKSPNTKVDKKAEPKSCDKTHTCPPELPGG 113

QY 267 ---PSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNVDGVVEVHNAKTPREE 323
Db 114 SEVSSVFIFPPKPKDVLITLTAKVTVVDVDSQDDPEVHFSWFDVDDVEVHTAQTPEE 173

QY 324 QYNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPS 383
Db 174 QFNSTFRVSSELPILHQLDWLNGRTFRCKVTSAAFPSPIEKTIKPEGRQVPHVYTMSTP 233

QY 384 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLTVDK 443
Db 234 KEEMTQNEVSTCWVGFYPPDIYVEWQMNGQPQENYKNTPTPTMDTDGSFYLYSLKLVKK 293
```

```
QY 444 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 476
Db 294 EKWQGNVTCFVSLHGLHNHHTKSLSHSPGK 326

RESULT 8
GCB_RAT ID_GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RL "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; IGc1; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 44.3%; Score 1142.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 1.4e-73;
Matches 214; Conservative 44; Mismatches 69; Indels 9; Gaps 3;

QY 147 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 206
Db 1 AQTAPSVYPLAPGCGDTTSSTVTLGCLVKGYFPEPTVWNSGALSSDVHTFPAVLQ-S 59

QY 207 GLYSLSVTVTPSSSLGTQYICNVNHNKSPNTKVDKKAEPKS-----CDKTHTCPPEA 260
Db 60 GLYTLTSSVT---SSTWPSQVTCNVNHNKSPNTKVDKKAEPKSGIGHKCTPTCTCHKCPV 117

QY 261 PELGGPSVFPLPKDLMISRTPEVTCVVDVSHEDPEVKFNVDGVVEVHNAKTKP 320
Db 118 PELGGPSVFIFPPKPKDILLISQNAKVCVVVDVSEEDPQVSWFNNVEVHTAQTQP 177

QY 321 REEQNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 380
Db 178 REEQNSTFRVSVLPIQHQDWMSGKFKCKVNNKALPSPIEKTISKPKGLVLRKPQVYVM 237

QY 381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLT 440
Db 238 GPTEQLTEQVTSVTLCTSLTSGPLNDIGVETNSGHIENKYNKTEPVMDSGSPFFMYSLN 297

QY 441 VDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 476
Db 298 VERSRWDSRAFCVSVVHGLNHNHVEKSLSRPFGK 333
```



```

DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> V (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 Y -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 47.6%; Score 1226.5; DB 1; Length 323;
Best Local Similarity 69.7%; Pred. No. 1.7e-79;
Matches 228; Conservative 34; Mismatches 58; Indels 7; Gaps 2;

QY 150 KGPSVFLPSSKSTGGTAALGCLVKDYPPETVTSWNSGALTSGVHTFPFPAVLQSSGLY 209
DB 4 KASVFPFLAPCCGDTSSVTGLCLVKGYLPEPVTVWNSGTLTGVRTPFSPVQSSGLY 63
QY 210 SLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSV 269
DB 64 SLSSVSVTSSS---QPVTNCVAHPATNTKVDKTVAPSTCSK---PTCPPELLGGPSV 116
QY 270 FLPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNSNY 329
DB 117 FIFPPKDTLMISRTPEVTCVVVDVSDPDPEVQFTWYINNEQVARTARPPRLREQPNSTI 176
QY 330 RVSVLTTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 389
DB 177 RVSTLTPIHQDLRGLKEFKCKVKHKNALPAPIEKTISKARGQPLEPKVYTMGPPREELSS 236
QY 390 NQVSLTCLVKGFPSDIATVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKRWQOG 449
DB 237 RSVSLACMNGFPPSDISVEWENKNGKAEDNYKTTTPAVLSDGSFYFLYLNKLSVPTSEWQRG 296
QY 450 NVFSCSVMEALHNHYTQKSLSLSPGK 476
DB 297 DVFTCSVMHEALHNHYTQKSISRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K.; Hussan Q.Z.; Cebra J.J.;

```

```

RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J.; Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E.; Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M.; Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B.; Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 47.1%; Score 1212.5; DB 1; Length 329;
Best Local Similarity 70.1%; Pred. No. 1.6e-78;
Matches 234; Conservative 28; Mismatches 63; Indels 9; Gaps 4;

QY 146 SASTKGPSVFPLAPSSKSTGGTAALGCLVKDYPPETVTSWNSGALTSGVHTFPFPAVLQS 205
DB 1 SARTTAPSVFPLAASCVDTSMMTLGCLVKGYFPEPVTVKNWSGALTSGVHTFPFPAVLQ- 59
QY 206 SGLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKAEPKSCDKTH--TCPPCPAPEL 263
DB 60 SGLYSLSVTVTPSSSQAT----CNVAHPASSTKVDKTVPEIPTP2BPBCTCPCPCPPEN 115
QY 264 LGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 323
DB 116 LGPSVFIFFPKPKDTLMISLTPTVTCVVVDVSDPEVQFTWYINNEQVARTARPPRLREQPNSTI 175
QY 324 QYNSTYRVVSVLTVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 383

```

16-OCT-2001 (Rel. 40, Last annotation update)
IG gamma-4 chain C region.
IGHG4.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=8115104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
[2]
SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSP; P01842; 7FAB.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGHG4; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98
FT CH1.
FT DOMAIN 99 110
FT HINGE.
FT DOMAIN 111 220
FT CH2.
FT DOMAIN 221 327
FT CH3.
FT INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 14 14
FT DISULFID 27 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106
FT DISULFID 109 109
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811BF208E7A CRC64;

Query Match 61.6%; Score 1586.5; DB 1; Length 327;
Best Local Similarity 90.6%; Pred. No. 6.9e-105;
Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

QY 147 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSMNSGALTSGVHTFPAVLQSS 206
DB 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSMNSGALTSGVHTFPAVLQSS 60

QY 207 GLYSLSSVTVPSSSLGITTYICNVNHSNTKVDKAEKPCDKTHCPCPAPELLGG 266
DB 1 GLYSLSSVTVPSSSLGITTYICNVNHSNTKVDKAEKPCDKTHCPCPAPELLGG 117

QY 267 PSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVN 326
DB 1 PSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVN 177

QY 327 STYRVSVLTVLHQDLNGKEYCKVKSNKALPAPIETKISKAKGPQRPVQVYTLPPSRDE 386
DB 1 STYRVSVLTVLHQDLNGKEYCKVKSNKALPAPIETKISKAKGPQRPVQVYTLPPSRDE 117

Db 178 STYRVSVLTVLHQDLNGKEYCKVKSNKALPAPIETKISKAKGPQRPVQVYTLPPSRDE 237
QY 387 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 446
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 297
QY 447 QGQNVFSCSVMEALHNYHTQKSLSPGK 476
Db 298 QGQNVFSCSVMEALHNYHTQKSLSPGK 327

RESULT 4
GC RABIT ID GC RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (in) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
CC -I- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
MARKERS AND REF.5 THE E15 MARKER.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; M16426; AAA31289.1; --
DR PIR; A02161; GHRB.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.

OX NCBF_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obara M., Nikaide T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IGG2 heavy chain: genetic,
evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
domains of a human IGG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
RN [11]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00230; AAB59393.1; -.
DR PIR; A02148; G2HU.
DR HSSP; P01857; 1FC1.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147110; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGH1; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
SQ SEQUENCE 326 AA; 35884 MW; 8310878C687CF9C CRC64;

Query Match 62.1%; Score 1600; DB 1; Length 326;
Best Local Similarity 90.9%; Pred. No. 7.7e-106;
Matches 300; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

Qy 147 ASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 206
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60

Qy 207 GLYSLSVTVTPSSSLGTQYICNNHKPSNTKVDKABPKSCDKTHTCPCPAPPELLGG 266
Db 61 GLYSLSVTVTPSSNFGTQYTCNVDPKPSNTKVDKVERKCCVE---CPPCAPP-VAG 116

Qy 267 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
Db 117 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVGFNWIYVDGVEVHNAKTKPREEQFN 176

Qy 327 STYRWVSVLTVHLDWLNKGEYCKVCKSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 386
Db 177 STFRVSVLTVHLDWLNKGEYCKVCKSNKGLPAPIETISKTKGQPREPQVYTLPPSRDE 236

Qy 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 446
Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 296

Qy 447 QQQNVFSCSVNHEALHNHYTQKSLSLSPGK 476
Db 297 QQQNVFSCSVNHEALHNHYTQKSLSLSPGK 326

RESULT 3
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPE MARKER, 97-K, & THE
CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
CC MARKER & THE GIM (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR Genew; HGNC:5525; IGHG1.
DR MIM; 147100; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGCL; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT STRAND 123 126

FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT STRAND 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT STRAND 238 240
FT HELIX 241 242
FT TURN 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT STRAND 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770BE106C2FA33D CRC64;
Query Match 68.4%; Score 1763; DB 1; Length 330;
Best Local Similarity 99.7%; Pred. No. 2.5e-117;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 207 GLYSLSVVTVVPSSSLGTOTYICNVNHPKSTNTKVKKAEPKSCDKHTHTCPPCPAPPELLGG 266
DB 61 GLYSLSVVTVVPSSSLGTOTYICNVNHPKSTNTKVKKAEPKSCDKHTHTCPPCPAPPELLGG 120
QY 267 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
DB 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 327 STYRVVSVLTVHLQDWLNQKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
DB 181 STYRVVSVLTVHLQDWLNQKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 387 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 446
DB 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
DB 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
RESULT 2
GC2 HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01559;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 11.3492 Seconds
(without alignments)
1739.566 Million cell updates/sec

Title: US-09-758-173-4

Perfect score: 2577

Sequence: 1 MKHLWFLLLVAAPRWLSQ.....MHEALHNYTQKSLSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1763	68.4	330	1 GCI_HUMAN	P01857 homo sapien
2	1600	62.1	326	1 GCI_HUMAN	P01859 homo sapien
3	1586.5	61.6	327	1 GC2_HUMAN	P01861 homo sapien
4	1226.5	47.6	323	1 GC_RABIT	P01870 oryctolagus
5	1122.5	47.1	329	1 GC2_CAVPO	P01862 cavia porce
6	1157	44.9	290	1 GC3_HUMAN	P01860 homo sapien
7	1148	44.5	326	1 GCI_RAT	P02759 rattus norv
8	1142.5	44.3	323	1 GCB_RAT	P02761 rattus norv
9	1138	44.2	324	1 GCI_MOUSE	P01868 mus musculu
10	1137	44.1	329	1 GCI_MOUSE	P22436 mus musculu
11	1133	44.0	393	1 GCIM_MOUSE	P01869 mus musculu
12	1126	43.7	398	1 GC3M_MOUSE	P03987 mus musculu
13	1122	43.5	330	1 GCAA_MOUSE	P01863 mus musculu
14	1119.5	43.4	335	1 GCAB_MOUSE	P01864 mus musculu
15	1117	43.3	399	1 GCAM_MOUSE	P01865 mus musculu
16	1114.5	43.2	329	1 GCC_RAT	P20762 rattus norv
17	1108	43.0	322	1 GCA_RAT	P20760 rattus norv
18	1085	42.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	41.9	405	1 GC3M_MOUSE	P01867 mus musculu
20	489	19.0	428	1 EPC_HUMAN	P01854 homo sapien
21	483.5	18.8	429	1 EPC_RAT	P01855 rattus norv
22	468	18.2	146	1 HVZ1_HUMAN	P06331 homo sapien
23	465	18.0	421	1 EPC_MOUSE	P06336 mus musculu
24	442	17.2	454	1 MUC_HUMAN	P01871 homo sapien
25	441.5	17.1	455	1 MUC_MOUSE	P01872 mus musculu
26	437	17.0	458	1 MUC_RABIT	P03988 oryctolagus
27	431.5	16.7	476	1 MUCM_MOUSE	P01873 mus musculu
28	427	16.6	479	1 MUCM_RABIT	P04221 oryctolagus
29	425	16.5	457	1 MUC_SUNMO	P20768 suncus muri
30	420	16.3	450	1 MUC_CANFA	P01874 canis fami
31	415.5	16.1	454	1 MUC_MESAU	P06337 mesocricetu
32	403	15.6	391	1 MUCB_HUMAN	P04220 homo sapien
33	394	15.3	438	1 HVCS_HETFR	P23087 heterodontu

ALIGNMENTS

```

RESULT 1
GCI_HUMAN
ID GCI_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
chymotryptic peptides of the H-chain, alignment of the tryptic
peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.

```

P23084 heterodontu
P23085 heterodontu
P23088 heterodontu
P01876 homo sapien
P20758 gorilla gor
P01877 homo sapien
P01824 homo sapien
P23086 heterodontu
P01825 homo sapien
P01822 mus musculu
P18531 mus musculu
P01878 mus musculu

34 390.5 15.2 370 1 HVC1_HETFR
35 386.5 15.0 438 1 HVC2_HETFR
36 385 14.9 461 1 HVC3_HETFR
37 383.5 14.9 353 1 ALC1_HUMAN
38 380.5 14.8 353 1 ALC1_GORGO
39 379 14.7 340 1 ALC2_HUMAN
40 371 14.4 129 1 HV2F_HUMAN
41 362.5 14.1 393 1 HVC3_HETFR
42 361 14.0 117 1 HV2G_HUMAN
43 356.5 13.8 137 1 HV46_MOUSE
44 355 13.8 116 1 HV60_MOUSE
45 344 13.3 344 1 ALC_MOUSE

```
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 36.8%; Score 948.5; DB 4; Length 597;
Best Local Similarity 37.7%; Pred. No. 5.1e-70;
Matches 222; Conservative 75; Mismatches 169; Indels 123; Gaps 20;

QY 1 MKHLWFFLLVAAPRWLSQVKLQWGGGLLOPSETLSRTCTVSGGSGISGYVYWTWIRQT 60
DB 1 MKHLWFFLLVAAPRWLSQVKLQWGGGLLOPSETLSRTCTVSGGSGISGYVYWTWIRQT 60
QY 61 PGRGLEWIGHIYVNGCATTYNPSLSKRVTSIKDTSKNQFFLNLSVTDADTAVYYCAR-- 118
DB 60 PGKGLEWIGEINHSG-ITNYPNLSKRVTSIVDTSKQSLSLSSVNAADTAVYYCARVI 118
QY 119 ---GPRPDCTTICYGWVDVWGPGDLVTSSASTKGPSVFPLAPSSKSTSG-GTAAALGCL 174
DB 119 TRASPQTDGR---YG-MDVWGQGTITVSSGSASAPTLFPLVSCENSPSDTSSVAVGCL 173
QY 175 VKDYFPEPVTVSW--NSGALTSQVHTFPVAVLOSSGLYSLSSVTVVPSSSL--GTQTY-IC 229
DB 174 AQDFLPDSITFSWKYKNNSDISSTRGFPVLR-GGKYAATSQVLLPSKDVMOGTDHVVVC 232
QY 230 NVNHKPSN-----TKVDKKAEPKS-----CDKTHTCP----- 256
DB 233 KVQHPNGNKEKNVPLVIAELPPKVSFVPRDGFNGNPKSKLICQATGSPRQIQVSW 292
QY 257 -----PCPAPELLGGPS----- 268
DB 293 LREGKQVSGVTTDQVQAEAKESGPTTKVYKVTSTLTIKESDWLSQSMFTCRVDRHGLTFQ 352
QY 269 -----VFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 313
DB 353 NASSMCMVPDQDAIRVFAIPPS-FASIFLTSTKTLCLVTLDTLTYD-SVTISWTRQGEA 410
QY 314 HNAKTKPREQNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGP- 372
DB 411 VKHTNISESHNPATFSVGEASICEDDWSGERFTCTVHTDLPSPKQIISRPKGVALL 470
QY 373 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVL 428
DB 471 HRPDVYLLPAREQLNRESAITCLVTGFSADVFQVMQMGQPLSPKQVTSAPMPEP 530
QY 429 -SDGSEFFLYSKLTVDKSRWQQGNVSCSWMEALHNHYTQKSLSLSPCK 476
DB 531 QAPGRYFAHSILTVSEEMNTGETYTCVVAHEALPNRVTERTVDSKSTGK 579

RESULT 15
Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 64.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIMPH;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
```

Search completed: March 29, 2003, 09:14:37
Job time : 46.1716 secs

DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 FT NON_TER 1
 SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 49.0%; Score 1262.5; DB 6; Length 337;
 Best Local Similarity 69.2%; Pred. No. 2.3e-96;
 Matches 234; Conservative 42; Mismatches 53; Indels 9; Gaps 3;

QY 147 ASTKGPSVFLPAPSSKSTSGTAAAGLCLVDFPEPVTYVSNWNGALTSVGHVTPPAVLQSS 206
 DB 1 ASITAPKVFALACGCTTSSTVALGCLVSGYFPEPKVSNWNGSLTSVGHVTPPAVLQSS 60

QY 207 GLYSLSSVTVPPSSLGSTQTYICNVNHPKNTKVDKAE-----KSCDKTHTCPPCA 260
 DB 61 GFYSLSSMTVPASTWTSETYICNVVHAASNFVKDKRIEIPDNHVKVCDMS-KCPKCPA 119

QY 261 PELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTP 320
 DB 120 PELLGGPSVFIFPNPKDITLMITRTPEVTCVVVDVSHEDPEVKFNWYMDGVEVRTATTP 179

QY 321 REQYNSTYRWVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPREPOVYTL 380
 DB 180 KERQFNSTYRWVSVLRHQDWLNGKGFCKVNNQALPQDIERTITTKRSGEPQVYVL 239

QY 381 PPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLDSDGSFFLYSK 438
 DB 240 AHPDELKSKSVTCLVKDFYPPENIEWQSQNGQPELETKYSTTQAQDSDGSFFLYSK 299

QY 439 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 476
 DB 300 LSVDRNRWQGGTFTTCVSMHEALHNHYTQKNVSKNPGK 337

RESULT 13
 Q9BU10 PRELIMINARY; PRT; 597 AA.

ID Q9BU10
 AC Q9BU10; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 65.3 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPH;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002963; AA02963.1; -.
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003600; Ig.like.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 5.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 4.
 DR SMART; SM00406; IG; 1.
 DR SMART; SM00410; IG like; 1.
 KW PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 597 AA; 65274 MW; 2DFA8FB7B055851 CRC64;

Query Match 36.9%; Score 950.5; DB 4; Length 597;
 Best Local Similarity 37.7%; Pred. No. 3.5e-70;
 Matches 222; Conservative 76; Mismatches 168; Indels 123; Gaps 20;

QY 1 MKHLWFFLLVAAPRWLSQVLQOQMGAGLLKPSSETLSLTCGVGGSGFSG-YVWSWIRQP 59
 QY 61 PGRGLEWIGHYGNAGATTNPNPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYCAR-- 118
 DB 60 PKGLEWIGEINHSG-STNPNPSLKSRTVTSKDTSKNQSLKLSVNAADTAVYCARV 118

QY 119 ---GRRPDCCTTCYGGWVDVNGPDLVTVSSASTKGRSPVFPPLAPSSKSTSG-GTAAALGCL 174
 DB 119 TRASPGETDGR---YG--MDVWGQGTTVTVSSGSASAPTLFPLVSCENSPTSSTSSAVAGCL 173

QY 175 VKDYFPEPVTYSM--NSGALTSVGHVTPPAVLQSSGLYSLSSVTVVPSSSL--GTQTY-IC 229
 DB 174 AQDFLPDSITFSWKYKNNSISSTRGFPFSLR-GGKYAATSQVLLPSKDVNQGTDEHVVC 232

QY 230 NVNHPKPS-----TKVDKKAEPKS-----CDKTHTCP----- 256
 DB 233 KVQHPNGNKEKNVPLPVIAELPPKVSFVFPDRDFFGNPKSKLICATGFSRQIQVSW 292

QY 257 -----PCPAPELLGGPS----- 268
 DB 293 LREGKQVSGVTTDQVQAEAKESGFTTYKVTSTLTIKESDWLSQSMFTCRVDHRLTFQ 352

QY 269 -----VFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 313
 DB 353 NASSNCVDPDQTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTYYD-SVTISWTRQNGEA 410

QY 314 HNAKTKPREQYNTYRWVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQP- 372
 DB 411 VKTHNTISESHPNATFSAVGEASICEDDWSGERFTCTVHTDLPSPKQTISRPKGV 470

QY 373 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLD- 428
 DB 471 HRPDVYLLPPAREQNLRESATITCLVTGFPADVFQWMQGOPLSPKQVTSAPMPEP 530

QY 429 -SDGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 476
 DB 531 QAPGRYFAHSILTVSBEWNTGETYTCVVAHEALPNRVTERTVTDKSTGK 579

RESULT 14
 Q9BQB8 PRELIMINARY; PRT; 597 AA.

ID Q9BQB8
 AC Q9BQB8; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Unknown (protein for MGC:1905) (protein for MGC:1228).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AA06180.1; -.
 DR EMBL; BC001872; AA01872.1; -.
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003600; Ig.like.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 5.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 4.

QY 1 MKHLWFFLLVAAPRWLSQVLQOQMGAGLLKPSSETLSLTCGVGGSGISGYYVWTWIROT 60

Ds 400 LNVQSNWEAGNTFTCSVLHGLHNNHTEKNLSHSPGK 437

RESULT 8

Q99L25 ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC03888; AAH0388.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 53.7%; Score 1383.5; DB 11; Length 473;

Best Local Similarity 55.3%; Pred. No. 3.5e-106;

Matches 269; Conservative 71; Mismatches 123; Indels 23; Gaps

7;

QY 1 MKHLWFLLLVAAPRWLSQVQLQWQEGLLQPSSETLSRTCVVSGSISGYIYWT-----YTFTDHTIH 54
DB 1 MENSWFLEPLSVTTGVHSQVQLQSDAELVKGASVKISCKVSG-----YTFTDHTIH 54
QY 56 WIRQTGRLGLEWTHGYNGATTNNPSLKSRTISKTSKNQFFLNLSVTDADTAVYY 115
DB 55 WVKRPEQGLEWIGYIYPRDGTSTKYNKPKGKATLTADKSSSTAYMQLNSLTSEDSAVCF 114
QY 116 CARGPRDCTTCYGV--GHVDVWPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALG 172
DB 115 CSRG-----GSIYGYGLYFDYWGQGTITVSSAKTTPSVPLAPVCGDITGSSVILG 169
QY 173 CLVKDYFPEPTVWMSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN 232
DB 170 CLVKGYFPEPTVLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQITCNVA 228
QY 233 HKPSNTKVKDKKABPKSCDKTHTCPP--CPAPELLGSPSVLPFPKPKDTLMISRPEVTC 290
DB 229 HPASSTKVKDKKIEPRG-PTIKPCPCPCAPNLLGGPSVFIFPPKIKDVLMISSLSPMVC 287
QY 291 VVVDVSHEDPEVKFNWVDCGEVHNNAKTKPREOYNSTYRVSVLTVLHODWLNKGEYK 350
DB 288 VVVDVSEDDPDVQISWPFVNNVEVHTAQTHREDYDINSTLRVVSALFIQHDWMSGKEFKC 347
QY 351 KVNKALPAPIETISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEM 410
DB 348 KVNKALPAPIETISKPKGSVRAPQVYVLPPEEETKKQVTLTCWVTFDFPEDIYVEW 407
QY 411 ESNQGPENNYKTPPVLDSGSPFLYSKLTVDKSRVQOQGNVFCSCVMHEALHNNHYTKSL 470
DB 408 TNGKTELNYKTEPVLDSGSPFYMSKLRVEKKNVERNSSCYSVVHGLHNNHHTKSF 467
QY 471 SLSPGK 476
DB 468 SRTPGK 473

RESULT 9

Q91Z05 ID Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 51.7%; Score 1333.5; DB 11; Length 473;

Best Local Similarity 54.0%; Pred. No. 4.9e-102;

Matches 259; Conservative 72; Mismatches 124; Indels 25; Gaps

7;

QY 7 FLLLVAAAPRWLSQVQLQWQEGLLQPSSETLSRTCVVSGSISGYIYWTWIRQTGRLGLE 66
DB 9 FLVLIL--KGVCQEVQLVSGGLVKGPSRKLSCAASGFTFSD-YGMHVRQAPKGLGLE 65
QY 67 WIGHYNGATTNNPSLKSRTISKTSKNQFFLNLSVTDADTAVYYCARGPRDCTT 126
DB 66 WVAVYNSGSTTIYYADTVKGRFTISRDNKNTLFLQWTSLSRSEDATMYCAREL----- 119
QY 127 ICYGM--VDVWPGDLVTVSSASTKGPSVFPPLAPSSKSTSGTAALGCLVKDYFPPEV 183
DB 120 -----WLRIDYWGQGTITVSSAKTTPSVYIPLAPCGDITGSSVTLGCLVKGYFPESV 174
QY 184 TVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKK 243
DB 175 TVWNSGSLSSVHTFPALLQ-SGLYTMSSSVTVTPSPSTQVTCVAHPASSTTVDDKK 233
QY 244 AEPKSCDKT-HTCAPP-----CPAPELLGSPSVLPFPKPKDTLMISRPEVTCVVDVS 296
DB 234 LEPSGPITINPCPCPKCKECHKCAPNLEGSPSVIFPPNKKDVLMISSLTPKVTCTVVDVS 293
QY 297 HEDPEVKFNWVDCGEVHNNAKTKPREOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKA 356
DB 294 EDDPDVQISWPFVNNVEVHTAQTHREDYDINSTLRVVSALFIQHDWMSGKEFKCKVNNKD 353
QY 357 LPAPIETISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQP 416
DB 354 LPSPIERTISKIKGLVRAPQVYVLPPEAEQLSRKDVSLTCLVWGFNPGDISVEWTSNGHT 413
QY 417 ENNYKTPPVLDSGSPFLYSKLTVDKSRVQOQGNVFCSCVMHEALHNNHYTKSLSPGK 476
DB 414 EENYKTDAPVLDSGSPFYISKDKTSKWEKTDSPFCNVRHGLKNYLYLKTISRSPGK 473

RESULT 10

Q8R3H6 ID Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)


```
GN IGH-4.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RX (1)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 55.2%; Score 1423.5; DB 11; Length 463;
Best Local Similarity 54.8%; Pred. No. 1.7e-109;
Matches 262; Conservative 84; Mismatches 115; Indels 17; Gaps 6;

QY 1 MKHLWPELLLVAAAPRWVLSQVQLQOMGEGILQPSSETLSRTCTVVGSGSISGYVYWTWIRT 60
DB 1 MEWIFLFLSCTAGVHSQVQLQSGAELRPGASVRLSCASGTFYTGYGV-SNVKQR 59
QY 61 PGRGLEWIGHYNGATTNPNLSKRVTSKDTSKNQFFLNLSVTDADTAVVYCARGP 120
DB 60 TGOGLEWVGIYSGSGNTYYSEKFGKATLTIDKSSSTAYMHLSSLTSEDSAVYFCARS 119
QY 121 RPDCTTCYGGWVDVWGPGDLVTVSSASTKGPSVFLPAPSKTSKGTALGLVVDYFP 180
DB 120 YSYVDLPA-----WGQGLVTVSAKTTTPSVYPLAPGSAQAATNSMTVLGLVKGYFP 173
QY 181 EPTVSNNSGALTSGVHTFPVAVLQSSGLSLSSVTVVPSSSLGTQTVICNVNHPKNTKV 240
DB 174 EPTVTWNSSGLSSGVHTFPVAVLQSD-LYTLSSSVTVVPSSTPSETVTCNVAHPASSTKV 232
QY 241 DKAEPKSCDKTHTCPP--CPAPELLGSPVFLPAPSKTSKGTALGLVVDYFP 298
DB 233 DKKIVPRDGG---CKPCITVPEV---SSVFIPLPKPKDVLTLITLPKVICVVVDISKD 285
QY 299 DPEVKFNWYDGVVEVHNAKTPREEQNVSTYRVSVLTVLHODWLNKGEYCKKVSNAKLP 358
DB 286 DPEVQFSWVDVDEVHTAQTPREEQNSTFRSVELPIHQDWLNKGEYCKRVNSAAPP 345
QY 359 APIEKTISKAKGPQEPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVWESNGOPEN 418
DB 346 APIEKTISKGRPKAFQVYTPPEQMAKDKVSLTCMITDFEPEDITVEWQMGQPAE 405
QY 419 NYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTKQSLSPGK 476
DB 406 NYKNTQPIMDTGSFYFYSKLVNQKSNWEAGNTFTCSVLHLEGLHNHHHTKSLSHSPGK 463

RESULT 5
Q99LJ31 PRELIMINARY; PRT; 468 AA.
ID Q99LJ31
AC Q99LJ31
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 54.5%; Score 1405; DB 11; Length 468;
Best Local Similarity 56.7%; Pred. No. 5.7e-108;
Matches 271; Conservative 65; Mismatches 130; Indels 12; Gaps 5;

QY 1 MKHLWPELLLVAAAPRWVLSQVQLQOMGEGILQPSSETLSRTCTVVGSGSISGYVYWTWIRT 60
DB 1 MKCSWVIFFLMAVVGIVNSEYVQLQSGAELRPGASVKLSCSTAGFNKID-SLMHMYKQR 59
QY 61 PGRGLEWIGHYNGATTNPNLSKRVTSKDTSKNQFFLNLSVTDADTAVVYCARGP 120
DB 60 PEGGLEWIGWIDPEDGETKYAPKQDKATITADTSSNTAYLQLSLTSSETAIYYCAR-- 117
QY 121 RPDCTTCYGGWVDVWGPGDLVTVSSASTKGPSVFLPAPSKTSKGTALGLVVDYFP 180
DB 118 -----NLLGYGYDYGQGTITTVSSAKTTAPSVYPLAPVCGDITGSSVTILGLVKGYFP 172
QY 181 EPTVSNNSGALTSGVHTFPVAVLQSSGLSLSSVTVVPSSSLGTQTVICNVNHPKNTKV 240
DB 173 EPTVTWNSSGLSSGVHTFPVAVLQSD-LYTLSSSVTVVPSSTPSETVTCNVAHPASSTKV 231
QY 241 DKAEPKSCDKTHTCPP--CPAPELLGSPVFLPAPSKTLMISRTPEVTCVVVDVSHS 298
DB 232 DKKTEPRG-PTIKCCPCKCPAPNLLGGPSVFIPLPKIKDVLMLSLSPMVTCCVVVDVSED 290
QY 299 DPEVKFNWYDGVVEVHNAKTPREEQNVSTYRVSVLTVLHODWLNKGEYCKKVSNAKLP 358
DB 291 DEDVQISWFNANNEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALP 350
QY 359 APIEKTISKAKGPQEPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVWESNGOPEN 418
DB 351 APIERTISKPKGSRAPQVYVLPPEEEMTKKQVTLTCWVTFDMPEDYVVEWTNNGKTEL 410
QY 419 NYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTKQSLSPGK 476
DB 411 NYKNTPEVLDSDGSFYFYSKLVNKKVSKLVEKKNVERNYSVCSVVHLEGLHNHHHTKFSRTPGK 468

RESULT 6
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1810060009Rik protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
```



```
Db 180 VSNWNGALTSVGHVTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKV 239
QY 245 EPKSCDKTHTCPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 304
Db 240 EPKSCDKTHTCPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 299
QY 305 NWYVDGVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 364
Db 300 NWYVDGVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 359
QY 365 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 424
Db 360 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 419
QY 425 PVLDSGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
Db 420 PVLDSGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 471

RESULT 2
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 78.3%; Score 2017; DB 4; Length 473;
Best Local Similarity 81.3%; Pred. No. 1.2e-158;
Matches 388; Conservative 29; Mismatches 48; Indels 12; Gaps 4;

QY 1 MKHLNFFLLVAAPRWLSQVKLQWGGGLQPSSTLRTCVWGGSI-SGYYYWTWIRQ 59
Db 8 MKHLNFFLLVAAPRWLSQVKLQWGGGLQPSSTLRTCVWGGSI-SGYYYWTWIRQ 67
QY 60 TPGRCLEWIGHYNGATNYPNLSKRVTSKDTSKNQFFLNLSVTDADTAVYYCARG 119
Db 68 PPGKGLEWIGTINFSG-NMYYSPLSRVMTMSADMSNSFYLKLDVSTAADTAVYYCAAG 126
QY 120 PRPDCTTCYGGWVDVWGPGLVTVSSASTKGPSVFLPAPSSKSTSGTAAIGCLVKDYF 179
Db 127 H-----LVMGFGAHWGQGLVSVSPASTKGPSVFLPAPCSRSTSTSGTAAIGCLVKDYF 179
QY 180 PEPVTVSNWNGALTSVGHVTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTK 239
Db 180 PEPVTVSNWNGALTSVGHVTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTK 239
QY 240 VDKKAEPSCKDTHTCPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHED 299
Db 240 VDKRVESK---YGPSPCSPAPEFLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSDQED 296
QY 300 PEVKNFNVYDGVVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
Db 297 PEVQNFNVYDGVVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPS 356
QY 360 PIEKTIISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
Db 357 SIEKTIISKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 416
QY 420 YKTPPPVSDSGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
```

```
Db 417 YKTPPPVSDSGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 3
Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024405; AAH24405.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 55.5%; Score 1429; DB 11; Length 469;
Best Local Similarity 56.0%; Pred. No. 5.9e-110;
Matches 270; Conservative 78; Mismatches 110; Indels 24; Gaps 9;

QY 4 LWF-FLLLVAAAPRWLSQVKLQWGGGLQPSSTLRTCVWGGSI-SGYYYWTWIRQTS 62
Db 3 LWNLFVFLVTLNGIOCEVNLVESGGGLVQPGGSLRLSCAASGFTFD-YVMSWVRQPG 61
QY 63 RGLIEWIGHI--YONGATTNYPNLSKRVTSKDTSKNQFFLNLSVTDADTAVYYCARG 120
Db 62 KALEWLGFIIRNKANGYTTSEYASVKGRFTISRDNSQSIYLNQNALRAEDSATYYCARD 121
QY 121 RPDG---TTICVGGWVDVWGPGLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVK 176
Db 122 RSSYYYSYSGTSFAY-----WGQTLTVVSAKTTTPSVVYPLAPGSAQTNSMVTGCLVK 175
QY 177 DYPEPPTVSNWNGALTSVGHVTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPK 236
Db 176 GYPEPPTVSNWNGALTSVGHVTFPAVLQSD-LYTLSSSVTVPSSTWPSQTVTCNVAHPAS 234
QY 237 NTKVDKKAEPKCDKTHTCPP--CPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVD 294
Db 235 STKVDKKIIVPRDGG---CKPCICTVPEV---SSVFIPEPPKPKDVLITLTPEKVTGVVD 287
QY 295 VSHEDPEVKNFNVYDGVVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSN 354
Db 288 ISKDDPEVQFSFVDDVEVHTAQTAPREEOFNSTFRSVSELFIMHQDWLNGKEFKCRVNS 347
QY 355 KALPAPIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 414
Db 348 AAPAPAPIEKTISKGRPKAPQVYTIPTPPKEQMAKDKVSLTCMTIDFFPEDITVEWQNG 407
QY 415 QPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSP 474
Db 408 QAENYKNTQPIINDIDGYSFYVSKLVNOKSNWEAGNTFTCSVLHGLNHNHHTKSLSHSP 467
QY 475 GK 476
Db 468 GK 469

RESULT 4
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 181006009 gene.
```

GenCore version 5.1.4_p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 43.1716 Seconds
(without alignments)
2271.829 Million cell updates/sec

Title: US-09-758-173-4
Perfect score: 2577
Sequence: 1 MKHLFFLLVAAPRWLSQ.....MHEALNHYTKSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2041.5	79.2	471	4	Q8TC77
2	2017	78.3	473	4	Q8TC63
3	1429	55.5	469	11	Q8R3V9
4	1423.5	55.2	463	11	Q99JLC4
5	1405	54.5	468	11	Q99L31
6	1403.5	54.5	473	11	Q99DL4
7	1389.5	53.9	437	11	Q99LA4
8	1383.5	53.7	473	11	Q99L25
9	1333.5	51.7	473	11	Q91Z05
10	1325	51.4	474	11	Q8R3H6
11	1268	49.2	701	4	Q96P08
12	1262.5	49.0	337	6	Q95W34
13	950.5	36.9	597	4	Q9BU10
14	948.5	36.8	597	4	Q9BQ88
15	940.5	36.5	588	4	Q8WUX4
16			618	4	Q96AA6

17	931	36.1	613	4	Q96EY0
18	856	33.2	496	4	Q96KX8
19	745.5	28.9	597	4	Q96BB9
20	727.5	28.2	479	11	Q99M22
21	719	27.9	613	11	Q8VCX7
22	718	27.9	613	4	Q8WUK1
23	712	27.6	278	11	Q921K1
24	691.5	26.8	614	4	Q96GA6
25	688	26.7	482	11	Q91X92
26	665	25.8	494	4	Q96K68
27	651	25.3	496	4	Q96DK0
28	640	24.8	500	4	Q9BRV0
29	632	24.5	488	11	Q91WR1
30	631.5	24.5	497	4	Q99KA4
31	630.5	24.5	497	4	Q8WY24
32	629.5	24.4	481	11	Q91WT1
33	625	24.3	486	11	Q91Z07
34	621.5	24.1	481	11	Q8VCV5
35	620.5	24.1	479	11	Q91WP5
36	618.5	24.0	484	11	Q8VEA0
37	617.5	24.0	480	11	Q91XE1
38	607.5	23.6	481	11	Q91WT3
39	600.5	23.3	489	11	Q8VCX4
40	584	22.7	416	4	Q9NP66
41	578	22.4	484	11	Q99LA6
42	509	19.8	573	4	Q8WU38
43	506.5	19.7	150	4	Q95973
44	504.5	19.6	426	11	Q9DCD9
45	457	17.7	384	4	Q9UP60

ALIGNMENTS

RESULT 1
Q8TC77
ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match	79.2%	Score	2041.5	DB	4	Length	471
Best Local Similarity	82.8%	Pred. No.	1.1e-160				
Matches	391	Conservative	22	Mismatches	52	Indels	7
Gaps							4
QY	5	WFLLVLAAPRWLSQVKLQWEGGLQPSLTSRTCTVVGSGISGYYTWTWIRQPGRG	64				
Db	7	WVF--LVALEGVQCEVQLVESGGGLVKGSGSLRSCAASGFTFSS-YSMNVWRQAPGKG	63				
QY	65	LEWIGHYNGATTTNNPSLKSRTVTSKDTSKNQFLLNLSVTDADTAVYYCARGPRDC	124				
Db	64	LEWVSSMSSSSYIYADSVKGRFTISRDNKNSLYLQWNSLRADTAVYYCARDLR-QL	122				
QY	125	TTICVGGWVDVNGDGLVTVSSASTKGPSPVFLPSSKTSSTGTAALGCLVKDYFPEPTV	184				
Db	123	TSYWY---FDLMGRGTLVTVSSASTKGPSPVFLPSSKTSSTGTAALGCLVKDYFPEPTV	179				
QY	185	VSNNSGALTSVHRTFPAVLQSSGLYSLSSVTVTPSSSSLGTTQYICNVNHNKPSNTKVKKKA	244				

Db 235 DKVESK---YGPCCPSCPAEFLLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVDSQEDP 291
Qy 301 EVKENWYVDGVEVHNNAKTPREEQVNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 292 EVQFNWYVDGVEVHNNAKTPREEQVNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSS 351
Qy 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
Db 352 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411
Qy 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVSNVMEALHNHYTQKSLSLSPGK 476
Db 412 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVSNVMEALHNHYTQKSLSLSPGK 467

RESULT 15
AAG63640
ID AAG63640 standard; Protein; 475 AA.
XX
AC AAG63640;
XX
DT 29-OCT-2001 (first entry)
XX
DE Amino acid sequence of a single chain antibody.
XX
KW Complementarity determining region; CDR; single chain antibody; ScFv;
KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW envelope glycoprotein.
XX
OS Homo sapiens.
XX
PN W0200158459-A1.
XX
PD 16-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-JF00967.
XX
PR 14-FEB-2000; 2000JP-0034906.
XX
PA (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
DR WPI; 2001-496986/54.
DR N-PSDB; AAH74680.
XX
PT Remedies for hepatitis C containing substances with antiviral effects
PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT compounds, by inhibiting binding of hepatitis C virus envelope
PT glycoprotein or CD81 -
XX
PS Disclosure; Page 105-108; 138pp; Japanese.
XX
CC The present sequence represents a single chain antibody of the invention.
CC The specification describes a substance can inhibit the binding between
CC hepatitis C virus (HCV) and cells with potential HCV infection, cells
CC with expression of CD81, or CD81. This substance is especially an
CC antibody with affinity towards HCV E2/NS1 protein, containing amino
CC acid sequences based on the complementarity determining region (CDR) 1,
CC CDR2 and CDR3 of the H and L chain variable regions. The antibody
CC inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor.
CC The antibodies and drugs are used for treatment and/or prevention of
CC hepatitis C, or for diagnosis of hepatitis C.
XX
SQ Sequence 475 AA;

Query Match 81.8%; Score 2107.5; DB 22; Length 475;
Best Local Similarity 84.3%; Pred. No. 1.6e-118;
Matches 402; Conservative 19; Mismatches 53; Indels 3; Gaps 3;

Qy 1 MKHLWFFLLVAAPRWLVLSQVQLQWGEGLQPSFELSRSCVVGSGISGYYYTWTWIRT 60
Db 1 MKHLWFFLLVAAPRWLVLSQVQLQWGEGLQPSFELSRSCVVGSGISGYYYTWTWIRT 60

Qy 61 PGRGLEWIGHIYCGNATTNYPNPSLKSRTVTSKDTSKNOFFLNLNSVTADTAVVYCARGP 120
Db 60 PGGLEWNGIIPLSGPPHYAQKFGVKYSITADESTAYLETLSTSETAVVYCARGV 119
Qy 121 RPDCTT-ICYGWDVWVGPDILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
Db 120 RGYCRRGSCY-DWLDPWGQGLVTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 178
Qy 180 PEPVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
Db 179 PEPVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 238
Qy 240 VDKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
Db 239 VDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 298
Qy 300 PEVKFNWYVDGVEVHNNAKTPREEQVNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
Db 299 PEVKFNWYVDGVEVHNNAKTPREEQVNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPA 358
Qy 360 PIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
Db 359 PIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 418
Qy 420 YKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVSNVMEALHNHYTQKSLSLSPGK 476
Db 419 YKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVSNVMEALHNHYTQKSLSLSPGK 475

Search completed: March 29, 2003, 09:10:16
Job time : 50.9575 secs